



Full wwPDB EM Validation Report ⓘ

Feb 24, 2025 – 04:49 PM JST

PDB ID : 8X4A
EMDB ID : EMD-38044
Title : Cryo-EM structure of Ryanodine receptor 1 (TM helix S0,100 nM Ca²⁺, closed state)
Authors : Chen, Q.; Hu, H.
Deposited on : 2023-11-15
Resolution : 3.80 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.2

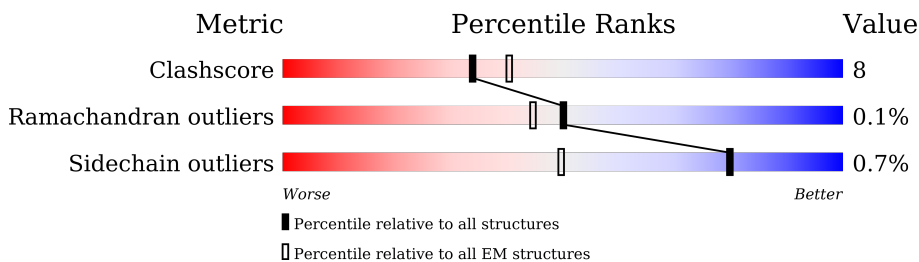
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	5037	<div> <div>7%</div> <div>65%</div> <div>14%</div> <div>21%</div> </div>
1	B	5037	<div> <div>7%</div> <div>65%</div> <div>13%</div> <div>21%</div> </div>
1	C	5037	<div> <div>7%</div> <div>65%</div> <div>14%</div> <div>21%</div> </div>
1	D	5037	<div> <div>7%</div> <div>65%</div> <div>14%</div> <div>21%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 118508 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3990	Total	C	N	O	S	0	0
			29626	18857	5143	5438	188		
1	B	3990	Total	C	N	O	S	0	0
			29626	18857	5143	5438	188		
1	C	3990	Total	C	N	O	S	0	0
			29626	18857	5143	5438	188		
1	D	3990	Total	C	N	O	S	0	0
			29626	18857	5143	5438	188		

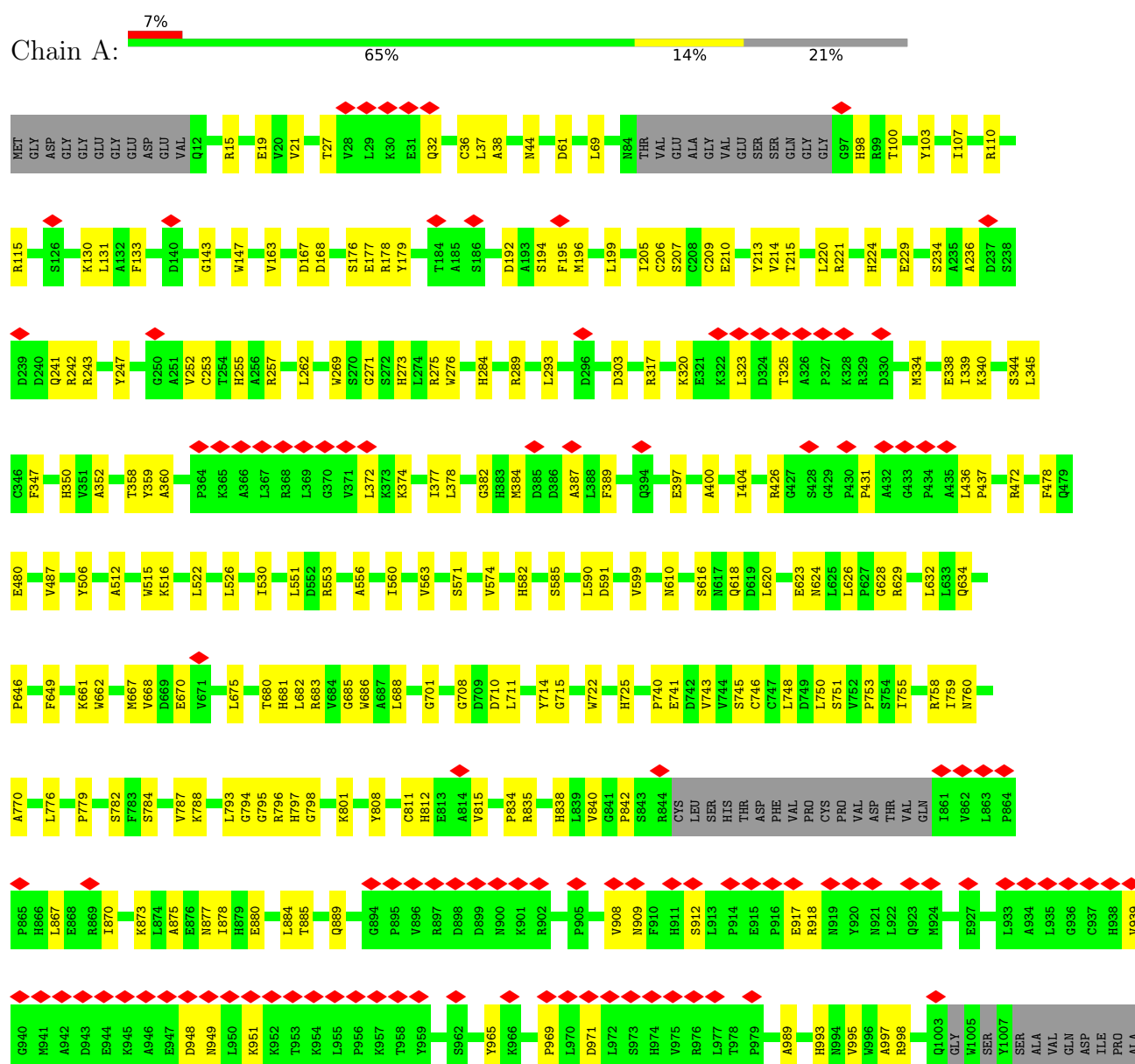
- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	Ca	0
			1	1	
2	B	1	Total	Ca	0
			1	1	
2	C	1	Total	Ca	0
			1	1	
2	D	1	Total	Ca	0
			1	1	

3 Residue-property plots

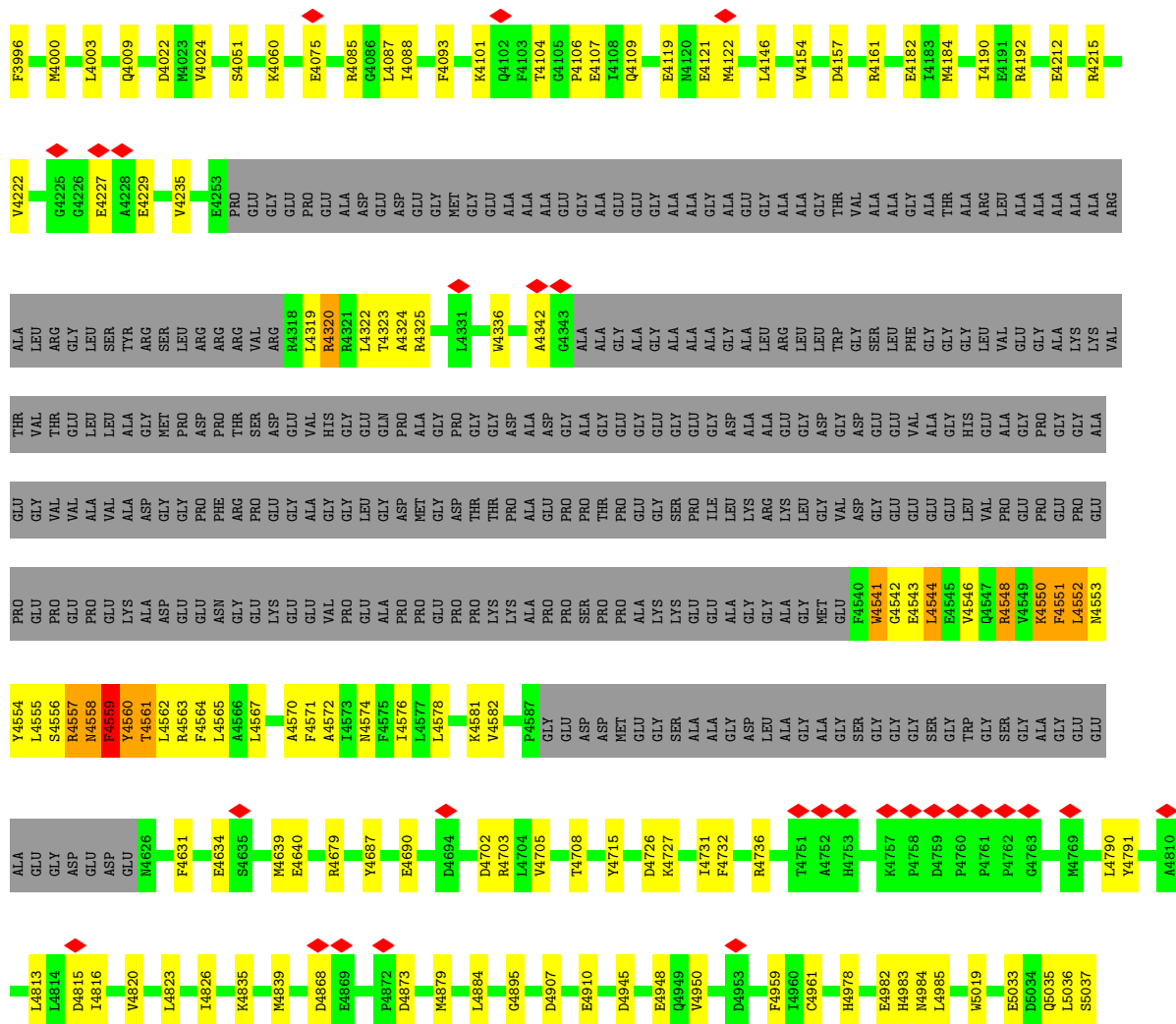
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Ryanodine receptor 1

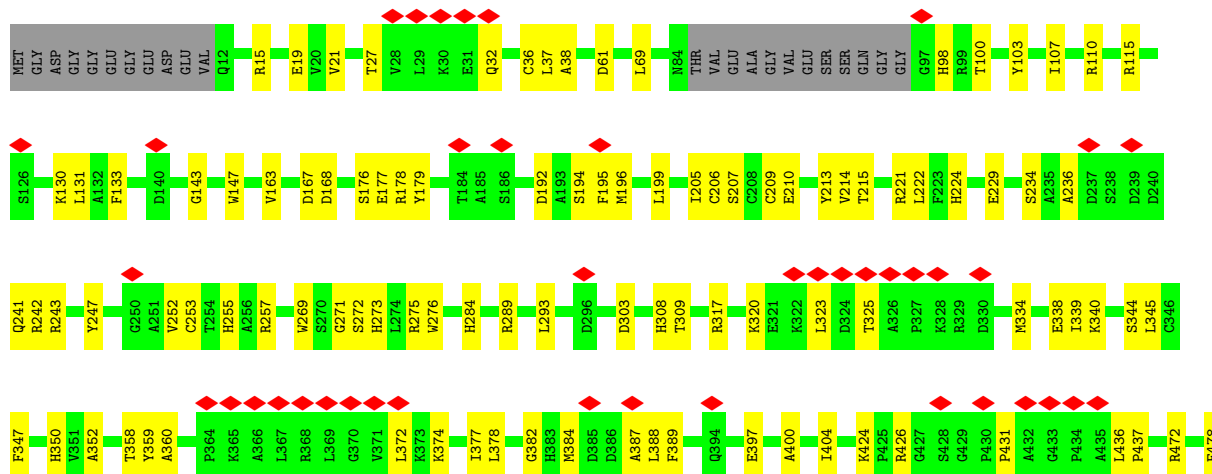


I2422	M2423	L2432	R2435	P2438	E2439	H2441	L2442	L2443	R2454	A2455	L2456	L2457	S2459	D2465	T2476	P2477	T2478	L2479	GLY	LYS	ASP	GLY	ALA	LEU	VAL	Q2487	P2488	K2489	A2492	V2495	P2496	D2497	H2498	F2505	R2508	I2512	Q2515	L2518	T2538	A2539	L2556							
K2316	G2317	Y2318	N2324	L2332	R2336	V2339	F2340	V2341	N2342	S2345	V2346	E2347	A2350	L2356	R2359	L2376	L2377	A2378	G2379	G2373	L2376	L2377	A2378	R2392	D2393	G2394	P2395	GLY	VAL	ARG	ASP	ARG	ARG	ARG	GLY	HIS	PHE	GLY	GLU	PRO	PRO	N2414	H2417	L2418				
PRO	GLU	GLU	LEU	PRO	ALA	GLU	K2089	K2090	V2103	Q2107	Y2110	F2121	L2131	L2138	P2139	Y2142	E2174	F2191	L2197	M2198	M2203	G2217	G2218	E2219	T2220	K2221	S2243	N2246	Y2256	N2260	I2263	T2281	V2299	C2310	L2314	A2315												
F1984	T1985	M1986	S1987	A1988	A1989	E1997	P2001	P2002	E2004	Q2005	L2009	F2012	D2017	C2021	P2022	L2023	L2039	E2047	G2048	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU						
Y1711	Y1712	D1713	L1714	L1715	S1716	S1717	I1718	H1719	L1720	E1721	M1730	I1735	F1748	P1749	P1750	G1751	R1752	K1753	G1754	G1755	N1756	A1757	V1765	G1766	R1772	H1775	F1782	V1783	A1784	A1785	L1786	P1787	A1788	ALA	GLY	VAL	ALA	E1793	A1794	P1795	A1796	R1797	L1798	L1844	M1851	I1866	E1869	
GLU	LEU	GLY	LYS	GLN	LYS	ASN	ILE	M1573	L1574	L1575	S1576	P1587	Q1590	R1594	L1600	V1615	GLU	THR	ARG	ARG	ALA	GLY	E1622	Q1629	P1633	E1644	N1645	R1646	C1647	M1648	L1657	D1658	L1659	L1667	R1671	A1672	V1673	M1679	H1688	L1694	P1704	L1707						
H1458	S1457	T1475	M1476	E1479	V1483	C1489	S1490	N1491	C1492	Y1493	M1494	V1495	W1496	D1499	Q1505	Q1506	G1507	R1508	I1516	D1521	L1522	A1523	T1524	G1525	L1526	M1527	T1528	F1529	T1530	A1531	K1534	E1535	S1536	M1537	T1538	F1539	F1540	E1543	P1544	N1545	T1546	K1547	L1548	P1556	Q1563	F1564		
PHE	LEU	PHE	LYS	ALA	LYS	LYS	ALA	ALA	MET	THR	GLN	PRO	PRO	ALA	THR	PRO	ARG	LEU	PRO	ALA	ASP	ASP	PRO	PRO	GLY	ILE	ILE	LEU	ASN	T1430	T1431	Y1434	Y1435	S1436	V1437	P1445	S1446	C1447	V1448	W1449	V1450	G1451	V1452	T1453	T1454			
ASP	PRO	TRP	GLU	ASN	LEU	ARG	ARG	SER	ALA	GLY	TRP	GLY	ALA	GLY	GLY	GLY	THR	THR	GLY	THR	GLN	GLN	GLY	VAL	ALA	ALA	ALA	GLN	PRO	LEU	ALA	ARG	ALA	GLY	ASN	LYS	ASP	ALA	ALA	THR	THR	GLU	LYS	ASN	LYS	ARG	GLU	PRO
ARG	ARG	ASN	R1020	L1021	V1022	F1023	Y1024	L1027	D1028	E1029	A1030	R1033	R1036	D1037	S1038	L1039	C1040	Q1041	A1042	V1043	R1044	T1045	L1046	L1047	Y1051	N1052	I1053	E1054	PRO	PRO	ASP	GLN	GLU	PRO	SER	GLN	SER	ARG	TRP	D1070	R1073	R1076	A1077	K1078	S1080	S1085		





• Molecule 1: Ryanodine receptor 1

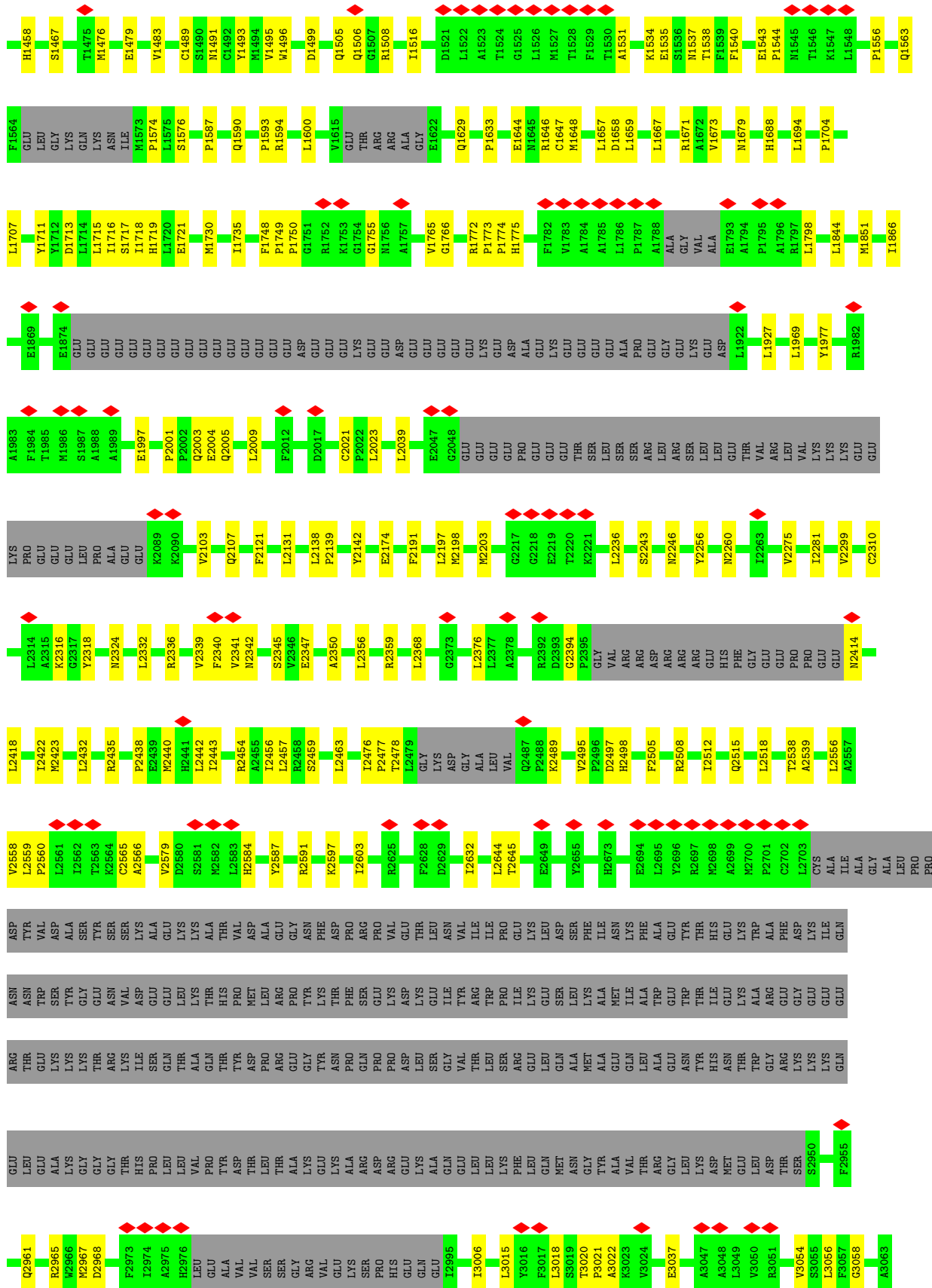




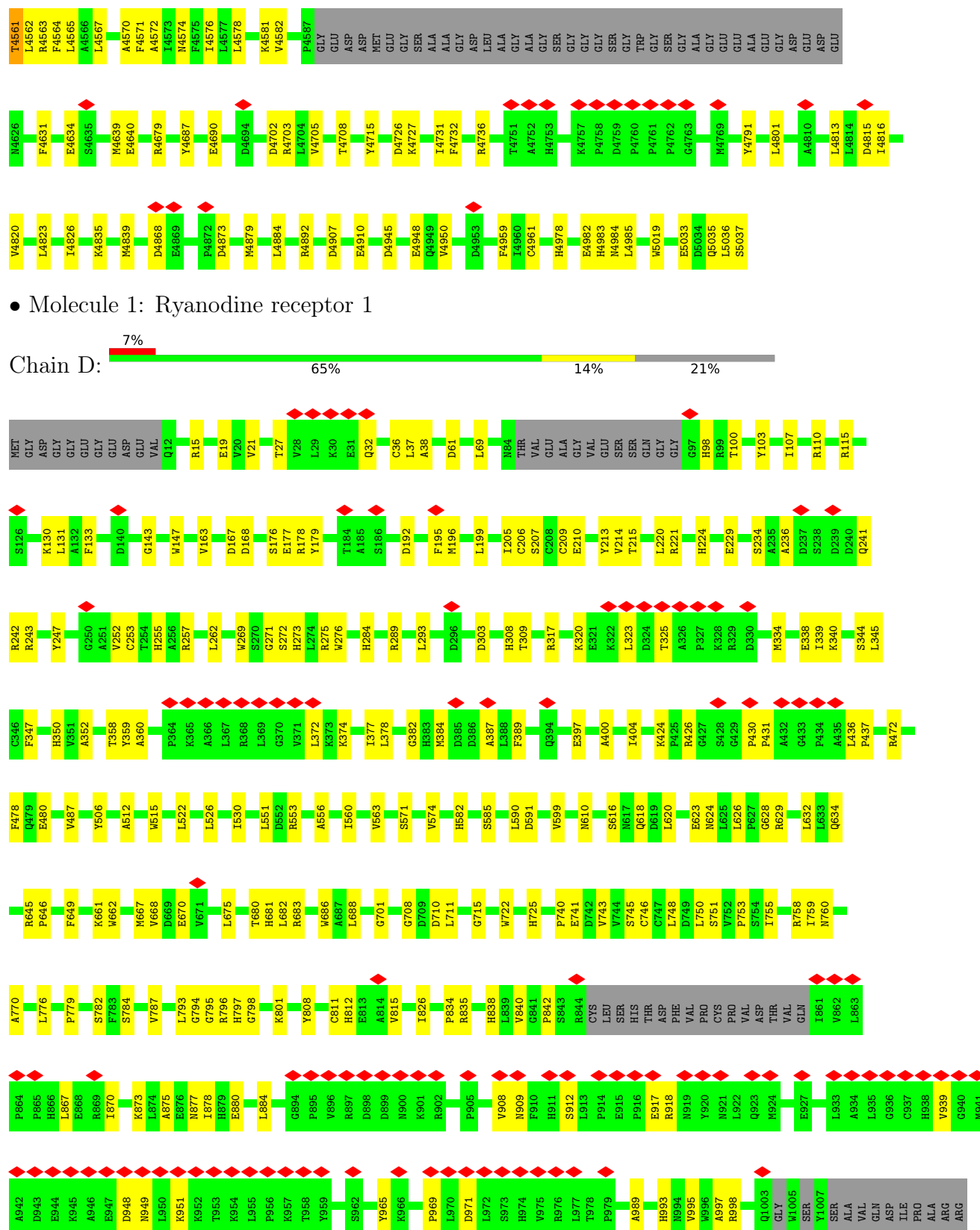
















[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	78641	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	1.566	Depositor
Minimum map value	-0.990	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.054	Depositor
Recommended contour level	0.254	Depositor
Map size (Å)	523.2, 523.2, 523.2	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.26	0/30247	0.43	0/41162
1	B	0.26	0/30247	0.43	0/41162
1	C	0.26	0/30247	0.43	0/41162
1	D	0.26	0/30247	0.43	0/41162
All	All	0.26	0/120988	0.43	0/164648

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	29626	0	27824	476	0
1	B	29626	0	27824	470	0
1	C	29626	0	27824	473	0
1	D	29626	0	27824	475	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
All	All	118508	0	111296	1844	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (1844) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4325:ARG:CD	1:B:4634:GLU:OE1	2.04	1.06
1:A:4325:ARG:CD	1:A:4634:GLU:OE1	2.04	1.06
1:C:4325:ARG:CD	1:C:4634:GLU:OE1	2.04	1.06
1:B:4325:ARG:HD2	1:B:4634:GLU:OE1	1.56	1.05
1:C:4325:ARG:HD3	1:C:4634:GLU:CD	1.77	1.05
1:D:4325:ARG:CD	1:D:4634:GLU:OE1	2.04	1.05
1:A:4325:ARG:HD3	1:A:4634:GLU:CD	1.77	1.05
1:B:4325:ARG:HD3	1:B:4634:GLU:CD	1.77	1.04
1:C:4325:ARG:HD2	1:C:4634:GLU:OE1	1.56	1.04
1:D:4325:ARG:HD3	1:D:4634:GLU:CD	1.77	1.04
1:A:4325:ARG:HD2	1:A:4634:GLU:OE1	1.56	1.03
1:B:4325:ARG:CD	1:B:4634:GLU:OE2	2.08	1.01
1:C:4325:ARG:CD	1:C:4634:GLU:CD	2.29	1.01
1:D:4325:ARG:HD2	1:D:4634:GLU:OE1	1.56	1.01
1:C:4325:ARG:CD	1:C:4634:GLU:OE2	2.08	1.01
1:A:4325:ARG:CD	1:A:4634:GLU:CD	2.29	1.01
1:B:4325:ARG:CD	1:B:4634:GLU:CD	2.29	1.01
1:A:4325:ARG:CD	1:A:4634:GLU:OE2	2.08	1.00
1:D:4325:ARG:CD	1:D:4634:GLU:OE2	2.08	1.00
1:D:4325:ARG:CD	1:D:4634:GLU:CD	2.29	1.00
1:B:4325:ARG:HD3	1:B:4634:GLU:OE2	1.67	0.94
1:D:4325:ARG:HD3	1:D:4634:GLU:OE2	1.67	0.93
1:C:4325:ARG:HD3	1:C:4634:GLU:OE2	1.67	0.93
1:B:4559:PHE:C	1:B:4561:THR:H	1.72	0.93
1:D:4559:PHE:C	1:D:4561:THR:H	1.72	0.93
1:A:4325:ARG:HD3	1:A:4634:GLU:OE2	1.67	0.92
1:C:4559:PHE:C	1:C:4561:THR:H	1.72	0.91
1:A:4559:PHE:C	1:A:4561:THR:H	1.72	0.90
1:A:4559:PHE:O	1:A:4561:THR:HG22	1.73	0.88
1:B:4559:PHE:O	1:B:4561:THR:HG22	1.73	0.88
1:C:4559:PHE:O	1:C:4561:THR:HG22	1.73	0.88
1:D:4559:PHE:O	1:D:4561:THR:HG22	1.73	0.87
1:B:4325:ARG:CB	1:B:4634:GLU:OE2	2.24	0.85
1:C:4325:ARG:CB	1:C:4634:GLU:OE2	2.24	0.85
1:A:4325:ARG:CB	1:A:4634:GLU:OE2	2.24	0.84
1:A:2318:TYR:HH	1:A:2414:ASN:N	1.76	0.84
1:D:4325:ARG:CB	1:D:4634:GLU:OE2	2.24	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4325:ARG:NH1	1:B:4634:GLU:OE1	2.11	0.83
1:D:2318:TYR:HH	1:D:2414:ASN:N	1.76	0.83
1:C:2318:TYR:HH	1:C:2414:ASN:N	1.77	0.83
1:D:4325:ARG:NH1	1:D:4634:GLU:OE1	2.11	0.83
1:B:2318:TYR:HH	1:B:2414:ASN:N	1.77	0.83
1:C:4325:ARG:NH1	1:C:4634:GLU:OE1	2.11	0.82
1:B:4550:LYS:O	1:B:4553:ASN:HB2	1.81	0.81
1:A:4325:ARG:NH1	1:A:4634:GLU:OE1	2.11	0.81
1:C:3535:LEU:HD12	1:C:3537:LYS:H	1.47	0.80
1:C:4550:LYS:O	1:C:4553:ASN:HB2	1.81	0.80
1:D:4550:LYS:O	1:D:4553:ASN:HB2	1.81	0.80
1:A:4342:ALA:O	1:A:4820:VAL:HG23	1.82	0.79
1:C:4342:ALA:O	1:C:4820:VAL:HG23	1.82	0.79
1:B:3535:LEU:HD12	1:B:3537:LYS:H	1.47	0.79
1:A:4336:TRP:HE3	1:A:4571:PHE:HE2	1.31	0.79
1:A:4550:LYS:O	1:A:4553:ASN:HB2	1.81	0.79
1:B:686:TRP:HE1	1:B:746:CYS:HG	1.28	0.79
1:D:3535:LEU:HD12	1:D:3537:LYS:H	1.47	0.79
1:B:4336:TRP:HE3	1:B:4571:PHE:HE2	1.31	0.79
1:B:4342:ALA:O	1:B:4820:VAL:HG23	1.82	0.78
1:A:4325:ARG:HD2	1:A:4634:GLU:CD	2.00	0.78
1:C:4336:TRP:HE3	1:C:4571:PHE:HE2	1.31	0.78
1:D:4325:ARG:HB2	1:D:4634:GLU:OE2	1.84	0.78
1:D:4336:TRP:HE3	1:D:4571:PHE:HE2	1.31	0.78
1:D:4342:ALA:O	1:D:4820:VAL:HG23	1.82	0.78
1:D:4336:TRP:HE3	1:D:4571:PHE:CE2	2.02	0.78
1:B:4325:ARG:HB2	1:B:4634:GLU:OE2	1.84	0.78
1:A:3535:LEU:HD12	1:A:3537:LYS:H	1.47	0.78
1:A:4336:TRP:HE3	1:A:4571:PHE:CE2	2.02	0.78
1:C:4325:ARG:HB2	1:C:4634:GLU:OE2	1.84	0.77
1:C:4336:TRP:HE3	1:C:4571:PHE:CE2	2.02	0.77
1:B:4336:TRP:HE3	1:B:4571:PHE:CE2	2.02	0.77
1:A:686:TRP:HE1	1:A:746:CYS:HG	1.30	0.77
1:D:4325:ARG:HD2	1:D:4634:GLU:CD	2.00	0.77
1:A:4325:ARG:HB2	1:A:4634:GLU:OE2	1.84	0.77
1:C:686:TRP:HE1	1:C:746:CYS:HG	1.30	0.76
1:C:794:GLY:H	1:C:798:GLY:HA3	1.51	0.76
1:B:794:GLY:H	1:B:798:GLY:HA3	1.51	0.76
1:A:794:GLY:H	1:A:798:GLY:HA3	1.51	0.76
1:D:794:GLY:H	1:D:798:GLY:HA3	1.51	0.76
1:B:4325:ARG:HD2	1:B:4634:GLU:CD	2.00	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:686:TRP:HE1	1:D:746:CYS:HG	1.32	0.74
1:C:4541:TRP:HA	1:C:4544:LEU:HD22	1.69	0.74
1:D:1152:MET:HB2	1:D:1161:ILE:HB	1.70	0.74
1:B:4541:TRP:HA	1:B:4544:LEU:HD22	1.69	0.74
1:C:1152:MET:HB2	1:C:1161:ILE:HB	1.70	0.74
1:C:4325:ARG:HD2	1:C:4634:GLU:CD	2.00	0.74
1:B:1152:MET:HB2	1:B:1161:ILE:HB	1.70	0.73
1:B:4961:CYS:SG	1:B:4983:HIS:NE2	2.61	0.73
1:A:4559:PHE:C	1:A:4561:THR:N	2.41	0.73
1:A:1152:MET:HB2	1:A:1161:ILE:HB	1.70	0.73
1:A:4961:CYS:SG	1:A:4983:HIS:NE2	2.61	0.73
1:C:4559:PHE:C	1:C:4561:THR:N	2.41	0.73
1:D:4961:CYS:SG	1:D:4983:HIS:NE2	2.61	0.73
1:B:3535:LEU:HD11	1:B:3538:THR:HG23	1.70	0.73
1:C:3535:LEU:HD11	1:C:3538:THR:HG23	1.70	0.73
1:D:4559:PHE:C	1:D:4561:THR:N	2.41	0.73
1:C:4961:CYS:SG	1:C:4983:HIS:NE2	2.61	0.72
1:D:4541:TRP:HA	1:D:4544:LEU:HD22	1.69	0.72
1:A:1434:TYR:HA	1:A:1449:TRP:HB3	1.71	0.72
1:A:4541:TRP:HA	1:A:4544:LEU:HD22	1.69	0.72
1:D:1434:TYR:HA	1:D:1449:TRP:HB3	1.71	0.72
1:D:3535:LEU:HD11	1:D:3538:THR:HG23	1.70	0.72
1:B:4559:PHE:C	1:B:4561:THR:N	2.41	0.72
1:C:1434:TYR:HA	1:C:1449:TRP:HB3	1.71	0.72
1:B:1434:TYR:HA	1:B:1449:TRP:HB3	1.71	0.71
1:D:2442:LEU:HG	1:D:2443:ILE:HG23	1.72	0.71
1:A:3535:LEU:HD11	1:A:3538:THR:HG23	1.70	0.71
1:C:3767:GLN:OE1	1:C:3809:ASN:ND2	2.22	0.71
1:D:3767:GLN:OE1	1:D:3809:ASN:ND2	2.22	0.71
1:B:2442:LEU:HG	1:B:2443:ILE:HG23	1.72	0.71
1:A:3767:GLN:OE1	1:A:3809:ASN:ND2	2.22	0.71
1:B:3767:GLN:OE1	1:B:3809:ASN:ND2	2.22	0.70
1:C:2442:LEU:HG	1:C:2443:ILE:HG23	1.72	0.70
1:C:2339:VAL:HB	1:C:2345:SER:HB2	1.74	0.70
1:D:2339:VAL:HB	1:D:2345:SER:HB2	1.74	0.70
1:A:2442:LEU:HG	1:A:2443:ILE:HG23	1.72	0.70
1:B:3897:ASN:O	1:B:3897:ASN:ND2	2.23	0.70
1:B:4559:PHE:O	1:B:4561:THR:N	2.25	0.70
1:B:2339:VAL:HB	1:B:2345:SER:HB2	1.74	0.69
1:C:4336:TRP:CE3	1:C:4571:PHE:CE2	2.81	0.69
1:A:4559:PHE:O	1:A:4561:THR:N	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4559:PHE:O	1:D:4561:THR:N	2.25	0.69
1:C:4559:PHE:O	1:C:4561:THR:N	2.25	0.69
1:D:4336:TRP:CE3	1:D:4571:PHE:CE2	2.81	0.69
1:A:667:MET:HB3	1:A:743:VAL:HG12	1.75	0.68
1:A:2339:VAL:HB	1:A:2345:SER:HB2	1.74	0.68
1:D:667:MET:HB3	1:D:743:VAL:HG12	1.75	0.68
1:A:4736:ARG:NH2	1:D:4075:GLU:OE2	2.27	0.68
1:A:36:CYS:SG	1:A:37:LEU:N	2.67	0.68
1:B:36:CYS:SG	1:B:37:LEU:N	2.67	0.68
1:B:4336:TRP:CE3	1:B:4571:PHE:CE2	2.81	0.68
1:A:4336:TRP:CE3	1:A:4571:PHE:CE2	2.81	0.68
1:B:4075:GLU:OE2	1:C:4736:ARG:NH2	2.27	0.68
1:D:36:CYS:SG	1:D:37:LEU:N	2.67	0.68
1:C:4075:GLU:OE2	1:D:4736:ARG:NH2	2.27	0.67
1:B:667:MET:HB3	1:B:743:VAL:HG12	1.75	0.67
1:C:3897:ASN:O	1:C:3897:ASN:ND2	2.23	0.67
1:A:618:GLN:NE2	1:A:1673:VAL:O	2.27	0.67
1:A:4075:GLU:OE2	1:B:4736:ARG:NH2	2.27	0.67
1:C:36:CYS:SG	1:C:37:LEU:N	2.67	0.67
1:C:667:MET:HB3	1:C:743:VAL:HG12	1.75	0.67
1:B:2644:LEU:HG	1:B:2645:THR:HG23	1.77	0.67
1:D:2644:LEU:HG	1:D:2645:THR:HG23	1.77	0.67
1:C:618:GLN:NE2	1:C:1673:VAL:O	2.27	0.66
1:C:2644:LEU:HG	1:C:2645:THR:HG23	1.77	0.66
1:D:3897:ASN:O	1:D:3897:ASN:ND2	2.23	0.66
1:A:359:TYR:HD2	1:A:374:LYS:HZ1	1.42	0.66
1:B:618:GLN:NE2	1:B:1673:VAL:O	2.27	0.66
1:C:209:CYS:SG	1:C:210:GLU:N	2.69	0.66
1:C:1493:TYR:HB3	1:C:1540:PHE:H	1.60	0.66
1:A:989:ALA:HB3	1:A:1036:ARG:HH22	1.60	0.66
1:C:811:CYS:HB3	1:C:815:VAL:HG21	1.78	0.66
1:C:989:ALA:HB3	1:C:1036:ARG:HH22	1.60	0.66
1:A:2644:LEU:HG	1:A:2645:THR:HG23	1.77	0.66
1:D:618:GLN:NE2	1:D:1673:VAL:O	2.27	0.66
1:D:811:CYS:HB3	1:D:815:VAL:HG21	1.78	0.66
1:B:209:CYS:SG	1:B:210:GLU:N	2.69	0.66
1:A:1647:CYS:SG	1:A:1648:MET:N	2.69	0.66
1:B:2131:LEU:HB3	1:B:3662:ILE:HG21	1.78	0.66
1:D:359:TYR:HD2	1:D:374:LYS:HZ1	1.42	0.66
1:D:2131:LEU:HB3	1:D:3662:ILE:HG21	1.78	0.66
1:A:2131:LEU:HB3	1:A:3662:ILE:HG21	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:989:ALA:HB3	1:D:1036:ARG:HH22	1.60	0.65
1:A:209:CYS:SG	1:A:210:GLU:N	2.69	0.65
1:A:3897:ASN:O	1:A:3897:ASN:ND2	2.23	0.65
1:B:989:ALA:HB3	1:B:1036:ARG:HH22	1.60	0.65
1:B:1647:CYS:SG	1:B:1648:MET:N	2.69	0.65
1:D:1647:CYS:SG	1:D:1648:MET:N	2.69	0.65
1:D:1493:TYR:HB3	1:D:1540:PHE:H	1.60	0.65
1:A:811:CYS:HB3	1:A:815:VAL:HG21	1.78	0.65
1:A:1162:PHE:H	1:A:1177:THR:HG21	1.62	0.65
1:B:1493:TYR:HB3	1:B:1540:PHE:H	1.60	0.65
1:D:209:CYS:SG	1:D:210:GLU:N	2.69	0.65
1:B:359:TYR:HD2	1:B:374:LYS:HZ1	1.45	0.65
1:C:359:TYR:HD2	1:C:374:LYS:HZ1	1.45	0.65
1:C:1647:CYS:SG	1:C:1648:MET:N	2.69	0.65
1:D:2368:LEU:HD13	1:D:2376:LEU:HD12	1.79	0.65
1:B:1162:PHE:H	1:B:1177:THR:HG21	1.62	0.64
1:D:213:TYR:HB3	1:D:273:HIS:HE1	1.62	0.64
1:B:1272:LEU:HD21	1:B:1287:LEU:HD21	1.79	0.64
1:B:3657:TYR:HB3	1:B:3661:TRP:NE1	2.12	0.64
1:D:3657:TYR:HB3	1:D:3661:TRP:NE1	2.12	0.64
1:B:551:LEU:HB3	1:B:553:ARG:HH11	1.61	0.64
1:D:1162:PHE:H	1:D:1177:THR:HG21	1.62	0.64
1:B:811:CYS:HB3	1:B:815:VAL:HG21	1.78	0.64
1:D:793:LEU:HG	1:D:795:GLY:H	1.63	0.64
1:A:1493:TYR:HB3	1:A:1540:PHE:H	1.60	0.64
1:C:551:LEU:HB3	1:C:553:ARG:HH11	1.61	0.64
1:C:2131:LEU:HB3	1:C:3662:ILE:HG21	1.78	0.64
1:C:2368:LEU:HD13	1:C:2376:LEU:HD12	1.79	0.64
1:C:3657:TYR:HB3	1:C:3661:TRP:NE1	2.12	0.64
1:A:1272:LEU:HD21	1:A:1287:LEU:HD21	1.79	0.64
1:A:213:TYR:HB3	1:A:273:HIS:HE1	1.62	0.64
1:C:69:LEU:HD22	1:C:107:ILE:HD11	1.80	0.64
1:A:2368:LEU:HD13	1:A:2376:LEU:HD12	1.79	0.64
1:D:551:LEU:HB3	1:D:553:ARG:HH11	1.61	0.64
1:B:2459:SER:HB2	1:C:131:LEU:HG	1.80	0.64
1:C:1162:PHE:H	1:C:1177:THR:HG21	1.62	0.64
1:C:1272:LEU:HD21	1:C:1287:LEU:HD21	1.79	0.64
1:C:2459:SER:HB2	1:D:131:LEU:HG	1.80	0.64
1:D:69:LEU:HD22	1:D:107:ILE:HD11	1.80	0.64
1:B:213:TYR:HB3	1:B:273:HIS:HE1	1.62	0.64
1:A:551:LEU:HB3	1:A:553:ARG:HH11	1.61	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2459:SER:HB2	1:B:131:LEU:HG	1.80	0.63
1:A:131:LEU:HG	1:D:2459:SER:HB2	1.80	0.63
1:A:3657:TYR:HB3	1:A:3661:TRP:NE1	2.12	0.63
1:B:69:LEU:HD22	1:B:107:ILE:HD11	1.80	0.63
1:A:793:LEU:HG	1:A:795:GLY:H	1.63	0.63
1:B:793:LEU:HG	1:B:795:GLY:H	1.63	0.63
1:C:1437:VAL:HA	1:C:1556:PRO:HA	1.81	0.63
1:D:1730:MET:O	1:D:1772:ARG:NH1	2.29	0.63
1:B:1437:VAL:HA	1:B:1556:PRO:HA	1.81	0.63
1:C:793:LEU:HG	1:C:795:GLY:H	1.63	0.63
1:A:1730:MET:O	1:A:1772:ARG:NH1	2.29	0.63
1:C:213:TYR:HB3	1:C:273:HIS:HE1	1.62	0.63
1:A:69:LEU:HD22	1:A:107:ILE:HD11	1.80	0.63
1:B:2368:LEU:HD13	1:B:2376:LEU:HD12	1.79	0.63
1:D:1272:LEU:HD21	1:D:1287:LEU:HD21	1.79	0.62
1:B:210:GLU:OE2	1:B:273:HIS:ND1	2.32	0.62
1:A:4184:MET:HB2	1:A:4190:ILE:HD13	1.81	0.62
1:C:835:ARG:HH12	1:C:1212:ARG:HH11	1.46	0.62
1:C:210:GLU:OE2	1:C:273:HIS:ND1	2.32	0.62
1:C:4104:THR:OG1	1:C:4107:GLU:OE1	2.18	0.62
1:D:210:GLU:OE2	1:D:273:HIS:ND1	2.32	0.62
1:A:835:ARG:HH12	1:A:1212:ARG:HH11	1.46	0.62
1:B:241:GLN:HB3	1:B:243:ARG:HG2	1.81	0.62
1:B:686:TRP:NE1	1:B:746:CYS:SG	2.70	0.62
1:D:4184:MET:HB2	1:D:4190:ILE:HD13	1.81	0.62
1:C:623:GLU:OE2	1:C:624:ASN:ND2	2.33	0.61
1:C:4570:ALA:O	1:C:4574:ASN:ND2	2.33	0.61
1:D:1496:TRP:O	1:D:1537:ASN:ND2	2.34	0.61
1:A:210:GLU:OE2	1:A:273:HIS:ND1	2.32	0.61
1:C:1496:TRP:O	1:C:1537:ASN:ND2	2.34	0.61
1:A:1496:TRP:O	1:A:1537:ASN:ND2	2.34	0.61
1:D:1437:VAL:HA	1:D:1556:PRO:HA	1.81	0.61
1:B:236:ALA:HA	1:B:242:ARG:HD2	1.83	0.61
1:B:1496:TRP:O	1:B:1537:ASN:ND2	2.34	0.61
1:B:4570:ALA:O	1:B:4574:ASN:ND2	2.33	0.61
1:C:236:ALA:HA	1:C:242:ARG:HD2	1.83	0.61
1:C:4325:ARG:HD3	1:C:4634:GLU:OE1	1.87	0.61
1:A:623:GLU:OE2	1:A:624:ASN:ND2	2.33	0.61
1:B:4104:THR:OG1	1:B:4107:GLU:OE1	2.18	0.61
1:D:835:ARG:HH12	1:D:1212:ARG:HH11	1.46	0.61
1:D:4570:ALA:O	1:D:4574:ASN:ND2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:629:ARG:HH12	1:B:1688:HIS:HA	1.66	0.61
1:B:4184:MET:HB2	1:B:4190:ILE:HD13	1.81	0.61
1:C:241:GLN:HB3	1:C:243:ARG:HG2	1.81	0.61
1:D:1505:GLN:OE1	1:D:1508:ARG:NH2	2.34	0.61
1:A:241:GLN:HB3	1:A:243:ARG:HG2	1.81	0.61
1:A:4104:THR:OG1	1:A:4107:GLU:OE1	2.18	0.61
1:A:4570:ALA:O	1:A:4574:ASN:ND2	2.33	0.61
1:C:4184:MET:HB2	1:C:4190:ILE:HD13	1.81	0.61
1:D:241:GLN:HB3	1:D:243:ARG:HG2	1.81	0.61
1:A:1437:VAL:HA	1:A:1556:PRO:HA	1.81	0.61
1:B:623:GLU:OE2	1:B:624:ASN:ND2	2.33	0.60
1:A:629:ARG:HH12	1:A:1688:HIS:HA	1.66	0.60
1:A:743:VAL:N	1:A:760:ASN:OD1	2.32	0.60
1:A:2310:CYS:HB2	1:A:2324:ASN:HB3	1.83	0.60
1:B:1505:GLN:OE1	1:B:1508:ARG:NH2	2.34	0.60
1:D:3556:ASN:OD1	1:D:3557:LEU:N	2.35	0.60
1:D:623:GLU:OE2	1:D:624:ASN:ND2	2.33	0.60
1:A:1735:ILE:HG22	1:A:2142:TYR:HB3	1.83	0.60
1:B:2310:CYS:HB2	1:B:2324:ASN:HB3	1.83	0.60
1:C:1505:GLN:OE1	1:C:1508:ARG:NH2	2.34	0.60
1:B:835:ARG:HH12	1:B:1212:ARG:HH11	1.46	0.60
1:B:3556:ASN:OD1	1:B:3557:LEU:N	2.35	0.60
1:D:629:ARG:HH12	1:D:1688:HIS:HA	1.66	0.60
1:D:2256:TYR:O	1:D:2260:ASN:ND2	2.34	0.60
1:A:1505:GLN:OE1	1:A:1508:ARG:NH2	2.34	0.60
1:B:743:VAL:N	1:B:760:ASN:OD1	2.32	0.60
1:B:4561:THR:O	1:B:4562:LEU:C	2.40	0.60
1:C:629:ARG:HH12	1:C:1688:HIS:HA	1.66	0.60
1:C:3556:ASN:OD1	1:C:3557:LEU:N	2.35	0.60
1:C:2256:TYR:O	1:C:2260:ASN:ND2	2.34	0.60
1:D:4104:THR:OG1	1:D:4107:GLU:OE1	2.18	0.60
1:A:236:ALA:HA	1:A:242:ARG:HD2	1.83	0.60
1:A:3556:ASN:OD1	1:A:3557:LEU:N	2.35	0.60
1:B:1730:MET:O	1:B:1772:ARG:NH1	2.29	0.60
1:B:4983:HIS:ND1	1:B:4983:HIS:O	2.35	0.60
1:C:686:TRP:NE1	1:C:746:CYS:SG	2.70	0.60
1:C:1735:ILE:HG22	1:C:2142:TYR:HB3	1.83	0.60
1:D:236:ALA:HA	1:D:242:ARG:HD2	1.83	0.60
1:D:1735:ILE:HG22	1:D:2142:TYR:HB3	1.83	0.60
1:B:989:ALA:O	1:B:993:HIS:ND1	2.31	0.60
1:C:2299:VAL:HG11	1:C:2356:LEU:HD13	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:743:VAL:N	1:D:760:ASN:OD1	2.32	0.60
1:A:2299:VAL:HG11	1:A:2356:LEU:HD13	1.84	0.59
1:A:4983:HIS:ND1	1:A:4983:HIS:O	2.35	0.59
1:B:4325:ARG:HD3	1:B:4634:GLU:OE1	1.87	0.59
1:C:3549:VAL:HG13	1:C:3553:LEU:HD23	1.84	0.59
1:C:4983:HIS:ND1	1:C:4983:HIS:O	2.35	0.59
1:C:2310:CYS:HB2	1:C:2324:ASN:HB3	1.83	0.59
1:A:2256:TYR:O	1:A:2260:ASN:ND2	2.34	0.59
1:C:743:VAL:N	1:C:760:ASN:OD1	2.32	0.59
1:B:4336:TRP:CE3	1:B:4571:PHE:HE2	2.18	0.59
1:B:4978:HIS:ND1	1:B:4982:GLU:OE1	2.35	0.59
1:C:1730:MET:O	1:C:1772:ARG:NH1	2.29	0.59
1:D:4978:HIS:ND1	1:D:4982:GLU:OE1	2.35	0.59
1:A:3549:VAL:HG13	1:A:3553:LEU:HD23	1.84	0.59
1:B:1735:ILE:HG22	1:B:2142:TYR:HB3	1.83	0.59
1:B:2256:TYR:O	1:B:2260:ASN:ND2	2.34	0.59
1:D:3549:VAL:HG13	1:D:3553:LEU:HD23	1.84	0.59
1:A:4561:THR:O	1:A:4562:LEU:C	2.40	0.59
1:C:4978:HIS:ND1	1:C:4982:GLU:OE1	2.35	0.59
1:D:2310:CYS:HB2	1:D:2324:ASN:HB3	1.83	0.59
1:D:4983:HIS:ND1	1:D:4983:HIS:O	2.35	0.59
1:A:686:TRP:NE1	1:A:746:CYS:SG	2.70	0.59
1:B:3549:VAL:HG13	1:B:3553:LEU:HD23	1.84	0.59
1:C:2243:SER:OG	1:C:2246:ASN:ND2	2.36	0.59
1:D:3322:ILE:O	1:D:3326:ASN:ND2	2.36	0.59
1:A:4978:HIS:ND1	1:A:4982:GLU:OE1	2.35	0.58
1:B:2299:VAL:HG11	1:B:2356:LEU:HD13	1.84	0.58
1:D:436:LEU:HD12	1:D:437:PRO:HD2	1.85	0.58
1:B:1748:PHE:O	1:B:1750:PRO:HD3	2.04	0.58
1:C:436:LEU:HD12	1:C:437:PRO:HD2	1.85	0.58
1:D:2299:VAL:HG11	1:D:2356:LEU:HD13	1.84	0.58
1:D:4325:ARG:CG	1:D:4634:GLU:OE2	2.51	0.58
1:B:3889:GLN:HG3	1:B:3967:GLU:HG3	1.85	0.58
1:C:2281:ILE:HG23	1:C:2341:VAL:HG21	1.85	0.58
1:B:4325:ARG:CG	1:B:4634:GLU:OE2	2.51	0.58
1:C:1748:PHE:O	1:C:1750:PRO:HD3	2.04	0.58
1:B:3842:LEU:O	1:B:3929:SER:OG	2.21	0.58
1:B:4325:ARG:HD2	1:B:4634:GLU:OE2	2.01	0.58
1:C:1196:PRO:O	1:C:1198:GLN:NE2	2.37	0.58
1:B:2281:ILE:HG23	1:B:2341:VAL:HG21	1.85	0.58
1:C:3322:ILE:O	1:C:3326:ASN:ND2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1748:PHE:O	1:A:1750:PRO:HD3	2.04	0.58
1:A:2281:ILE:HG23	1:A:2341:VAL:HG21	1.85	0.58
1:B:323:LEU:HG	1:B:325:THR:H	1.68	0.58
1:C:3569:LEU:HB2	1:C:3573:MET:HG3	1.86	0.58
1:A:4325:ARG:CG	1:A:4634:GLU:OE2	2.51	0.58
1:B:3322:ILE:O	1:B:3326:ASN:ND2	2.36	0.58
1:C:3889:GLN:HG3	1:C:3967:GLU:HG3	1.85	0.58
1:D:323:LEU:HG	1:D:325:THR:H	1.68	0.58
1:A:3569:LEU:HB2	1:A:3573:MET:HG3	1.86	0.58
1:C:4325:ARG:CG	1:C:4634:GLU:OE2	2.51	0.58
1:C:4544:LEU:HB3	1:C:4548:ARG:NH1	2.19	0.58
1:C:4791:TYR:OH	1:C:4815:ASP:O	2.21	0.58
1:D:1748:PHE:O	1:D:1750:PRO:HD3	2.04	0.58
1:D:2243:SER:OG	1:D:2246:ASN:ND2	2.36	0.58
1:D:4544:LEU:HB3	1:D:4548:ARG:NH1	2.19	0.58
1:A:1658:ASP:OD1	1:A:1659:LEU:N	2.37	0.57
1:A:323:LEU:HG	1:A:325:THR:H	1.68	0.57
1:A:3322:ILE:O	1:A:3326:ASN:ND2	2.36	0.57
1:D:4561:THR:O	1:D:4562:LEU:C	2.40	0.57
1:A:358:THR:HG21	1:A:382:GLY:HA3	1.86	0.57
1:A:436:LEU:HD12	1:A:437:PRO:HD2	1.85	0.57
1:B:4544:LEU:HB3	1:B:4548:ARG:NH1	2.19	0.57
1:D:1196:PRO:O	1:D:1198:GLN:NE2	2.37	0.57
1:D:1658:ASP:OD1	1:D:1659:LEU:N	2.37	0.57
1:D:3569:LEU:HB2	1:D:3573:MET:HG3	1.86	0.57
1:B:4157:ASP:O	1:B:4161:ARG:NH1	2.37	0.57
1:C:2438:PRO:HG3	1:C:2454:ARG:HB2	1.87	0.57
1:D:3889:GLN:HG3	1:D:3967:GLU:HG3	1.85	0.57
1:A:2243:SER:OG	1:A:2246:ASN:ND2	2.36	0.57
1:A:4157:ASP:O	1:A:4161:ARG:NH1	2.37	0.57
1:B:2243:SER:OG	1:B:2246:ASN:ND2	2.36	0.57
1:B:2438:PRO:HG3	1:B:2454:ARG:HB2	1.87	0.57
1:C:682:LEU:HD11	1:C:787:VAL:HG21	1.87	0.57
1:C:1658:ASP:OD1	1:C:1659:LEU:N	2.37	0.57
1:C:4157:ASP:O	1:C:4161:ARG:NH1	2.37	0.57
1:D:1089:TYR:HE1	1:D:1150:GLY:HA3	1.70	0.57
1:A:176:SER:HA	1:D:2456:ILE:HD11	1.87	0.57
1:B:646:PRO:HD2	1:B:779:PRO:HG2	1.87	0.57
1:D:358:THR:HG21	1:D:382:GLY:HA3	1.86	0.57
1:D:4813:LEU:HA	1:D:4816:ILE:HG22	1.87	0.57
1:A:2456:ILE:HD11	1:B:176:SER:HA	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3889:GLN:HG3	1:A:3967:GLU:HG3	1.85	0.57
1:B:3569:LEU:HB2	1:B:3573:MET:HG3	1.86	0.57
1:C:3529:ASP:HA	1:D:1220:GLN:HE21	1.70	0.57
1:A:4544:LEU:HB3	1:A:4548:ARG:NH1	2.19	0.57
1:B:436:LEU:HD12	1:B:437:PRO:HD2	1.85	0.57
1:D:2438:PRO:HG3	1:D:2454:ARG:HB2	1.87	0.57
1:A:1089:TYR:HE1	1:A:1150:GLY:HA3	1.70	0.57
1:A:3529:ASP:HA	1:B:1220:GLN:HE21	1.70	0.57
1:A:4562:LEU:O	1:A:4565:LEU:N	2.37	0.57
1:B:358:THR:HG21	1:B:382:GLY:HA3	1.86	0.57
1:B:682:LEU:HD11	1:B:787:VAL:HG21	1.87	0.57
1:C:646:PRO:HD2	1:C:779:PRO:HG2	1.87	0.57
1:D:1516:ILE:HB	1:D:1531:ALA:HB3	1.86	0.57
1:A:2103:VAL:O	1:A:2107:GLN:NE2	2.38	0.57
1:C:591:ASP:O	1:C:1594:ARG:NH2	2.38	0.57
1:C:1516:ILE:HB	1:C:1531:ALA:HB3	1.86	0.57
1:C:4562:LEU:O	1:C:4565:LEU:N	2.37	0.57
1:D:2281:ILE:HG23	1:D:2341:VAL:HG21	1.85	0.57
1:A:1196:PRO:O	1:A:1198:GLN:NE2	2.37	0.56
1:A:1220:GLN:HE21	1:D:3529:ASP:HA	1.70	0.56
1:B:1089:TYR:HE1	1:B:1150:GLY:HA3	1.70	0.56
1:B:1658:ASP:OD1	1:B:1659:LEU:N	2.37	0.56
1:A:4813:LEU:HA	1:A:4816:ILE:HG22	1.87	0.56
1:B:4562:LEU:O	1:B:4565:LEU:N	2.37	0.56
1:D:1505:GLN:HG3	1:D:1506:GLN:H	1.71	0.56
1:A:1505:GLN:HG3	1:A:1506:GLN:H	1.71	0.56
1:A:2438:PRO:HG3	1:A:2454:ARG:HB2	1.87	0.56
1:B:591:ASP:O	1:B:1594:ARG:NH2	2.38	0.56
1:C:323:LEU:HG	1:C:325:THR:H	1.68	0.56
1:C:2456:ILE:HD11	1:D:176:SER:HA	1.87	0.56
1:C:3272:ILE:HG22	1:C:3276:MET:HG2	1.87	0.56
1:D:591:ASP:O	1:D:1594:ARG:NH2	2.38	0.56
1:D:4324:ALA:O	1:D:4325:ARG:C	2.44	0.56
1:A:591:ASP:O	1:A:1594:ARG:NH2	2.38	0.56
1:A:1516:ILE:HB	1:A:1531:ALA:HB3	1.86	0.56
1:C:1089:TYR:HE1	1:C:1150:GLY:HA3	1.70	0.56
1:C:4561:THR:O	1:C:4562:LEU:C	2.40	0.56
1:C:4813:LEU:HA	1:C:4816:ILE:HG22	1.87	0.56
1:D:670:GLU:HB3	1:D:787:VAL:HG13	1.87	0.56
1:D:686:TRP:NE1	1:D:746:CYS:SG	2.70	0.56
1:D:3272:ILE:HG22	1:D:3276:MET:HG2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:646:PRO:HD2	1:A:779:PRO:HG2	1.87	0.56
1:B:682:LEU:HD21	1:B:787:VAL:HG11	1.88	0.56
1:D:949:ASN:OD1	1:D:951:LYS:NZ	2.38	0.56
1:D:3842:LEU:O	1:D:3929:SER:OG	2.21	0.56
1:A:4324:ALA:O	1:A:4325:ARG:C	2.44	0.56
1:B:2191:PHE:HD1	1:B:2198:MET:HG3	1.70	0.56
1:C:358:THR:HG21	1:C:382:GLY:HA3	1.86	0.56
1:C:2191:PHE:HD1	1:C:2198:MET:HG3	1.70	0.56
1:D:682:LEU:HD11	1:D:787:VAL:HG21	1.87	0.56
1:D:2103:VAL:O	1:D:2107:GLN:NE2	2.38	0.56
1:D:2005:GLN:HG2	1:D:3641:LEU:HD12	1.88	0.56
1:D:4157:ASP:O	1:D:4161:ARG:NH1	2.37	0.56
1:A:949:ASN:OD1	1:A:951:LYS:NZ	2.38	0.56
1:B:4336:TRP:CE3	1:B:4571:PHE:CD2	2.94	0.56
1:B:4813:LEU:HA	1:B:4816:ILE:HG22	1.87	0.56
1:C:4324:ALA:O	1:C:4325:ARG:C	2.44	0.56
1:D:2191:PHE:HD1	1:D:2198:MET:HG3	1.70	0.56
1:D:4562:LEU:O	1:D:4565:LEU:N	2.37	0.56
1:A:1209:SER:HB3	1:D:3577:ARG:HH22	1.71	0.56
1:B:3529:ASP:HA	1:C:1220:GLN:HE21	1.70	0.56
1:C:2005:GLN:HG2	1:C:3641:LEU:HD12	1.88	0.56
1:C:3194:LEU:HG	1:C:3196:ARG:H	1.71	0.56
1:C:4336:TRP:CE3	1:C:4571:PHE:CD2	2.94	0.56
1:B:2005:GLN:HG2	1:B:3641:LEU:HD12	1.88	0.55
1:C:949:ASN:OD1	1:C:951:LYS:NZ	2.38	0.55
1:A:682:LEU:HD11	1:A:787:VAL:HG21	1.87	0.55
1:B:1516:ILE:HB	1:B:1531:ALA:HB3	1.86	0.55
1:B:2456:ILE:HD11	1:C:176:SER:HA	1.87	0.55
1:B:3272:ILE:HG22	1:B:3276:MET:HG2	1.87	0.55
1:D:15:ARG:NH2	1:D:98:HIS:O	2.39	0.55
1:D:646:PRO:HD2	1:D:779:PRO:HG2	1.87	0.55
1:A:670:GLU:HB3	1:A:787:VAL:HG13	1.87	0.55
1:A:1109:LEU:HA	1:A:1120:LEU:HD23	1.89	0.55
1:A:2005:GLN:HG2	1:A:3641:LEU:HD12	1.88	0.55
1:A:3272:ILE:HG22	1:A:3276:MET:HG2	1.87	0.55
1:B:2103:VAL:O	1:B:2107:GLN:NE2	2.38	0.55
1:C:670:GLU:HB3	1:C:787:VAL:HG13	1.87	0.55
1:A:2191:PHE:HD1	1:A:2198:MET:HG3	1.70	0.55
1:C:682:LEU:HD21	1:C:787:VAL:HG11	1.88	0.55
1:C:1109:LEU:HA	1:C:1120:LEU:HD23	1.89	0.55
1:C:1505:GLN:HG3	1:C:1506:GLN:H	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:ARG:NH2	1:A:98:HIS:O	2.39	0.55
1:A:3842:LEU:O	1:A:3929:SER:OG	2.21	0.55
1:B:670:GLU:HB3	1:B:787:VAL:HG13	1.87	0.55
1:D:4336:TRP:CE3	1:D:4571:PHE:CD2	2.94	0.55
1:C:472:ARG:NH1	1:C:3712:GLU:OE2	2.40	0.55
1:D:682:LEU:HD21	1:D:787:VAL:HG11	1.88	0.55
1:B:1109:LEU:HA	1:B:1120:LEU:HD23	1.89	0.55
1:B:4324:ALA:O	1:B:4325:ARG:C	2.44	0.55
1:C:4119:GLU:HG2	1:C:4121:GLU:HG2	1.88	0.55
1:A:472:ARG:NH1	1:A:3712:GLU:OE2	2.40	0.55
1:A:682:LEU:HD21	1:A:787:VAL:HG11	1.88	0.55
1:A:3577:ARG:HH22	1:B:1209:SER:HB3	1.71	0.55
1:A:4119:GLU:HG2	1:A:4121:GLU:HG2	1.88	0.55
1:B:472:ARG:NH1	1:B:3712:GLU:OE2	2.40	0.55
1:B:1505:GLN:HG3	1:B:1506:GLN:H	1.71	0.55
1:B:3577:ARG:HH22	1:C:1209:SER:HB3	1.71	0.55
1:C:995:VAL:HG22	1:C:998:ARG:HH12	1.72	0.55
1:A:3805:LEU:HB3	1:A:3812:VAL:HG21	1.89	0.55
1:A:4336:TRP:CE3	1:A:4571:PHE:CD2	2.94	0.55
1:B:1196:PRO:O	1:B:1198:GLN:NE2	2.37	0.55
1:B:3221:THR:HB	1:B:3224:PRO:HG3	1.88	0.55
1:C:15:ARG:NH2	1:C:98:HIS:O	2.39	0.55
1:C:3221:THR:HB	1:C:3224:PRO:HG3	1.88	0.55
1:C:3805:LEU:HB3	1:C:3812:VAL:HG21	1.89	0.55
1:D:1576:SER:OG	1:D:1590:GLN:O	2.25	0.55
1:D:3194:LEU:HG	1:D:3196:ARG:H	1.71	0.55
1:A:1671:ARG:NH1	1:A:1713:ASP:OD2	2.40	0.55
1:B:4119:GLU:HG2	1:B:4121:GLU:HG2	1.88	0.55
1:C:2103:VAL:O	1:C:2107:GLN:NE2	2.38	0.55
1:D:3378:GLN:HG3	1:D:3381:LEU:HD12	1.89	0.55
1:D:3805:LEU:HB3	1:D:3812:VAL:HG21	1.89	0.55
1:D:4119:GLU:HG2	1:D:4121:GLU:HG2	1.88	0.55
1:A:711:LEU:HD13	1:A:1534:LYS:HD2	1.89	0.54
1:A:3194:LEU:HG	1:A:3196:ARG:H	1.71	0.54
1:B:15:ARG:NH2	1:B:98:HIS:O	2.39	0.54
1:D:1671:ARG:NH1	1:D:1713:ASP:OD2	2.40	0.54
1:D:3221:THR:HB	1:D:3224:PRO:HG3	1.88	0.54
1:A:4791:TYR:OH	1:A:4815:ASP:O	2.21	0.54
1:B:143:GLY:HA3	1:B:147:TRP:HE1	1.72	0.54
1:C:3577:ARG:HH22	1:D:1209:SER:HB3	1.71	0.54
1:C:4823:LEU:HD22	1:D:4839:MET:HE2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:949:ASN:OD1	1:B:951:LYS:NZ	2.38	0.54
1:B:3805:LEU:HB3	1:B:3812:VAL:HG21	1.89	0.54
1:C:2339:VAL:O	1:C:2435:ARG:NH2	2.31	0.54
1:D:1109:LEU:HA	1:D:1120:LEU:HD23	1.89	0.54
1:A:995:VAL:HG22	1:A:998:ARG:HH12	1.72	0.54
1:A:2457:LEU:HD21	1:A:2505:PHE:HE1	1.72	0.54
1:B:711:LEU:HD13	1:B:1534:LYS:HD2	1.89	0.54
1:B:1126:GLY:HA3	1:B:1143:TRP:CE2	2.43	0.54
1:A:1576:SER:OG	1:A:1590:GLN:O	2.25	0.54
1:A:3221:THR:HB	1:A:3224:PRO:HG3	1.88	0.54
1:B:995:VAL:HG22	1:B:998:ARG:HH12	1.72	0.54
1:B:3378:GLN:HG3	1:B:3381:LEU:HD12	1.89	0.54
1:A:224:HIS:N	1:A:229:GLU:O	2.41	0.54
1:B:224:HIS:N	1:B:229:GLU:O	2.41	0.54
1:B:1671:ARG:NH1	1:B:1713:ASP:OD2	2.40	0.54
1:B:3194:LEU:HG	1:B:3196:ARG:H	1.71	0.54
1:C:711:LEU:HD13	1:C:1534:LYS:HD2	1.89	0.54
1:D:472:ARG:NH1	1:D:3712:GLU:OE2	2.40	0.54
1:A:3378:GLN:HG3	1:A:3381:LEU:HD12	1.89	0.54
1:D:2457:LEU:HD21	1:D:2505:PHE:HE1	1.72	0.54
1:B:668:VAL:O	1:B:741:GLU:N	2.37	0.54
1:C:224:HIS:N	1:C:229:GLU:O	2.41	0.54
1:C:4559:PHE:O	1:C:4561:THR:CG2	2.53	0.54
1:A:1126:GLY:HA3	1:A:1143:TRP:CE2	2.43	0.54
1:A:2961:GLN:O	1:A:2965:ARG:NH2	2.41	0.54
1:A:4839:MET:HE2	1:D:4823:LEU:HD22	1.90	0.54
1:B:5033:GLU:O	1:B:5037:SER:OG	2.24	0.54
1:C:19:GLU:HB2	1:C:206:CYS:HB3	1.90	0.54
1:C:2457:LEU:HD21	1:C:2505:PHE:HE1	1.72	0.54
1:D:143:GLY:HA3	1:D:147:TRP:HE1	1.72	0.54
1:D:487:VAL:HG13	1:D:522:LEU:HD12	1.90	0.54
1:D:711:LEU:HD13	1:D:1534:LYS:HD2	1.89	0.54
1:D:1679:ASN:ND2	1:D:1798:LEU:O	2.41	0.54
1:D:4561:THR:O	1:D:4564:PHE:N	2.40	0.54
1:B:917:GLU:HG3	1:B:918:ARG:HG2	1.90	0.54
1:B:4823:LEU:HD22	1:C:4839:MET:HE2	1.89	0.54
1:D:989:ALA:O	1:D:993:HIS:ND1	2.31	0.54
1:B:1078:GLU:HG3	1:B:1080:SER:H	1.73	0.53
1:C:15:ARG:NH1	1:C:100:THR:OG1	2.36	0.53
1:C:1576:SER:OG	1:C:1590:GLN:O	2.25	0.53
1:C:2961:GLN:O	1:C:2965:ARG:NH2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:670:GLU:H	1:D:740:PRO:HB3	1.73	0.53
1:D:4177:TYR:OH	1:D:4199:GLU:OE1	2.19	0.53
1:C:487:VAL:HG13	1:C:522:LEU:HD12	1.90	0.53
1:C:1671:ARG:NH1	1:C:1713:ASP:OD2	2.40	0.53
1:C:4561:THR:O	1:C:4564:PHE:N	2.40	0.53
1:A:143:GLY:HA3	1:A:147:TRP:HE1	1.72	0.53
1:A:917:GLU:HG3	1:A:918:ARG:HG2	1.90	0.53
1:A:4823:LEU:HD22	1:B:4839:MET:HE2	1.90	0.53
1:B:4561:THR:O	1:B:4564:PHE:N	2.40	0.53
1:C:143:GLY:HA3	1:C:147:TRP:HE1	1.72	0.53
1:D:995:VAL:HG22	1:D:998:ARG:HH12	1.72	0.53
1:D:5033:GLU:O	1:D:5037:SER:OG	2.24	0.53
1:A:1679:ASN:ND2	1:A:1798:LEU:O	2.41	0.53
1:B:19:GLU:HB2	1:B:206:CYS:HB3	1.90	0.53
1:B:1679:ASN:ND2	1:B:1798:LEU:O	2.41	0.53
1:B:2565:CYS:SG	1:B:2566:ALA:N	2.82	0.53
1:C:917:GLU:HG3	1:C:918:ARG:HG2	1.90	0.53
1:C:1126:GLY:HA3	1:C:1143:TRP:CE2	2.43	0.53
1:C:1679:ASN:ND2	1:C:1798:LEU:O	2.41	0.53
1:C:2565:CYS:SG	1:C:2566:ALA:N	2.82	0.53
1:D:917:GLU:HG3	1:D:918:ARG:HG2	1.90	0.53
1:A:487:VAL:HG13	1:A:522:LEU:HD12	1.90	0.53
1:A:2565:CYS:SG	1:A:2566:ALA:N	2.82	0.53
1:A:2587:TYR:O	1:A:2591:ARG:N	2.31	0.53
1:A:4567:LEU:HD12	1:A:4816:ILE:HG13	1.91	0.53
1:B:1085:SER:O	1:B:1088:TRP:NE1	2.38	0.53
1:D:224:HIS:N	1:D:229:GLU:O	2.41	0.53
1:D:2565:CYS:SG	1:D:2566:ALA:N	2.82	0.53
1:A:1765:VAL:HG22	1:A:1766:GLY:H	1.74	0.53
1:A:4581:LYS:HE2	1:A:4581:LYS:HA	1.91	0.53
1:A:5033:GLU:O	1:A:5037:SER:OG	2.24	0.53
1:B:2961:GLN:O	1:B:2965:ARG:NH2	2.41	0.53
1:C:5033:GLU:O	1:C:5037:SER:OG	2.24	0.53
1:D:19:GLU:HB2	1:D:206:CYS:HB3	1.90	0.53
1:D:1033:ARG:NE	1:D:1037:ASP:OD2	2.41	0.53
1:A:1033:ARG:NE	1:A:1037:ASP:OD2	2.41	0.53
1:A:1078:GLU:HG3	1:A:1080:SER:H	1.73	0.53
1:A:4561:THR:O	1:A:4564:PHE:N	2.40	0.53
1:B:487:VAL:HG13	1:B:522:LEU:HD12	1.90	0.53
1:C:793:LEU:HD11	1:C:796:ARG:HG2	1.91	0.53
1:D:2961:GLN:O	1:D:2965:ARG:NH2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4581:LYS:HE2	1:D:4581:LYS:HA	1.91	0.53
1:B:2457:LEU:HD21	1:B:2505:PHE:HE1	1.72	0.53
1:D:745:SER:HB2	1:D:758:ARG:HB3	1.91	0.53
1:B:1576:SER:OG	1:B:1590:GLN:O	2.25	0.53
1:C:3378:GLN:HG3	1:C:3381:LEU:HD12	1.89	0.53
1:A:3983:SER:OG	1:A:3984:ARG:N	2.42	0.53
1:B:2587:TYR:O	1:B:2591:ARG:N	2.31	0.53
1:D:15:ARG:NH1	1:D:100:THR:OG1	2.36	0.53
1:A:668:VAL:O	1:A:741:GLU:N	2.37	0.52
1:A:670:GLU:H	1:A:740:PRO:HB3	1.73	0.52
1:B:745:SER:HB2	1:B:758:ARG:HB3	1.91	0.52
1:B:793:LEU:HD11	1:B:796:ARG:HG2	1.91	0.52
1:B:426:ARG:HD2	1:B:431:PRO:HB3	1.92	0.52
1:C:989:ALA:O	1:C:993:HIS:ND1	2.31	0.52
1:C:4567:LEU:HD12	1:C:4816:ILE:HG13	1.91	0.52
1:D:1126:GLY:HA3	1:D:1143:TRP:CE2	2.43	0.52
1:B:3983:SER:OG	1:B:3984:ARG:N	2.42	0.52
1:C:1078:GLU:HG3	1:C:1080:SER:H	1.73	0.52
1:A:19:GLU:HB2	1:A:206:CYS:HB3	1.90	0.52
1:C:269:TRP:HZ3	1:C:334:MET:HG2	1.75	0.52
1:C:3842:LEU:O	1:C:3929:SER:OG	2.21	0.52
1:D:269:TRP:HZ3	1:D:334:MET:HG2	1.75	0.52
1:D:793:LEU:HD11	1:D:796:ARG:HG2	1.91	0.52
1:B:269:TRP:HZ3	1:B:334:MET:HG2	1.75	0.52
1:B:670:GLU:H	1:B:740:PRO:HB3	1.73	0.52
1:C:317:ARG:HH21	1:C:323:LEU:HB3	1.75	0.52
1:B:4567:LEU:HD12	1:B:4816:ILE:HG13	1.91	0.52
1:C:1765:VAL:HG22	1:C:1766:GLY:H	1.74	0.52
1:D:4567:LEU:HD12	1:D:4816:ILE:HG13	1.91	0.52
1:A:1085:SER:O	1:A:1088:TRP:NE1	2.38	0.52
1:C:426:ARG:HD2	1:C:431:PRO:HB3	1.92	0.52
1:D:1765:VAL:HG22	1:D:1766:GLY:H	1.74	0.52
1:A:793:LEU:HD11	1:A:796:ARG:HG2	1.91	0.52
1:A:2339:VAL:O	1:A:2435:ARG:NH2	2.31	0.52
1:B:2559:LEU:HD11	1:B:2603:ILE:HG13	1.91	0.52
1:C:3538:THR:O	1:C:3542:LEU:N	2.43	0.52
1:C:4556:SER:O	1:C:4557:ARG:C	2.48	0.52
1:C:4581:LYS:HE2	1:C:4581:LYS:HA	1.91	0.52
1:D:3983:SER:OG	1:D:3984:ARG:N	2.42	0.52
1:A:2559:LEU:HD11	1:A:2603:ILE:HG13	1.91	0.52
1:B:4581:LYS:HA	1:B:4581:LYS:HE2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:213:TYR:HB3	1:D:273:HIS:CE1	2.44	0.52
1:D:1078:GLU:HG3	1:D:1080:SER:H	1.73	0.52
1:A:745:SER:HB2	1:A:758:ARG:HB3	1.91	0.52
1:B:317:ARG:HH21	1:B:323:LEU:HB3	1.75	0.52
1:A:3541:ALA:O	1:A:3545:THR:N	2.43	0.51
1:A:4826:ILE:HD12	1:B:4839:MET:HE3	1.91	0.51
1:B:1765:VAL:HG22	1:B:1766:GLY:H	1.74	0.51
1:D:3538:THR:O	1:D:3542:LEU:N	2.43	0.51
1:A:317:ARG:HH21	1:A:323:LEU:HB3	1.75	0.51
1:B:340:LYS:O	1:B:344:SER:OG	2.20	0.51
1:B:4791:TYR:OH	1:B:4815:ASP:O	2.21	0.51
1:C:670:GLU:H	1:C:740:PRO:HB3	1.73	0.51
1:C:4177:TYR:OH	1:C:4199:GLU:OE1	2.19	0.51
1:A:842:PRO:HG3	1:A:1073:ARG:HG3	1.93	0.51
1:B:1033:ARG:NE	1:B:1037:ASP:OD2	2.41	0.51
1:C:870:ILE:HA	1:C:873:LYS:HB2	1.93	0.51
1:D:345:LEU:HD23	1:D:389:PHE:HB3	1.93	0.51
1:D:1450:VAL:HG12	1:D:1452:TRP:HE3	1.76	0.51
1:D:1458:HIS:CE1	1:D:1483:VAL:HG21	2.46	0.51
1:A:870:ILE:HA	1:A:873:LYS:HB2	1.93	0.51
1:A:1535:GLU:HB3	1:A:1537:ASN:OD1	2.11	0.51
1:B:345:LEU:HD23	1:B:389:PHE:HB3	1.93	0.51
1:C:1033:ARG:NE	1:C:1037:ASP:OD2	2.41	0.51
1:D:4559:PHE:O	1:D:4561:THR:CG2	2.53	0.51
1:A:168:ASP:HB3	1:A:199:LEU:HD22	1.92	0.51
1:A:426:ARG:HD2	1:A:431:PRO:HB3	1.92	0.51
1:A:838:HIS:HA	1:A:1201:HIS:HB3	1.93	0.51
1:B:838:HIS:HA	1:B:1201:HIS:HB3	1.93	0.51
1:B:1458:HIS:CE1	1:B:1483:VAL:HG21	2.46	0.51
1:B:4556:SER:O	1:B:4557:ARG:C	2.48	0.51
1:C:213:TYR:HB3	1:C:273:HIS:CE1	2.44	0.51
1:C:745:SER:HB2	1:C:758:ARG:HB3	1.91	0.51
1:C:1458:HIS:CE1	1:C:1483:VAL:HG21	2.46	0.51
1:D:257:ARG:O	1:D:284:HIS:NE2	2.40	0.51
1:D:1535:GLU:HB3	1:D:1537:ASN:OD1	2.11	0.51
1:D:2587:TYR:O	1:D:2591:ARG:N	2.31	0.51
1:A:1458:HIS:CE1	1:A:1483:VAL:HG21	2.46	0.51
1:A:3538:THR:O	1:A:3542:LEU:N	2.43	0.51
1:B:213:TYR:HB3	1:B:273:HIS:CE1	2.44	0.51
1:C:2559:LEU:HD11	1:C:2603:ILE:HG13	1.91	0.51
1:C:3983:SER:OG	1:C:3984:ARG:N	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:247:TYR:HB2	1:D:374:LYS:HB3	1.92	0.51
1:A:213:TYR:HB3	1:A:273:HIS:CE1	2.44	0.51
1:A:989:ALA:O	1:A:993:HIS:ND1	2.31	0.51
1:A:269:TRP:HZ3	1:A:334:MET:HG2	1.75	0.51
1:A:1495:VAL:HG12	1:A:1538:THR:H	1.76	0.51
1:B:842:PRO:HG3	1:B:1073:ARG:HG3	1.93	0.51
1:C:4336:TRP:CE3	1:C:4571:PHE:HE2	2.18	0.51
1:D:842:PRO:HG3	1:D:1073:ARG:HG3	1.93	0.51
1:D:2174:GLU:OE1	1:D:2174:GLU:N	2.34	0.51
1:A:192:ASP:OD1	1:A:192:ASP:N	2.44	0.51
1:A:4088:ILE:HD11	1:A:4093:PHE:HD2	1.76	0.51
1:B:192:ASP:N	1:B:192:ASP:OD1	2.44	0.51
1:B:247:TYR:HB2	1:B:374:LYS:HB3	1.92	0.51
1:C:842:PRO:HG3	1:C:1073:ARG:HG3	1.93	0.51
1:C:1450:VAL:HG12	1:C:1452:TRP:HE3	1.76	0.51
1:C:1495:VAL:HG12	1:C:1538:THR:H	1.76	0.51
1:C:1535:GLU:HB3	1:C:1537:ASN:OD1	2.11	0.51
1:D:1495:VAL:HG12	1:D:1538:THR:H	1.76	0.51
1:B:1495:VAL:HG12	1:B:1538:THR:H	1.76	0.51
1:C:345:LEU:HD23	1:C:389:PHE:HB3	1.93	0.51
1:D:317:ARG:HH21	1:D:323:LEU:HB3	1.75	0.51
1:D:1114:GLU:HB3	1:D:1117:ALA:HB2	1.93	0.51
1:D:4731:ILE:HG13	1:D:4732:PHE:HD1	1.76	0.51
1:A:345:LEU:HD23	1:A:389:PHE:HB3	1.93	0.50
1:A:3722:TYR:OH	1:A:3797:THR:HG22	2.11	0.50
1:B:3538:THR:O	1:B:3542:LEU:N	2.43	0.50
1:C:247:TYR:HB2	1:C:374:LYS:HB3	1.92	0.50
1:C:4558:ASN:O	1:C:4559:PHE:O	2.29	0.50
1:A:4558:ASN:O	1:A:4559:PHE:O	2.29	0.50
1:B:590:LEU:HB2	1:B:599:VAL:HG11	1.93	0.50
1:C:168:ASP:HB3	1:C:199:LEU:HD22	1.92	0.50
1:C:192:ASP:N	1:C:192:ASP:OD1	2.44	0.50
1:D:426:ARG:HD2	1:D:431:PRO:HB3	1.92	0.50
1:D:2559:LEU:HD11	1:D:2603:ILE:HG13	1.91	0.50
1:D:4319:LEU:HB3	1:D:4320:ARG:HH12	1.77	0.50
1:D:4336:TRP:CE3	1:D:4571:PHE:HE2	2.18	0.50
1:A:1114:GLU:HB3	1:A:1117:ALA:HB2	1.93	0.50
1:A:1450:VAL:HG12	1:A:1452:TRP:HE3	1.76	0.50
1:A:2465:ASP:OD1	1:A:2465:ASP:N	2.45	0.50
1:A:4561:THR:O	1:A:4564:PHE:HB3	2.12	0.50
1:B:870:ILE:HA	1:B:873:LYS:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1535:GLU:HB3	1:B:1537:ASN:OD1	2.11	0.50
1:B:3722:TYR:OH	1:B:3797:THR:HG22	2.11	0.50
1:B:4561:THR:O	1:B:4564:PHE:HB3	2.12	0.50
1:C:3805:LEU:CD1	1:C:3890:LEU:HB3	2.41	0.50
1:D:793:LEU:HD21	1:D:797:HIS:H	1.76	0.50
1:D:4558:ASN:O	1:D:4559:PHE:O	2.29	0.50
1:B:1166:GLY:HA2	1:B:1216:ILE:HG13	1.94	0.50
1:B:2339:VAL:O	1:B:2435:ARG:NH2	2.31	0.50
1:D:4325:ARG:HD2	1:D:4634:GLU:OE2	2.01	0.50
1:D:4561:THR:O	1:D:4564:PHE:HB3	2.12	0.50
1:D:4791:TYR:OH	1:D:4815:ASP:O	2.21	0.50
1:A:1704:PRO:HG2	1:A:1707:LEU:HD12	1.94	0.50
1:B:15:ARG:NH1	1:B:100:THR:OG1	2.36	0.50
1:B:1704:PRO:HG2	1:B:1707:LEU:HD12	1.94	0.50
1:B:2336:ARG:O	1:B:2340:PHE:HB2	2.12	0.50
1:B:2556:LEU:HD12	1:B:2597:LYS:HA	1.93	0.50
1:B:4558:ASN:O	1:B:4559:PHE:O	2.29	0.50
1:C:590:LEU:HB2	1:C:599:VAL:HG11	1.93	0.50
1:D:347:PHE:HE1	1:D:387:ALA:H	1.60	0.50
1:A:4731:ILE:HG13	1:A:4732:PHE:HD1	1.76	0.50
1:B:234:SER:O	1:B:242:ARG:NH1	2.45	0.50
1:B:4562:LEU:O	1:B:4563:ARG:C	2.50	0.50
1:C:2556:LEU:HD12	1:C:2597:LYS:HA	1.93	0.50
1:C:4088:ILE:HD11	1:C:4093:PHE:HD2	1.76	0.50
1:C:4731:ILE:HG13	1:C:4732:PHE:HD1	1.76	0.50
1:D:1166:GLY:HA2	1:D:1216:ILE:HG13	1.94	0.50
1:A:1275:ARG:O	1:A:1281:ASN:ND2	2.45	0.50
1:A:2556:LEU:HD12	1:A:2597:LYS:HA	1.93	0.50
1:A:3941:ASP:OD1	1:A:3942:VAL:N	2.45	0.50
1:A:4556:SER:O	1:A:4557:ARG:C	2.48	0.50
1:A:4839:MET:HE3	1:D:4826:ILE:HD12	1.93	0.50
1:B:276:TRP:N	1:B:338:GLU:OE1	2.39	0.50
1:B:3941:ASP:OD1	1:B:3942:VAL:N	2.45	0.50
1:C:1100:MET:HB2	1:C:1143:TRP:HZ3	1.77	0.50
1:C:2359:ARG:NH2	1:D:177:GLU:O	2.45	0.50
1:C:3722:TYR:OH	1:C:3797:THR:HG22	2.11	0.50
1:D:234:SER:O	1:D:242:ARG:NH1	2.45	0.50
1:D:1085:SER:O	1:D:1088:TRP:NE1	2.38	0.50
1:A:247:TYR:HB2	1:A:374:LYS:HB3	1.92	0.50
1:A:793:LEU:HD21	1:A:797:HIS:H	1.76	0.50
1:B:206:CYS:SG	1:B:207:SER:N	2.84	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:793:LEU:HD21	1:C:797:HIS:H	1.76	0.50
1:C:1114:GLU:HB3	1:C:1117:ALA:HB2	1.93	0.50
1:C:2336:ARG:O	1:C:2340:PHE:HB2	2.12	0.50
1:C:4319:LEU:HB3	1:C:4320:ARG:HH12	1.77	0.50
1:D:110:ARG:HH21	1:D:115:ARG:HD2	1.77	0.50
1:D:168:ASP:HB3	1:D:199:LEU:HD22	1.92	0.50
1:D:1969:LEU:HD13	1:D:2023:LEU:HD21	1.94	0.50
1:A:206:CYS:SG	1:A:207:SER:N	2.84	0.50
1:B:1024:TYR:HA	1:B:1027:LEU:HG	1.94	0.50
1:B:1467:SER:HB2	1:B:1489:CYS:SG	2.52	0.50
1:B:4319:LEU:HB3	1:B:4320:ARG:HH12	1.77	0.50
1:D:206:CYS:SG	1:D:207:SER:N	2.84	0.50
1:D:1450:VAL:HG21	1:D:1454:THR:HG21	1.94	0.50
1:D:3941:ASP:OD1	1:D:3942:VAL:N	2.45	0.50
1:A:177:GLU:O	1:D:2359:ARG:NH2	2.45	0.49
1:A:215:THR:OG1	1:A:271:GLY:O	2.31	0.49
1:A:234:SER:O	1:A:242:ARG:NH1	2.45	0.49
1:A:340:LYS:O	1:A:344:SER:OG	2.20	0.49
1:A:840:VAL:O	1:A:1073:ARG:NH2	2.45	0.49
1:A:1450:VAL:HG21	1:A:1454:THR:HG21	1.94	0.49
1:A:3805:LEU:CD1	1:A:3890:LEU:HB3	2.41	0.49
1:B:1450:VAL:HG12	1:B:1452:TRP:HE3	1.76	0.49
1:B:2359:ARG:NH2	1:C:177:GLU:O	2.45	0.49
1:C:1694:LEU:HD23	1:C:1715:LEU:HB2	1.94	0.49
1:D:131:LEU:HD12	1:D:133:PHE:CE1	2.47	0.49
1:D:870:ILE:HA	1:D:873:LYS:HB2	1.93	0.49
1:A:15:ARG:NH1	1:A:100:THR:OG1	2.36	0.49
1:B:131:LEU:HD12	1:B:133:PHE:CE1	2.47	0.49
1:B:1114:GLU:HB3	1:B:1117:ALA:HB2	1.93	0.49
1:B:4088:ILE:HD11	1:B:4093:PHE:HD2	1.76	0.49
1:C:1024:TYR:HA	1:C:1027:LEU:HG	1.94	0.49
1:D:192:ASP:OD1	1:D:192:ASP:N	2.44	0.49
1:D:1467:SER:HB2	1:D:1489:CYS:SG	2.52	0.49
1:A:347:PHE:HE1	1:A:387:ALA:H	1.60	0.49
1:A:1100:MET:HB2	1:A:1143:TRP:HZ3	1.77	0.49
1:A:1166:GLY:HA2	1:A:1216:ILE:HG13	1.94	0.49
1:A:1969:LEU:HD13	1:A:2023:LEU:HD21	1.94	0.49
1:B:632:LEU:O	1:B:634:GLN:NE2	2.45	0.49
1:B:1100:MET:HB2	1:B:1143:TRP:HZ3	1.77	0.49
1:C:131:LEU:HD12	1:C:133:PHE:CE1	2.47	0.49
1:C:206:CYS:SG	1:C:207:SER:N	2.84	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:347:PHE:HE1	1:C:387:ALA:H	1.60	0.49
1:C:838:HIS:HA	1:C:1201:HIS:HB3	1.93	0.49
1:D:590:LEU:HB2	1:D:599:VAL:HG11	1.93	0.49
1:D:2336:ARG:O	1:D:2340:PHE:HB2	2.12	0.49
1:D:4088:ILE:HD11	1:D:4093:PHE:HD2	1.76	0.49
1:A:131:LEU:HD12	1:A:133:PHE:CE1	2.47	0.49
1:B:1079:LYS:NZ	1:B:1655:GLU:OE2	2.33	0.49
1:B:3805:LEU:CD1	1:B:3890:LEU:HB3	2.41	0.49
1:C:257:ARG:O	1:C:284:HIS:NE2	2.40	0.49
1:C:1275:ARG:O	1:C:1281:ASN:ND2	2.45	0.49
1:C:1467:SER:HB2	1:C:1489:CYS:SG	2.52	0.49
1:C:1969:LEU:HD13	1:C:2023:LEU:HD21	1.94	0.49
1:D:3722:TYR:OH	1:D:3797:THR:HG22	2.11	0.49
1:A:110:ARG:HH21	1:A:115:ARG:HD2	1.77	0.49
1:A:632:LEU:O	1:A:634:GLN:NE2	2.45	0.49
1:A:1024:TYR:HA	1:A:1027:LEU:HG	1.94	0.49
1:A:1694:LEU:HD23	1:A:1715:LEU:HB2	1.94	0.49
1:A:2336:ARG:O	1:A:2340:PHE:HB2	2.12	0.49
1:B:168:ASP:HB3	1:B:199:LEU:HD22	1.92	0.49
1:B:2174:GLU:OE1	1:B:2174:GLU:N	2.34	0.49
1:D:838:HIS:HA	1:D:1201:HIS:HB3	1.93	0.49
1:D:1694:LEU:HD23	1:D:1715:LEU:HB2	1.94	0.49
1:D:3805:LEU:CD1	1:D:3890:LEU:HB3	2.41	0.49
1:A:178:ARG:HH11	1:A:195:PHE:HA	1.78	0.49
1:B:793:LEU:HD21	1:B:797:HIS:H	1.76	0.49
1:C:3941:ASP:OD1	1:C:3942:VAL:N	2.45	0.49
1:C:4561:THR:O	1:C:4564:PHE:HB3	2.12	0.49
1:A:590:LEU:HB2	1:A:599:VAL:HG11	1.93	0.49
1:A:1467:SER:HB2	1:A:1489:CYS:SG	2.52	0.49
1:A:4319:LEU:HB3	1:A:4320:ARG:HH12	1.77	0.49
1:B:110:ARG:HH21	1:B:115:ARG:HD2	1.77	0.49
1:B:556:ALA:HB1	1:B:560:ILE:HG12	1.95	0.49
1:B:1694:LEU:HD23	1:B:1715:LEU:HB2	1.94	0.49
1:D:582:HIS:O	1:D:585:SER:OG	2.27	0.49
1:D:1139:PHE:HZ	1:D:1177:THR:HG22	1.78	0.49
1:D:1704:PRO:HG2	1:D:1707:LEU:HD12	1.94	0.49
1:D:3554:GLN:O	1:D:3558:HIS:ND1	2.46	0.49
1:A:4325:ARG:HD3	1:A:4634:GLU:OE1	1.87	0.49
1:B:1139:PHE:HZ	1:B:1177:THR:HG22	1.78	0.49
1:B:1450:VAL:HG21	1:B:1454:THR:HG21	1.94	0.49
1:B:4227:GLU:HG2	1:B:4229:GLU:HG3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:215:THR:OG1	1:C:271:GLY:O	2.31	0.49
1:C:1139:PHE:HZ	1:C:1177:THR:HG22	1.78	0.49
1:C:4227:GLU:HG2	1:C:4229:GLU:HG3	1.95	0.49
1:C:4562:LEU:O	1:C:4563:ARG:C	2.50	0.49
1:D:167:ASP:N	1:D:167:ASP:OD1	2.46	0.49
1:D:1024:TYR:HA	1:D:1027:LEU:HG	1.94	0.49
1:D:4562:LEU:O	1:D:4563:ARG:C	2.50	0.49
1:A:1139:PHE:HZ	1:A:1177:THR:HG22	1.78	0.49
1:C:234:SER:O	1:C:242:ARG:NH1	2.45	0.49
1:D:909:ASN:HB3	1:D:912:SER:HB3	1.95	0.49
1:D:4556:SER:O	1:D:4557:ARG:C	2.48	0.49
1:A:556:ALA:HB1	1:A:560:ILE:HG12	1.95	0.49
1:A:4562:LEU:O	1:A:4563:ARG:C	2.50	0.49
1:B:4731:ILE:HG13	1:B:4732:PHE:HD1	1.76	0.49
1:B:4959:PHE:HD2	1:B:4985:LEU:HD22	1.78	0.49
1:D:1100:MET:HB2	1:D:1143:TRP:HZ3	1.77	0.49
1:A:2359:ARG:NH2	1:B:177:GLU:O	2.45	0.48
1:A:4227:GLU:HG2	1:A:4229:GLU:HG3	1.95	0.48
1:B:675:LEU:HD21	1:B:1633:PRO:HB3	1.95	0.48
1:C:276:TRP:N	1:C:338:GLU:OE1	2.39	0.48
1:C:1450:VAL:HG21	1:C:1454:THR:HG21	1.94	0.48
1:D:556:ALA:HB1	1:D:560:ILE:HG12	1.95	0.48
1:D:2556:LEU:HD12	1:D:2597:LYS:HA	1.93	0.48
1:A:1176:GLU:O	1:A:1180:ARG:NH2	2.33	0.48
1:B:215:THR:OG1	1:B:271:GLY:O	2.31	0.48
1:B:1969:LEU:HD13	1:B:2023:LEU:HD21	1.94	0.48
1:C:110:ARG:HH21	1:C:115:ARG:HD2	1.77	0.48
1:C:1085:SER:O	1:C:1088:TRP:NE1	2.38	0.48
1:C:1166:GLY:HA2	1:C:1216:ILE:HG13	1.94	0.48
1:C:1704:PRO:HG2	1:C:1707:LEU:HD12	1.94	0.48
1:C:2316:LYS:HB3	1:C:2318:TYR:HE1	1.78	0.48
1:C:3302:PRO:HG2	1:C:3303:PRO:HD3	1.95	0.48
1:D:2512:ILE:O	1:D:2512:ILE:HG13	2.14	0.48
1:D:3289:PRO:HA	1:D:3338:LEU:HD22	1.95	0.48
1:A:3435:PHE:HA	1:A:3438:VAL:HG23	1.95	0.48
1:B:2512:ILE:HG13	1:B:2512:ILE:O	2.14	0.48
1:C:556:ALA:HB1	1:C:560:ILE:HG12	1.95	0.48
1:C:675:LEU:HD21	1:C:1633:PRO:HB3	1.95	0.48
1:C:971:ASP:OD1	1:C:971:ASP:N	2.46	0.48
1:C:2512:ILE:HG13	1:C:2512:ILE:O	2.14	0.48
1:C:3554:GLN:O	1:C:3558:HIS:ND1	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:840:VAL:O	1:D:1073:ARG:NH2	2.45	0.48
1:A:971:ASP:OD1	1:A:971:ASP:N	2.46	0.48
1:A:2512:ILE:O	1:A:2512:ILE:HG13	2.14	0.48
1:B:178:ARG:HH11	1:B:195:PHE:HA	1.78	0.48
1:B:347:PHE:HE1	1:B:387:ALA:H	1.60	0.48
1:C:4959:PHE:HD2	1:C:4985:LEU:HD22	1.78	0.48
1:A:1076:ARG:HB3	1:A:1191:VAL:HG23	1.96	0.48
1:A:3289:PRO:HA	1:A:3338:LEU:HD22	1.95	0.48
1:B:167:ASP:N	1:B:167:ASP:OD1	2.46	0.48
1:B:4561:THR:OG1	1:B:4562:LEU:N	2.45	0.48
1:B:4835:LYS:HD3	1:B:4835:LYS:HA	1.63	0.48
1:C:178:ARG:HH11	1:C:195:PHE:HA	1.78	0.48
1:C:404:ILE:HD11	1:C:478:PHE:CE1	2.49	0.48
1:D:908:VAL:O	1:D:965:TYR:OH	2.29	0.48
1:A:2316:LYS:HB3	1:A:2318:TYR:HE1	1.78	0.48
1:B:4342:ALA:O	1:B:4820:VAL:CG2	2.58	0.48
1:C:909:ASN:HB3	1:C:912:SER:HB3	1.95	0.48
1:C:3285:TRP:HZ3	1:C:3296:LEU:HD13	1.79	0.48
1:C:4679:ARG:NH1	1:C:4715:TYR:OH	2.25	0.48
1:D:178:ARG:HH11	1:D:195:PHE:HA	1.78	0.48
1:A:551:LEU:O	1:A:553:ARG:NE	2.47	0.48
1:A:1543:GLU:HB3	1:A:1544:PRO:HD3	1.96	0.48
1:A:1977:TYR:OH	1:A:1997:GLU:HB3	2.14	0.48
1:A:4087:LEU:HD22	1:A:4122:MET:HA	1.96	0.48
1:B:4679:ARG:NH1	1:B:4715:TYR:OH	2.25	0.48
1:C:3289:PRO:HA	1:C:3338:LEU:HD22	1.95	0.48
1:C:3541:ALA:O	1:C:3545:THR:N	2.43	0.48
1:D:404:ILE:HD11	1:D:478:PHE:CE1	2.49	0.48
1:D:668:VAL:O	1:D:741:GLU:N	2.37	0.48
1:A:3375:GLU:O	1:A:3379:LEU:N	2.46	0.48
1:B:404:ILE:HD11	1:B:478:PHE:CE1	2.49	0.48
1:B:3285:TRP:HZ3	1:B:3296:LEU:HD13	1.79	0.48
1:B:3302:PRO:HG2	1:B:3303:PRO:HD3	1.95	0.48
1:C:167:ASP:OD1	1:C:167:ASP:N	2.46	0.48
1:C:4325:ARG:HD2	1:C:4634:GLU:OE2	2.01	0.48
1:D:551:LEU:O	1:D:553:ARG:NE	2.47	0.48
1:D:1243:PRO:HB2	1:D:1600:LEU:HD13	1.96	0.48
1:D:2316:LYS:HB3	1:D:2318:TYR:HE1	1.78	0.48
1:A:3302:PRO:HG2	1:A:3303:PRO:HD3	1.95	0.48
1:B:3194:LEU:HD23	1:B:3194:LEU:H	1.79	0.48
1:D:971:ASP:OD1	1:D:971:ASP:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:3285:TRP:HZ3	1:D:3296:LEU:HD13	1.79	0.48
1:A:908:VAL:O	1:A:965:TYR:OH	2.29	0.48
1:A:3285:TRP:HZ3	1:A:3296:LEU:HD13	1.79	0.48
1:A:4959:PHE:HD2	1:A:4985:LEU:HD22	1.78	0.48
1:B:130:LYS:NZ	1:B:131:LEU:O	2.47	0.48
1:B:1275:ARG:O	1:B:1281:ASN:ND2	2.45	0.48
1:B:1543:GLU:HB3	1:B:1544:PRO:HD3	1.96	0.48
1:C:4550:LYS:HZ2	1:C:4550:LYS:HA	1.78	0.48
1:C:4556:SER:OG	1:C:4557:ARG:N	2.47	0.48
1:D:215:THR:OG1	1:D:271:GLY:O	2.31	0.48
1:D:1021:LEU:HD23	1:D:1021:LEU:H	1.79	0.48
1:D:4556:SER:OG	1:D:4557:ARG:N	2.47	0.48
1:B:1076:ARG:HB3	1:B:1191:VAL:HG23	1.96	0.47
1:C:103:TYR:OH	1:C:167:ASP:OD2	2.31	0.47
1:C:1543:GLU:HB3	1:C:1544:PRO:HD3	1.96	0.47
1:C:1977:TYR:OH	1:C:1997:GLU:HB3	2.14	0.47
1:C:3194:LEU:HD23	1:C:3194:LEU:H	1.79	0.47
1:D:675:LEU:HD21	1:D:1633:PRO:HB3	1.95	0.47
1:D:1275:ARG:O	1:D:1281:ASN:ND2	2.45	0.47
1:D:3015:LEU:HD23	1:D:3018:LEU:HD13	1.96	0.47
1:A:2174:GLU:OE1	1:A:2174:GLU:N	2.34	0.47
1:B:1977:TYR:OH	1:B:1997:GLU:HB3	2.14	0.47
1:B:3289:PRO:HA	1:B:3338:LEU:HD22	1.95	0.47
1:C:2587:TYR:O	1:C:2591:ARG:N	2.31	0.47
1:D:1977:TYR:OH	1:D:1997:GLU:HB3	2.14	0.47
1:D:2539:ALA:H	1:D:2584:HIS:HE1	1.62	0.47
1:D:4959:PHE:HD2	1:D:4985:LEU:HD22	1.78	0.47
1:A:2539:ALA:H	1:A:2584:HIS:HE1	1.62	0.47
1:A:4559:PHE:HD2	1:A:4560:TYR:H	1.57	0.47
1:C:840:VAL:O	1:C:1073:ARG:NH2	2.45	0.47
1:C:997:ALA:HA	1:C:1021:LEU:HD21	1.96	0.47
1:C:1243:PRO:HB2	1:C:1600:LEU:HD13	1.96	0.47
1:C:3015:LEU:HD23	1:C:3018:LEU:HD13	1.96	0.47
1:D:997:ALA:HA	1:D:1021:LEU:HD21	1.96	0.47
1:D:3555:ASN:HA	1:D:3597:GLN:HE22	1.79	0.47
1:D:4227:GLU:HG2	1:D:4229:GLU:HG3	1.95	0.47
1:A:130:LYS:NZ	1:A:131:LEU:O	2.47	0.47
1:A:276:TRP:N	1:A:338:GLU:OE1	2.39	0.47
1:A:748:LEU:HA	1:A:755:ILE:HD13	1.97	0.47
1:A:909:ASN:HB3	1:A:912:SER:HB3	1.95	0.47
1:A:997:ALA:HA	1:A:1021:LEU:HD21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1021:LEU:H	1:A:1021:LEU:HD23	1.79	0.47
1:A:1243:PRO:HB2	1:A:1600:LEU:HD13	1.96	0.47
1:A:3555:ASN:HA	1:A:3597:GLN:HE22	1.79	0.47
1:B:2316:LYS:HB3	1:B:2318:TYR:HE1	1.78	0.47
1:B:3555:ASN:HA	1:B:3597:GLN:HE22	1.79	0.47
1:C:1021:LEU:HD23	1:C:1021:LEU:H	1.79	0.47
1:C:3435:PHE:HA	1:C:3438:VAL:HG23	1.95	0.47
1:D:3302:PRO:HG2	1:D:3303:PRO:HD3	1.95	0.47
1:D:3761:GLN:C	1:D:3763:LEU:H	2.18	0.47
1:D:4087:LEU:HD22	1:D:4122:MET:HA	1.96	0.47
1:D:4679:ARG:NH1	1:D:4715:TYR:OH	2.25	0.47
1:A:404:ILE:HD11	1:A:478:PHE:CE1	2.49	0.47
1:B:909:ASN:HB3	1:B:912:SER:HB3	1.95	0.47
1:B:971:ASP:N	1:B:971:ASP:OD1	2.46	0.47
1:B:1021:LEU:HD23	1:B:1021:LEU:H	1.79	0.47
1:B:3006:ILE:HA	1:B:3056:LEU:HG	1.97	0.47
1:B:3435:PHE:HA	1:B:3438:VAL:HG23	1.95	0.47
1:B:4868:ASP:OD1	1:B:4868:ASP:N	2.48	0.47
1:C:3006:ILE:HA	1:C:3056:LEU:HG	1.97	0.47
1:D:2339:VAL:O	1:D:2435:ARG:NH2	2.31	0.47
1:A:675:LEU:HD21	1:A:1633:PRO:HB3	1.95	0.47
1:A:3554:GLN:O	1:A:3558:HIS:ND1	2.46	0.47
1:B:2539:ALA:H	1:B:2584:HIS:HE1	1.62	0.47
1:B:3949:ARG:O	1:B:3949:ARG:NH2	2.44	0.47
1:B:4548:ARG:O	1:B:4551:PHE:HD2	1.98	0.47
1:C:632:LEU:O	1:C:634:GLN:NE2	2.45	0.47
1:C:3551:GLU:O	1:C:3555:ASN:ND2	2.48	0.47
1:D:632:LEU:O	1:D:634:GLN:NE2	2.45	0.47
1:D:748:LEU:HA	1:D:755:ILE:HD13	1.97	0.47
1:A:103:TYR:OH	1:A:167:ASP:OD2	2.31	0.47
1:A:680:THR:OG1	1:A:784:SER:HB2	2.15	0.47
1:A:4548:ARG:O	1:A:4551:PHE:HD2	1.98	0.47
1:A:4868:ASP:OD1	1:A:4868:ASP:N	2.48	0.47
1:B:426:ARG:HG2	1:B:506:TYR:HA	1.96	0.47
1:B:840:VAL:O	1:B:1073:ARG:NH2	2.45	0.47
1:B:997:ALA:HA	1:B:1021:LEU:HD21	1.96	0.47
1:B:3990:VAL:HG23	1:B:4051:SER:HB3	1.97	0.47
1:B:4087:LEU:HD22	1:B:4122:MET:HA	1.96	0.47
1:C:551:LEU:O	1:C:553:ARG:NE	2.47	0.47
1:C:680:THR:OG1	1:C:784:SER:HB2	2.15	0.47
1:C:908:VAL:O	1:C:965:TYR:OH	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2539:ALA:H	1:C:2584:HIS:HE1	1.62	0.47
1:C:3990:VAL:HG23	1:C:4051:SER:HB3	1.97	0.47
1:C:4182:GLU:HG2	1:C:4192:ARG:HD3	1.96	0.47
1:C:4541:TRP:O	1:C:4544:LEU:HB2	2.15	0.47
1:D:1543:GLU:HB3	1:D:1544:PRO:HD3	1.96	0.47
1:D:3435:PHE:HA	1:D:3438:VAL:HG23	1.95	0.47
1:D:3990:VAL:HG23	1:D:4051:SER:HB3	1.97	0.47
1:D:4559:PHE:HD2	1:D:4560:TYR:H	1.57	0.47
1:A:3761:GLN:C	1:A:3763:LEU:H	2.18	0.47
1:B:551:LEU:O	1:B:553:ARG:NE	2.47	0.47
1:C:2174:GLU:OE1	1:C:2174:GLU:N	2.34	0.47
1:D:3054:VAL:O	1:D:3058:GLY:N	2.48	0.47
1:D:3551:GLU:O	1:D:3555:ASN:ND2	2.48	0.47
1:A:257:ARG:O	1:A:284:HIS:NE2	2.40	0.47
1:A:2476:ILE:HG12	1:A:2478:THR:HG23	1.97	0.47
1:A:3194:LEU:HD23	1:A:3194:LEU:H	1.79	0.47
1:A:4336:TRP:CE3	1:A:4571:PHE:HE2	2.18	0.47
1:C:178:ARG:NE	1:C:194:SER:O	2.45	0.47
1:C:3555:ASN:HA	1:C:3597:GLN:HE22	1.79	0.47
1:D:130:LYS:NZ	1:D:131:LEU:O	2.47	0.47
1:D:2476:ILE:HG12	1:D:2478:THR:HG23	1.97	0.47
1:D:3770:LEU:HD23	1:D:3804:ILE:HG12	1.97	0.47
1:D:3949:ARG:O	1:D:3949:ARG:NH2	2.44	0.47
1:D:4835:LYS:HD3	1:D:4835:LYS:HA	1.63	0.47
1:A:167:ASP:N	1:A:167:ASP:OD1	2.46	0.47
1:A:2394:GLY:H	1:A:2418:LEU:HD23	1.80	0.47
1:B:289:ARG:HG3	1:B:303:ASP:HA	1.97	0.47
1:B:1243:PRO:HB2	1:B:1600:LEU:HD13	1.96	0.47
1:B:3015:LEU:HD23	1:B:3018:LEU:HD13	1.96	0.47
1:B:3375:GLU:O	1:B:3379:LEU:N	2.46	0.47
1:B:3761:GLN:C	1:B:3763:LEU:H	2.18	0.47
1:B:4182:GLU:HG2	1:B:4192:ARG:HD3	1.96	0.47
1:B:4559:PHE:O	1:B:4561:THR:CG2	2.53	0.47
1:C:130:LYS:NZ	1:C:131:LEU:O	2.47	0.47
1:C:2394:GLY:H	1:C:2418:LEU:HD23	1.80	0.47
1:C:4868:ASP:OD1	1:C:4868:ASP:N	2.48	0.47
1:D:1076:ARG:HB3	1:D:1191:VAL:HG23	1.96	0.47
1:D:3006:ILE:HA	1:D:3056:LEU:HG	1.97	0.47
1:A:3006:ILE:HA	1:A:3056:LEU:HG	1.97	0.46
1:B:3551:GLU:O	1:B:3555:ASN:ND2	2.48	0.46
1:C:748:LEU:HA	1:C:755:ILE:HD13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3281:LEU:O	1:C:3285:TRP:N	2.49	0.46
1:C:4551:PHE:O	1:C:4552:LEU:C	2.53	0.46
1:D:680:THR:OG1	1:D:784:SER:HB2	2.15	0.46
1:A:875:ALA:HA	1:A:878:ILE:HD12	1.97	0.46
1:A:3015:LEU:HD23	1:A:3018:LEU:HD13	1.96	0.46
1:A:3990:VAL:HG23	1:A:4051:SER:HB3	1.97	0.46
1:A:4182:GLU:HG2	1:A:4192:ARG:HD3	1.96	0.46
1:A:4550:LYS:HA	1:A:4550:LYS:HZ2	1.80	0.46
1:B:512:ALA:HA	1:B:515:TRP:HB2	1.98	0.46
1:B:680:THR:OG1	1:B:784:SER:HB2	2.15	0.46
1:B:748:LEU:HA	1:B:755:ILE:HD13	1.97	0.46
1:C:1076:ARG:HB3	1:C:1191:VAL:HG23	1.96	0.46
1:D:289:ARG:HG3	1:D:303:ASP:HA	1.97	0.46
1:D:4541:TRP:O	1:D:4544:LEU:HB2	2.15	0.46
1:B:683:ARG:HB2	1:B:782:SER:HB3	1.97	0.46
1:B:1283:LEU:H	1:B:1283:LEU:HD23	1.80	0.46
1:B:3541:ALA:O	1:B:3545:THR:N	2.43	0.46
1:B:4559:PHE:HD2	1:B:4560:TYR:H	1.57	0.46
1:C:875:ALA:HA	1:C:878:ILE:HD12	1.97	0.46
1:C:3054:VAL:O	1:C:3058:GLY:N	2.48	0.46
1:C:4087:LEU:HD22	1:C:4122:MET:HA	1.96	0.46
1:D:2394:GLY:H	1:D:2418:LEU:HD23	1.80	0.46
1:D:2440:MET:SD	1:D:2508:ARG:NH2	2.84	0.46
1:D:3194:LEU:HD23	1:D:3194:LEU:H	1.79	0.46
1:D:4182:GLU:HG2	1:D:4192:ARG:HD3	1.96	0.46
1:A:2418:LEU:O	1:A:2422:ILE:HG12	2.16	0.46
1:A:3551:GLU:O	1:A:3555:ASN:ND2	2.48	0.46
1:A:3770:LEU:HD23	1:A:3804:ILE:HG12	1.97	0.46
1:A:4561:THR:OG1	1:A:4562:LEU:N	2.45	0.46
1:B:293:LEU:HD13	1:B:378:LEU:HG	1.97	0.46
1:B:870:ILE:HG12	1:B:1051:TYR:HE2	1.81	0.46
1:B:1574:PRO:HD3	1:B:1587:PRO:HA	1.97	0.46
1:C:426:ARG:HG2	1:C:506:TYR:HA	1.96	0.46
1:C:1574:PRO:HD3	1:C:1587:PRO:HA	1.97	0.46
1:C:4222:VAL:HG11	1:C:4950:VAL:HG23	1.98	0.46
1:D:683:ARG:HB2	1:D:782:SER:HB3	1.97	0.46
1:D:4548:ARG:O	1:D:4551:PHE:HD2	1.98	0.46
1:A:289:ARG:HG3	1:A:303:ASP:HA	1.97	0.46
1:A:293:LEU:HD13	1:A:378:LEU:HG	1.97	0.46
1:A:683:ARG:HB2	1:A:782:SER:HB3	1.97	0.46
1:B:2318:TYR:OH	1:B:2414:ASN:N	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3054:VAL:O	1:B:3058:GLY:N	2.48	0.46
1:B:4325:ARG:NH1	1:B:4639:MET:SD	2.84	0.46
1:B:4541:TRP:O	1:B:4544:LEU:HB2	2.15	0.46
1:C:289:ARG:HG3	1:C:303:ASP:HA	1.97	0.46
1:C:3770:LEU:HD23	1:C:3804:ILE:HG12	1.97	0.46
1:B:103:TYR:OH	1:B:167:ASP:OD2	2.31	0.46
1:B:3201:MET:HE3	1:B:3204:ALA:HB3	1.98	0.46
1:B:4556:SER:OG	1:B:4557:ARG:N	2.47	0.46
1:C:1225:PRO:HG2	1:C:1228:ILE:HD13	1.98	0.46
1:D:426:ARG:HG2	1:D:506:TYR:HA	1.96	0.46
1:D:4235:VAL:HG11	1:D:5019:TRP:CH2	2.51	0.46
1:A:3201:MET:HE3	1:A:3204:ALA:HB3	1.98	0.46
1:A:4559:PHE:O	1:A:4561:THR:CG2	2.53	0.46
1:B:103:TYR:HE1	1:B:163:VAL:HA	1.81	0.46
1:B:908:VAL:O	1:B:965:TYR:OH	2.29	0.46
1:B:2394:GLY:H	1:B:2418:LEU:HD23	1.80	0.46
1:C:715:GLY:HA3	1:C:722:TRP:HB2	1.97	0.46
1:C:2318:TYR:OH	1:C:2414:ASN:N	2.46	0.46
1:D:1225:PRO:HG2	1:D:1228:ILE:HD13	1.98	0.46
1:D:3375:GLU:O	1:D:3379:LEU:N	2.46	0.46
1:A:835:ARG:NH1	1:A:1212:ARG:HH11	2.13	0.46
1:A:1499:ASP:OD1	1:A:1499:ASP:N	2.49	0.46
1:A:4235:VAL:HG11	1:A:5019:TRP:CH2	2.51	0.46
1:B:257:ARG:O	1:B:284:HIS:NE2	2.40	0.46
1:B:835:ARG:NH1	1:B:1212:ARG:HH11	2.13	0.46
1:B:948:ASP:N	1:B:948:ASP:OD1	2.49	0.46
1:B:3554:GLN:O	1:B:3558:HIS:ND1	2.46	0.46
1:B:4235:VAL:HG11	1:B:5019:TRP:CH2	2.51	0.46
1:C:103:TYR:HE1	1:C:163:VAL:HA	1.81	0.46
1:C:835:ARG:NH1	1:C:1212:ARG:HH11	2.13	0.46
1:C:1499:ASP:N	1:C:1499:ASP:OD1	2.49	0.46
1:C:4235:VAL:HG11	1:C:5019:TRP:CH2	2.51	0.46
1:C:4548:ARG:O	1:C:4551:PHE:HD2	1.98	0.46
1:D:3281:LEU:O	1:D:3285:TRP:N	2.49	0.46
1:D:4222:VAL:HG11	1:D:4950:VAL:HG23	1.98	0.46
1:A:2003:GLN:OE1	1:A:3656:SER:OG	2.30	0.46
1:B:715:GLY:HA3	1:B:722:TRP:HB2	1.97	0.46
1:B:875:ALA:HA	1:B:878:ILE:HD12	1.97	0.46
1:C:1164:LEU:O	1:C:1167:GLU:HG3	2.16	0.46
1:C:2476:ILE:HG12	1:C:2478:THR:HG23	1.97	0.46
1:C:2477:PRO:HB3	1:C:2489:LYS:H	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:27:THR:HG22	1:D:32:GLN:HA	1.98	0.46
1:D:512:ALA:HA	1:D:515:TRP:HB2	1.98	0.46
1:D:875:ALA:HA	1:D:878:ILE:HD12	1.97	0.46
1:D:884:LEU:HD22	1:D:969:PRO:HB3	1.98	0.46
1:A:4541:TRP:O	1:A:4544:LEU:HB2	2.15	0.46
1:B:1716:ILE:HD11	1:B:1844:LEU:HA	1.98	0.46
1:B:2440:MET:SD	1:B:2508:ARG:NH2	2.84	0.46
1:B:2476:ILE:HG12	1:B:2478:THR:HG23	1.97	0.46
1:B:4726:ASP:OD1	1:B:4727:LYS:N	2.49	0.46
1:C:1283:LEU:HD23	1:C:1283:LEU:H	1.80	0.46
1:C:2418:LEU:O	1:C:2422:ILE:HG12	2.16	0.46
1:C:4559:PHE:HD2	1:C:4560:TYR:H	1.57	0.46
1:D:103:TYR:HE1	1:D:163:VAL:HA	1.81	0.46
1:D:4726:ASP:OD1	1:D:4727:LYS:N	2.49	0.46
1:A:4342:ALA:O	1:A:4820:VAL:CG2	2.58	0.45
1:A:4687:TYR:OH	1:A:4702:ASP:OD1	2.34	0.45
1:B:3770:LEU:HD23	1:B:3804:ILE:HG12	1.97	0.45
1:C:404:ILE:HD11	1:C:478:PHE:CD1	2.51	0.45
1:C:870:ILE:HG12	1:C:1051:TYR:HE2	1.81	0.45
1:C:4325:ARG:NH1	1:C:4639:MET:SD	2.84	0.45
1:C:4687:TYR:OH	1:C:4702:ASP:OD1	2.34	0.45
1:D:2477:PRO:HB3	1:D:2489:LYS:H	1.81	0.45
1:D:4561:THR:OG1	1:D:4562:LEU:N	2.45	0.45
1:A:426:ARG:HG2	1:A:506:TYR:HA	1.96	0.45
1:A:2131:LEU:HD22	1:A:3662:ILE:HD12	1.99	0.45
1:A:4726:ASP:OD1	1:A:4727:LYS:N	2.49	0.45
1:B:404:ILE:HD11	1:B:478:PHE:CD1	2.51	0.45
1:B:1164:LEU:O	1:B:1167:GLU:HG3	2.16	0.45
1:B:1667:LEU:HD21	1:B:1711:TYR:CE1	2.52	0.45
1:C:27:THR:HG22	1:C:32:GLN:HA	1.98	0.45
1:C:582:HIS:O	1:C:585:SER:OG	2.27	0.45
1:C:668:VAL:O	1:C:741:GLU:N	2.37	0.45
1:C:884:LEU:HD22	1:C:969:PRO:HB3	1.98	0.45
1:C:4561:THR:OG1	1:C:4562:LEU:N	2.45	0.45
1:C:4726:ASP:OD1	1:C:4727:LYS:N	2.49	0.45
1:D:1283:LEU:HD23	1:D:1283:LEU:H	1.80	0.45
1:D:2967:MET:HG2	1:D:3037:GLU:OE2	2.16	0.45
1:D:4342:ALA:O	1:D:4820:VAL:CG2	2.58	0.45
1:A:103:TYR:HE1	1:A:163:VAL:HA	1.81	0.45
1:A:1228:ILE:HD11	1:D:3572:GLN:OE1	2.17	0.45
1:A:4222:VAL:HG11	1:A:4950:VAL:HG23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4325:ARG:NH1	1:A:4639:MET:SD	2.84	0.45
1:B:1499:ASP:OD1	1:B:1499:ASP:N	2.49	0.45
1:B:2418:LEU:O	1:B:2422:ILE:HG12	2.16	0.45
1:B:2967:MET:HG2	1:B:3037:GLU:OE2	2.16	0.45
1:B:4687:TYR:HE1	1:B:4703:ARG:HE	1.65	0.45
1:C:683:ARG:HB2	1:C:782:SER:HB3	1.97	0.45
1:C:2967:MET:HG2	1:C:3037:GLU:OE2	2.16	0.45
1:D:293:LEU:HD13	1:D:378:LEU:HG	1.97	0.45
1:D:1716:ILE:HD11	1:D:1844:LEU:HA	1.98	0.45
1:D:2423:MET:SD	1:D:2498:HIS:ND1	2.80	0.45
1:D:4687:TYR:HE1	1:D:4703:ARG:HE	1.65	0.45
1:A:404:ILE:HD11	1:A:478:PHE:CD1	2.51	0.45
1:A:2967:MET:HG2	1:A:3037:GLU:OE2	2.16	0.45
1:B:884:LEU:HD22	1:B:969:PRO:HB3	1.98	0.45
1:B:2131:LEU:HD22	1:B:3662:ILE:HD12	1.99	0.45
1:B:2191:PHE:CD1	1:B:2198:MET:HG3	2.51	0.45
1:C:750:LEU:HD12	1:C:751:SER:N	2.32	0.45
1:C:3228:ALA:HB1	1:C:3302:PRO:HB3	1.99	0.45
1:D:1499:ASP:OD1	1:D:1499:ASP:N	2.49	0.45
1:D:1574:PRO:HD3	1:D:1587:PRO:HA	1.97	0.45
1:A:512:ALA:HA	1:A:515:TRP:HB2	1.98	0.45
1:A:870:ILE:HG12	1:A:1051:TYR:HE2	1.81	0.45
1:A:1574:PRO:HD3	1:A:1587:PRO:HA	1.97	0.45
1:A:2191:PHE:CD1	1:A:2198:MET:HG3	2.51	0.45
1:C:1667:LEU:HD21	1:C:1711:TYR:CE1	2.52	0.45
1:C:1716:ILE:HD11	1:C:1844:LEU:HA	1.98	0.45
1:C:2191:PHE:CD1	1:C:2198:MET:HG3	2.51	0.45
1:C:4687:TYR:HE1	1:C:4703:ARG:HE	1.65	0.45
1:D:2131:LEU:HD22	1:D:3662:ILE:HD12	1.99	0.45
1:D:3657:TYR:CZ	1:D:3660:ALA:HB3	2.52	0.45
1:A:1164:LEU:O	1:A:1167:GLU:HG3	2.16	0.45
1:A:4581:LYS:HD3	1:A:4582:VAL:H	1.82	0.45
1:B:1176:GLU:O	1:B:1180:ARG:NH2	2.33	0.45
1:B:2342:ASN:OD1	1:B:2342:ASN:N	2.50	0.45
1:B:2477:PRO:HB3	1:B:2489:LYS:H	1.81	0.45
1:C:4581:LYS:HD3	1:C:4582:VAL:H	1.82	0.45
1:D:715:GLY:HA3	1:D:722:TRP:HB2	1.97	0.45
1:D:870:ILE:HG12	1:D:1051:TYR:HE2	1.81	0.45
1:D:2009:LEU:HD12	1:D:2009:LEU:HA	1.79	0.45
1:D:4687:TYR:OH	1:D:4702:ASP:OD1	2.34	0.45
1:D:4820:VAL:CG1	1:D:4823:LEU:HD23	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3572:GLN:OE1	1:B:1228:ILE:HD11	2.17	0.45
1:C:512:ALA:HA	1:C:515:TRP:HB2	1.98	0.45
1:C:3761:GLN:C	1:C:3763:LEU:H	2.18	0.45
1:D:103:TYR:OH	1:D:167:ASP:OD2	2.31	0.45
1:D:2418:LEU:O	1:D:2422:ILE:HG12	2.16	0.45
1:D:4967:TYR:OH	1:D:5033:GLU:OE2	2.28	0.45
1:A:221:ARG:NE	1:A:253:CYS:O	2.50	0.45
1:A:1225:PRO:HG2	1:A:1228:ILE:HD13	1.98	0.45
1:A:1644:GLU:HG2	1:A:1646:ARG:HE	1.81	0.45
1:A:3878:ASP:N	1:A:3878:ASP:OD1	2.50	0.45
1:A:4325:ARG:HD2	1:A:4634:GLU:OE2	2.01	0.45
1:B:3228:ALA:HB1	1:B:3302:PRO:HB3	1.99	0.45
1:B:4826:ILE:HD12	1:C:4839:MET:HE3	1.97	0.45
1:C:293:LEU:HD13	1:C:378:LEU:HG	1.97	0.45
1:C:2579:VAL:HG11	1:C:2632:ILE:HD11	1.98	0.45
1:C:4342:ALA:O	1:C:4820:VAL:CG2	2.58	0.45
1:D:4550:LYS:HA	1:D:4550:LYS:HZ2	1.82	0.45
1:A:2342:ASN:OD1	1:A:2342:ASN:N	2.50	0.45
1:A:2579:VAL:HG11	1:A:2632:ILE:HD11	1.98	0.45
1:A:4839:MET:CE	1:D:4826:ILE:HD12	2.47	0.45
1:B:27:THR:HG22	1:B:32:GLN:HA	1.98	0.45
1:B:317:ARG:HH11	1:B:317:ARG:HA	1.82	0.45
1:B:4551:PHE:O	1:B:4552:LEU:C	2.53	0.45
1:C:3572:GLN:OE1	1:D:1228:ILE:HD11	2.17	0.45
1:D:404:ILE:HD11	1:D:478:PHE:CD1	2.51	0.45
1:D:1644:GLU:HG2	1:D:1646:ARG:HE	1.81	0.45
1:D:4325:ARG:NH1	1:D:4639:MET:SD	2.84	0.45
1:A:27:THR:HG22	1:A:32:GLN:HA	1.98	0.45
1:A:1283:LEU:HD23	1:A:1283:LEU:H	1.80	0.45
1:A:2009:LEU:HD12	1:A:2009:LEU:HA	1.79	0.45
1:A:4551:PHE:O	1:A:4552:LEU:C	2.53	0.45
1:B:582:HIS:O	1:B:585:SER:OG	2.27	0.45
1:B:1225:PRO:HG2	1:B:1228:ILE:HD13	1.98	0.45
1:B:2316:LYS:HB3	1:B:2318:TYR:CE1	2.52	0.45
1:B:2423:MET:SD	1:B:2498:HIS:ND1	2.80	0.45
1:C:221:ARG:NE	1:C:253:CYS:O	2.50	0.45
1:C:948:ASP:OD1	1:C:948:ASP:N	2.49	0.45
1:C:3878:ASP:N	1:C:3878:ASP:OD1	2.50	0.45
1:C:4826:ILE:HD12	1:D:4839:MET:CE	2.47	0.45
1:D:340:LYS:O	1:D:344:SER:OG	2.20	0.45
1:D:1164:LEU:O	1:D:1167:GLU:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:3228:ALA:HB1	1:D:3302:PRO:HB3	1.99	0.45
1:D:4106:PRO:O	1:D:4109:GLN:NE2	2.50	0.45
1:D:4581:LYS:HD3	1:D:4582:VAL:H	1.82	0.45
1:A:1667:LEU:HD21	1:A:1711:TYR:CE1	2.52	0.44
1:A:4556:SER:OG	1:A:4557:ARG:N	2.47	0.44
1:B:3657:TYR:CZ	1:B:3660:ALA:HB3	2.52	0.44
1:B:4106:PRO:O	1:B:4109:GLN:NE2	2.50	0.44
1:C:317:ARG:HA	1:C:317:ARG:HH11	1.82	0.44
1:D:424:LYS:HE2	1:D:424:LYS:HB2	1.80	0.44
1:D:835:ARG:NH1	1:D:1212:ARG:HH11	2.13	0.44
1:D:867:LEU:HD21	1:D:939:VAL:HB	1.99	0.44
1:D:2316:LYS:HB3	1:D:2318:TYR:CE1	2.52	0.44
1:D:2579:VAL:HG11	1:D:2632:ILE:HD11	1.98	0.44
1:A:867:LEU:HD21	1:A:939:VAL:HB	1.99	0.44
1:A:3368:ARG:O	1:A:3372:VAL:N	2.48	0.44
1:B:424:LYS:HE2	1:B:424:LYS:HB2	1.80	0.44
1:B:626:LEU:HG	1:B:628:GLY:H	1.81	0.44
1:B:4222:VAL:HG11	1:B:4950:VAL:HG23	1.98	0.44
1:B:4581:LYS:HD3	1:B:4582:VAL:H	1.82	0.44
1:C:323:LEU:HD23	1:C:323:LEU:H	1.82	0.44
1:C:340:LYS:O	1:C:344:SER:OG	2.20	0.44
1:C:2131:LEU:HD22	1:C:3662:ILE:HD12	1.99	0.44
1:C:4820:VAL:CG1	1:C:4823:LEU:HD23	2.47	0.44
1:D:2463:LEU:HD12	1:D:2463:LEU:HA	1.88	0.44
1:D:4154:VAL:O	1:D:4154:VAL:HG13	2.17	0.44
1:A:715:GLY:HA3	1:A:722:TRP:HB2	1.97	0.44
1:A:2316:LYS:HB3	1:A:2318:TYR:CE1	2.52	0.44
1:A:3228:ALA:HB1	1:A:3302:PRO:HB3	1.99	0.44
1:A:3281:LEU:O	1:A:3285:TRP:N	2.49	0.44
1:A:4687:TYR:HE1	1:A:4703:ARG:HE	1.65	0.44
1:B:750:LEU:HD12	1:B:751:SER:N	2.32	0.44
1:B:1644:GLU:HG2	1:B:1646:ARG:HE	1.81	0.44
1:B:3572:GLN:OE1	1:C:1228:ILE:HD11	2.17	0.44
1:B:4820:VAL:CG1	1:B:4823:LEU:HD23	2.47	0.44
1:B:4826:ILE:HD12	1:C:4839:MET:CE	2.47	0.44
1:C:3657:TYR:CZ	1:C:3660:ALA:HB3	2.52	0.44
1:C:4154:VAL:HG13	1:C:4154:VAL:O	2.17	0.44
1:D:323:LEU:HD23	1:D:323:LEU:H	1.82	0.44
1:A:884:LEU:HD22	1:A:969:PRO:HB3	1.98	0.44
1:A:1716:ILE:HD11	1:A:1844:LEU:HA	1.98	0.44
1:A:3577:ARG:HH12	1:B:1209:SER:HA	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3577:ARG:HH12	1:C:1209:SER:HA	1.83	0.44
1:C:626:LEU:HG	1:C:628:GLY:H	1.81	0.44
1:C:1644:GLU:HG2	1:C:1646:ARG:HE	1.81	0.44
1:C:3577:ARG:HH12	1:D:1209:SER:HA	1.83	0.44
1:D:276:TRP:N	1:D:338:GLU:OE1	2.39	0.44
1:D:3541:ALA:O	1:D:3545:THR:N	2.43	0.44
1:A:750:LEU:HD12	1:A:751:SER:N	2.32	0.44
1:A:4154:VAL:O	1:A:4154:VAL:HG13	2.17	0.44
1:A:4873:ASP:OD1	1:A:4873:ASP:N	2.50	0.44
1:B:221:ARG:NE	1:B:253:CYS:O	2.50	0.44
1:D:626:LEU:HG	1:D:628:GLY:H	1.81	0.44
1:D:3201:MET:HE3	1:D:3204:ALA:HB3	1.99	0.44
1:D:4868:ASP:N	1:D:4868:ASP:OD1	2.48	0.44
1:A:317:ARG:HA	1:A:317:ARG:HH11	1.82	0.44
1:A:2477:PRO:HB3	1:A:2489:LYS:H	1.81	0.44
1:A:3657:TYR:CZ	1:A:3660:ALA:HB3	2.52	0.44
1:B:1189:LEU:HD12	1:B:1190:PRO:HD2	1.99	0.44
1:B:4551:PHE:CD2	1:B:4552:LEU:N	2.86	0.44
1:C:626:LEU:HG	1:C:628:GLY:N	2.33	0.44
1:C:2001:PRO:HD2	1:C:2004:GLU:HB2	2.00	0.44
1:C:2342:ASN:OD1	1:C:2342:ASN:N	2.50	0.44
1:C:3147:ILE:HG23	1:C:3197:LEU:HD21	2.00	0.44
1:C:4835:LYS:HD3	1:C:4835:LYS:HA	1.63	0.44
1:D:4212:GLU:OE2	1:D:4215:ARG:NH2	2.51	0.44
1:D:4557:ARG:HA	1:D:4557:ARG:HD3	1.78	0.44
1:A:877:ASN:ND2	1:A:880:GLU:OE1	2.51	0.44
1:A:1491:ASN:OD1	1:A:1491:ASN:N	2.51	0.44
1:A:3054:VAL:O	1:A:3058:GLY:N	2.48	0.44
1:A:4212:GLU:OE2	1:A:4215:ARG:NH2	2.51	0.44
1:B:2579:VAL:HG11	1:B:2632:ILE:HD11	1.98	0.44
1:B:4212:GLU:OE2	1:B:4215:ARG:NH2	2.51	0.44
1:C:1189:LEU:HD12	1:C:1190:PRO:HD2	1.99	0.44
1:C:1491:ASN:OD1	1:C:1491:ASN:N	2.51	0.44
1:C:3242:ASP:HB2	1:C:3267:PRO:HB3	2.00	0.44
1:D:750:LEU:HD12	1:D:751:SER:N	2.32	0.44
1:A:1215:ALA:C	1:A:1219:LEU:HD22	2.38	0.44
1:A:4826:ILE:HD12	1:B:4839:MET:CE	2.47	0.44
1:C:681:HIS:ND1	1:C:784:SER:OG	2.51	0.44
1:C:1176:GLU:O	1:C:1180:ARG:NH2	2.33	0.44
1:C:4551:PHE:CD2	1:C:4552:LEU:N	2.86	0.44
1:D:681:HIS:ND1	1:D:784:SER:OG	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:877:ASN:ND2	1:D:880:GLU:OE1	2.51	0.44
1:A:626:LEU:HG	1:A:628:GLY:H	1.81	0.44
1:A:2021:CYS:SG	1:A:2023:LEU:HB2	2.58	0.44
1:B:255:HIS:CG	1:B:480:GLU:HG3	2.53	0.44
1:B:323:LEU:H	1:B:323:LEU:HD23	1.82	0.44
1:B:3020:THR:HB	1:B:3021:PRO:HD3	2.00	0.44
1:C:3375:GLU:O	1:C:3379:LEU:N	2.46	0.44
1:D:1667:LEU:HD21	1:D:1711:TYR:CE1	2.52	0.44
1:A:582:HIS:O	1:A:585:SER:OG	2.27	0.43
1:A:753:PRO:HB2	1:A:770:ALA:H	1.83	0.43
1:B:1215:ALA:C	1:B:1219:LEU:HD22	2.38	0.43
1:B:4687:TYR:OH	1:B:4702:ASP:OD1	2.34	0.43
1:C:2021:CYS:SG	1:C:2023:LEU:HB2	2.58	0.43
1:C:2316:LYS:HB3	1:C:2318:TYR:CE1	2.52	0.43
1:C:4212:GLU:OE2	1:C:4215:ARG:NH2	2.51	0.43
1:D:221:ARG:NE	1:D:253:CYS:O	2.50	0.43
1:D:1152:MET:N	1:D:1161:ILE:O	2.51	0.43
1:D:1215:ALA:C	1:D:1219:LEU:HD22	2.38	0.43
1:D:2001:PRO:HD2	1:D:2004:GLU:HB2	2.00	0.43
1:D:4060:LYS:HA	1:D:4060:LYS:HD2	1.77	0.43
1:A:214:VAL:HG12	1:A:339:ILE:HB	2.00	0.43
1:A:323:LEU:HD23	1:A:323:LEU:H	1.82	0.43
1:A:2440:MET:SD	1:A:2508:ARG:NH2	2.84	0.43
1:A:3147:ILE:HG23	1:A:3197:LEU:HD21	2.00	0.43
1:A:4820:VAL:CG1	1:A:4823:LEU:HD23	2.47	0.43
1:B:681:HIS:ND1	1:B:784:SER:OG	2.51	0.43
1:B:1491:ASN:OD1	1:B:1491:ASN:N	2.51	0.43
1:B:2021:CYS:SG	1:B:2023:LEU:HB2	2.58	0.43
1:C:2003:GLN:OE1	1:C:3656:SER:OG	2.30	0.43
1:C:3020:THR:HB	1:C:3021:PRO:HD3	2.00	0.43
1:D:1189:LEU:HD12	1:D:1190:PRO:HD2	1.99	0.43
1:A:1189:LEU:HD12	1:A:1190:PRO:HD2	1.99	0.43
1:A:4106:PRO:O	1:A:4109:GLN:NE2	2.50	0.43
1:B:626:LEU:HG	1:B:628:GLY:N	2.33	0.43
1:B:3147:ILE:HG23	1:B:3197:LEU:HD21	2.00	0.43
1:B:3281:LEU:O	1:B:3285:TRP:N	2.49	0.43
1:B:3843:ASP:OD1	1:B:3845:ASN:N	2.51	0.43
1:B:3996:PHE:O	1:B:4000:MET:HG2	2.18	0.43
1:C:4826:ILE:HD12	1:D:4839:MET:HE3	2.00	0.43
1:C:5035:GLN:O	1:C:5036:LEU:HD22	2.18	0.43
1:D:255:HIS:CG	1:D:480:GLU:HG3	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2142:TYR:CG	1:A:2197:LEU:HD13	2.54	0.43
1:B:5035:GLN:O	1:B:5036:LEU:HD22	2.18	0.43
1:C:610:ASN:N	1:C:610:ASN:OD1	2.52	0.43
1:C:867:LEU:HD21	1:C:939:VAL:HB	1.99	0.43
1:C:2121:PHE:CD2	1:C:3701:LEU:HD13	2.54	0.43
1:C:2440:MET:SD	1:C:2508:ARG:NH2	2.84	0.43
1:C:3996:PHE:O	1:C:4000:MET:HG2	2.18	0.43
1:C:4542:GLY:O	1:C:4546:VAL:HG23	2.19	0.43
1:D:610:ASN:OD1	1:D:610:ASN:N	2.52	0.43
1:D:626:LEU:HG	1:D:628:GLY:N	2.33	0.43
1:D:2021:CYS:SG	1:D:2023:LEU:HB2	2.58	0.43
1:D:2357:LEU:HD12	1:D:2357:LEU:HA	1.89	0.43
1:D:3878:ASP:N	1:D:3878:ASP:OD1	2.50	0.43
1:A:626:LEU:HG	1:A:628:GLY:N	2.33	0.43
1:A:2967:MET:SD	1:A:2968:ASP:N	2.92	0.43
1:B:2538:THR:OG1	1:B:2539:ALA:N	2.52	0.43
1:B:4154:VAL:O	1:B:4154:VAL:HG13	2.17	0.43
1:C:759:ILE:HG22	1:C:760:ASN:N	2.34	0.43
1:C:1152:MET:N	1:C:1161:ILE:O	2.51	0.43
1:C:1177:THR:O	1:C:1180:ARG:NH1	2.48	0.43
1:C:1215:ALA:C	1:C:1219:LEU:HD22	2.38	0.43
1:C:4578:LEU:HA	1:D:4879:MET:HG2	2.00	0.43
1:D:214:VAL:HG12	1:D:339:ILE:HB	2.00	0.43
1:D:2121:PHE:CD2	1:D:3701:LEU:HD13	2.54	0.43
1:D:3996:PHE:O	1:D:4000:MET:HG2	2.18	0.43
1:A:3292:PRO:O	1:A:3294:PRO:HD3	2.19	0.43
1:A:4060:LYS:HA	1:A:4060:LYS:HD2	1.77	0.43
1:A:4551:PHE:CD2	1:A:4552:LEU:N	2.86	0.43
1:A:4835:LYS:HD3	1:A:4835:LYS:HA	1.63	0.43
1:A:4945:ASP:O	1:A:4948:GLU:HG3	2.19	0.43
1:B:753:PRO:HB2	1:B:770:ALA:H	1.83	0.43
1:B:867:LEU:HD21	1:B:939:VAL:HB	1.99	0.43
1:B:877:ASN:ND2	1:B:880:GLU:OE1	2.51	0.43
1:B:2121:PHE:CD2	1:B:3701:LEU:HD13	2.54	0.43
1:B:3242:ASP:HB2	1:B:3267:PRO:HB3	2.00	0.43
1:B:3878:ASP:OD1	1:B:3878:ASP:N	2.50	0.43
1:C:571:SER:O	1:C:574:VAL:HG12	2.19	0.43
1:D:1491:ASN:OD1	1:D:1491:ASN:N	2.51	0.43
1:D:2967:MET:SD	1:D:2968:ASP:N	2.92	0.43
1:D:3722:TYR:CZ	1:D:3782:MET:HE1	2.53	0.43
1:D:4551:PHE:CD2	1:D:4552:LEU:N	2.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4702:ASP:OD1	1:D:4702:ASP:N	2.52	0.43
1:A:681:HIS:ND1	1:A:784:SER:OG	2.51	0.43
1:A:3780:LEU:HD12	1:A:3780:LEU:HA	1.91	0.43
1:A:4578:LEU:HA	1:B:4879:MET:HG2	2.00	0.43
1:A:5035:GLN:O	1:A:5036:LEU:HD22	2.18	0.43
1:B:526:LEU:O	1:B:530:ILE:HG12	2.19	0.43
1:B:610:ASN:OD1	1:B:610:ASN:N	2.52	0.43
1:B:1717:SER:HA	1:B:1721:GLU:HB2	2.01	0.43
1:B:2142:TYR:CG	1:B:2197:LEU:HD13	2.54	0.43
1:B:4945:ASP:O	1:B:4948:GLU:HG3	2.19	0.43
1:C:753:PRO:HB2	1:C:770:ALA:H	1.83	0.43
1:C:805:PRO:HA	1:C:806:PRO:HD3	1.92	0.43
1:C:877:ASN:ND2	1:C:880:GLU:OE1	2.51	0.43
1:C:3201:MET:HE3	1:C:3204:ALA:HB3	2.00	0.43
1:C:3566:SER:O	1:C:3571:TRP:HB2	2.19	0.43
1:D:801:LYS:HE2	1:D:801:LYS:HB2	1.77	0.43
1:D:2003:GLN:OE1	1:D:3656:SER:OG	2.30	0.43
1:D:2336:ARG:HG2	1:D:2340:PHE:HB2	2.00	0.43
1:D:3242:ASP:HB2	1:D:3267:PRO:HB3	2.00	0.43
1:D:4542:GLY:O	1:D:4546:VAL:HG23	2.19	0.43
1:A:526:LEU:O	1:A:530:ILE:HG12	2.19	0.43
1:A:759:ILE:HG22	1:A:760:ASN:N	2.34	0.43
1:A:1152:MET:N	1:A:1161:ILE:O	2.51	0.43
1:A:3996:PHE:O	1:A:4000:MET:HG2	2.18	0.43
1:A:4542:GLY:O	1:A:4546:VAL:HG23	2.19	0.43
1:B:214:VAL:HG12	1:B:339:ILE:HB	2.00	0.43
1:B:675:LEU:HD12	1:B:675:LEU:HA	1.92	0.43
1:B:759:ILE:HG22	1:B:760:ASN:H	1.84	0.43
1:B:2967:MET:SD	1:B:2968:ASP:N	2.92	0.43
1:B:4705:VAL:O	1:B:4708:THR:HG22	2.19	0.43
1:C:255:HIS:CG	1:C:480:GLU:HG3	2.53	0.43
1:C:3292:PRO:O	1:C:3294:PRO:HD3	2.19	0.43
1:D:759:ILE:HG22	1:D:760:ASN:N	2.34	0.43
1:D:1430:THR:O	1:D:1431:THR:OG1	2.37	0.43
1:D:3566:SER:O	1:D:3571:TRP:HB2	2.19	0.43
1:A:610:ASN:OD1	1:A:610:ASN:N	2.52	0.43
1:A:1209:SER:HA	1:D:3577:ARG:HH12	1.83	0.43
1:A:3843:ASP:OD1	1:A:3845:ASN:N	2.51	0.43
1:B:1177:THR:O	1:B:1180:ARG:NH1	2.48	0.43
1:D:317:ARG:HA	1:D:317:ARG:HH11	1.82	0.43
1:D:4544:LEU:HB3	1:D:4548:ARG:HH12	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:VAL:HG21	1:A:257:ARG:HH21	1.84	0.43
1:A:571:SER:O	1:A:574:VAL:HG12	2.19	0.43
1:A:801:LYS:HE2	1:A:801:LYS:HB2	1.77	0.43
1:A:1430:THR:O	1:A:1431:THR:OG1	2.37	0.43
1:A:4679:ARG:NH1	1:A:4715:TYR:OH	2.25	0.43
1:B:3292:PRO:O	1:B:3294:PRO:HD3	2.19	0.43
1:B:4631:PHE:HE2	1:B:4640:GLU:HA	1.84	0.43
1:C:2142:TYR:CG	1:C:2197:LEU:HD13	2.54	0.43
1:C:2336:ARG:HG2	1:C:2340:PHE:HB2	2.00	0.43
1:C:3843:ASP:OD1	1:C:3845:ASN:N	2.51	0.43
1:D:753:PRO:HB2	1:D:770:ALA:H	1.83	0.43
1:D:948:ASP:N	1:D:948:ASP:OD1	2.49	0.43
1:D:2191:PHE:CD1	1:D:2198:MET:HG3	2.51	0.43
1:D:2342:ASN:OD1	1:D:2342:ASN:N	2.50	0.43
1:D:3020:THR:HB	1:D:3021:PRO:HD3	2.00	0.43
1:D:3147:ILE:HG23	1:D:3197:LEU:HD21	2.00	0.43
1:D:4690:GLU:OE1	1:D:4690:GLU:N	2.52	0.43
1:A:255:HIS:CG	1:A:480:GLU:HG3	2.53	0.42
1:A:2001:PRO:HD2	1:A:2004:GLU:HB2	2.00	0.42
1:B:616:SER:O	1:B:620:LEU:HG	2.20	0.42
1:B:710:ASP:OD1	1:B:710:ASP:N	2.52	0.42
1:B:2001:PRO:HD2	1:B:2004:GLU:HB2	2.00	0.42
1:D:4024:VAL:HG23	1:D:4146:LEU:HD22	2.01	0.42
1:D:4705:VAL:O	1:D:4708:THR:HG22	2.19	0.42
1:D:4945:ASP:O	1:D:4948:GLU:HG3	2.19	0.42
1:A:1717:SER:HA	1:A:1721:GLU:HB2	2.01	0.42
1:A:2423:MET:SD	1:A:2498:HIS:ND1	2.80	0.42
1:A:3242:ASP:HB2	1:A:3267:PRO:HB3	2.00	0.42
1:A:4790:LEU:HD23	1:A:4790:LEU:HA	1.90	0.42
1:A:4879:MET:HG2	1:D:4578:LEU:HA	2.00	0.42
1:C:214:VAL:HG12	1:C:339:ILE:HB	2.00	0.42
1:C:1430:THR:O	1:C:1431:THR:OG1	2.37	0.42
1:C:1717:SER:HA	1:C:1721:GLU:HB2	2.01	0.42
1:C:2538:THR:OG1	1:C:2539:ALA:N	2.52	0.42
1:D:372:LEU:HD23	1:D:372:LEU:H	1.85	0.42
1:D:1717:SER:HA	1:D:1721:GLU:HB2	2.01	0.42
1:D:2142:TYR:CG	1:D:2197:LEU:HD13	2.54	0.42
1:A:4024:VAL:HG23	1:A:4146:LEU:HD22	2.01	0.42
1:B:2003:GLN:NE2	1:B:3652:MET:SD	2.93	0.42
1:C:2967:MET:SD	1:C:2968:ASP:N	2.92	0.42
1:C:4884:LEU:HD12	1:C:4884:LEU:HA	1.94	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:616:SER:O	1:D:620:LEU:HG	2.20	0.42
1:D:3396:ASP:O	1:D:3400:VAL:HG12	2.20	0.42
1:D:4541:TRP:CD2	1:D:4541:TRP:N	2.85	0.42
1:D:4551:PHE:O	1:D:4552:LEU:C	2.53	0.42
1:D:5035:GLN:O	1:D:5036:LEU:HD22	2.18	0.42
1:A:3020:THR:HB	1:A:3021:PRO:HD3	2.00	0.42
1:B:215:THR:OG1	1:B:272:SER:O	2.38	0.42
1:B:1435:TYR:O	1:B:1447:CYS:HB2	2.20	0.42
1:B:2336:ARG:HG2	1:B:2340:PHE:HB2	2.00	0.42
1:B:3722:TYR:CZ	1:B:3782:MET:HE1	2.55	0.42
1:B:4542:GLY:O	1:B:4546:VAL:HG23	2.19	0.42
1:B:4713:SER:OG	1:B:4775:TYR:OH	2.27	0.42
1:C:710:ASP:OD1	1:C:710:ASP:N	2.52	0.42
1:C:1435:TYR:O	1:C:1447:CYS:HB2	2.20	0.42
1:C:4544:LEU:HB3	1:C:4548:ARG:HH12	1.84	0.42
1:C:4801:LEU:HD12	1:C:4801:LEU:HA	1.90	0.42
1:D:308:HIS:O	1:D:309:THR:OG1	2.34	0.42
1:D:571:SER:O	1:D:574:VAL:HG12	2.19	0.42
1:D:1176:GLU:O	1:D:1180:ARG:NH2	2.33	0.42
1:A:2332:LEU:HD22	1:A:2432:LEU:HD22	2.01	0.42
1:A:2336:ARG:HG2	1:A:2340:PHE:HB2	2.00	0.42
1:A:4557:ARG:HA	1:A:4557:ARG:HD3	1.78	0.42
1:B:2347:GLU:HA	1:B:2350:ALA:HB3	2.02	0.42
1:C:526:LEU:O	1:C:530:ILE:HG12	2.19	0.42
1:C:616:SER:O	1:C:620:LEU:HG	2.20	0.42
1:C:3949:ARG:O	1:C:3949:ARG:NH2	2.44	0.42
1:C:4631:PHE:HE2	1:C:4640:GLU:HA	1.84	0.42
1:D:430:PRO:HA	1:D:431:PRO:HD3	1.94	0.42
1:D:710:ASP:N	1:D:710:ASP:OD1	2.52	0.42
1:D:2495:VAL:HG12	1:D:2497:ASP:H	1.85	0.42
1:D:3843:ASP:OD1	1:D:3845:ASN:N	2.51	0.42
1:A:948:ASP:N	1:A:948:ASP:OD1	2.49	0.42
1:A:2121:PHE:CD2	1:A:3701:LEU:HD13	2.54	0.42
1:A:3949:ARG:O	1:A:3949:ARG:NH2	2.44	0.42
1:B:103:TYR:CD1	1:B:163:VAL:HG22	2.55	0.42
1:B:2641:LEU:HD23	1:B:2641:LEU:HA	1.86	0.42
1:B:3566:SER:O	1:B:3571:TRP:HB2	2.19	0.42
1:B:4003:LEU:HA	1:B:4009:GLN:HE21	1.85	0.42
1:B:4544:LEU:HB3	1:B:4548:ARG:HH12	1.84	0.42
1:C:759:ILE:HG22	1:C:760:ASN:H	1.84	0.42
1:C:2495:VAL:HG12	1:C:2497:ASP:H	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:759:ILE:HG22	1:D:760:ASN:H	1.84	0.42
1:A:103:TYR:CD1	1:A:163:VAL:HG22	2.55	0.42
1:A:710:ASP:OD1	1:A:710:ASP:N	2.52	0.42
1:A:2347:GLU:HA	1:A:2350:ALA:HB3	2.02	0.42
1:A:3434:LEU:HD23	1:A:3434:LEU:H	1.84	0.42
1:A:4690:GLU:OE1	1:A:4690:GLU:N	2.52	0.42
1:B:308:HIS:O	1:B:309:THR:OG1	2.34	0.42
1:B:1152:MET:N	1:B:1161:ILE:O	2.51	0.42
1:C:320:LYS:HE3	1:C:384:MET:SD	2.60	0.42
1:C:1479:GLU:O	1:C:1563:GLN:NE2	2.52	0.42
1:C:4106:PRO:O	1:C:4109:GLN:NE2	2.50	0.42
1:D:2003:GLN:NE2	1:D:3652:MET:SD	2.93	0.42
1:D:3434:LEU:H	1:D:3434:LEU:HD23	1.84	0.42
1:D:4801:LEU:HD12	1:D:4801:LEU:HA	1.90	0.42
1:A:759:ILE:HG22	1:A:760:ASN:H	1.84	0.42
1:A:794:GLY:N	1:A:798:GLY:HA3	2.28	0.42
1:A:3396:ASP:O	1:A:3400:VAL:HG12	2.20	0.42
1:A:4003:LEU:HA	1:A:4009:GLN:HE21	1.85	0.42
1:A:4631:PHE:HE2	1:A:4640:GLU:HA	1.84	0.42
1:B:759:ILE:HG22	1:B:760:ASN:N	2.34	0.42
1:B:1773:PRO:HA	1:B:1774:PRO:HD3	1.91	0.42
1:B:3396:ASP:O	1:B:3400:VAL:HG12	2.20	0.42
1:B:3434:LEU:HD23	1:B:3434:LEU:H	1.84	0.42
1:C:372:LEU:H	1:C:372:LEU:HD23	1.85	0.42
1:C:2003:GLN:NE2	1:C:3652:MET:SD	2.93	0.42
1:C:2463:LEU:HD12	1:C:2463:LEU:HA	1.88	0.42
1:C:3188:PRO:HA	1:C:3232:LEU:HD21	2.02	0.42
1:C:3782:MET:HE2	1:C:3782:MET:HB2	1.87	0.42
1:C:4572:ALA:O	1:C:4576:ILE:HG12	2.20	0.42
1:D:1435:TYR:O	1:D:1447:CYS:HB2	2.20	0.42
1:D:3188:PRO:HA	1:D:3232:LEU:HD21	2.02	0.42
1:D:3292:PRO:O	1:D:3294:PRO:HD3	2.19	0.42
1:D:4572:ALA:O	1:D:4576:ILE:HG12	2.20	0.42
1:A:661:LYS:HB3	1:A:808:TYR:HD1	1.84	0.42
1:A:1866:ILE:HG23	1:A:1927:LEU:HD22	2.02	0.42
1:A:2538:THR:OG1	1:A:2539:ALA:N	2.52	0.42
1:A:3566:SER:O	1:A:3571:TRP:HB2	2.19	0.42
1:A:4705:VAL:O	1:A:4708:THR:HG22	2.19	0.42
1:B:1866:ILE:HG23	1:B:1927:LEU:HD22	2.02	0.42
1:B:2003:GLN:OE1	1:B:3656:SER:OG	2.30	0.42
1:B:2332:LEU:HD22	1:B:2432:LEU:HD22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1866:ILE:HG23	1:C:1927:LEU:HD22	2.02	0.42
1:C:3434:LEU:HD23	1:C:3434:LEU:H	1.84	0.42
1:C:3959:LYS:HG3	1:C:4022:ASP:OD2	2.20	0.42
1:C:4024:VAL:HG23	1:C:4146:LEU:HD22	2.01	0.42
1:C:4557:ARG:HA	1:C:4557:ARG:HD3	1.78	0.42
1:C:4705:VAL:O	1:C:4708:THR:HG22	2.19	0.42
1:C:4945:ASP:O	1:C:4948:GLU:HG3	2.19	0.42
1:D:37:LEU:HD12	1:D:38:ALA:H	1.85	0.42
1:D:526:LEU:O	1:D:530:ILE:HG12	2.19	0.42
1:D:3959:LYS:HG3	1:D:4022:ASP:OD2	2.20	0.42
1:A:616:SER:O	1:A:620:LEU:HG	2.20	0.42
1:A:3959:LYS:HG3	1:A:4022:ASP:OD2	2.20	0.42
1:B:1092:PHE:HD1	1:B:1202:LEU:HB3	1.85	0.42
1:B:4543:GLU:O	1:B:4544:LEU:C	2.58	0.42
1:B:4578:LEU:HA	1:C:4879:MET:HG2	2.00	0.42
1:B:4690:GLU:OE1	1:B:4690:GLU:N	2.52	0.42
1:C:252:VAL:HG21	1:C:257:ARG:HH21	1.84	0.42
1:C:397:GLU:HA	1:C:400:ALA:HB3	2.02	0.42
1:C:1101:ARG:HB3	1:C:1123:VAL:CG2	2.50	0.42
1:C:3396:ASP:O	1:C:3400:VAL:HG12	2.20	0.42
1:C:3723:MET:H	1:C:3723:MET:HG2	1.70	0.42
1:C:4892:ARG:NH2	1:D:4895:GLY:O	2.52	0.42
1:D:103:TYR:CD1	1:D:163:VAL:HG22	2.55	0.42
1:D:1092:PHE:HD1	1:D:1202:LEU:HB3	1.85	0.42
1:D:1101:ARG:HB3	1:D:1123:VAL:CG2	2.50	0.42
1:A:37:LEU:HD12	1:A:38:ALA:H	1.85	0.41
1:A:179:TYR:HB2	1:A:196:MET:O	2.20	0.41
1:A:360:ALA:HB2	1:A:377:ILE:HG12	2.02	0.41
1:A:993:HIS:O	1:A:997:ALA:N	2.48	0.41
1:A:1435:TYR:O	1:A:1447:CYS:HB2	2.20	0.41
1:A:4543:GLU:O	1:A:4544:LEU:C	2.58	0.41
1:B:252:VAL:HG21	1:B:257:ARG:HH21	1.84	0.41
1:B:571:SER:O	1:B:574:VAL:HG12	2.19	0.41
1:B:1718:ILE:HG22	1:B:1719:HIS:CD2	2.55	0.41
1:C:21:VAL:HG11	1:C:205:ILE:HD13	2.02	0.41
1:C:360:ALA:HB2	1:C:377:ILE:HG12	2.02	0.41
1:C:688:LEU:HD23	1:C:688:LEU:H	1.85	0.41
1:D:130:LYS:HE2	1:D:130:LYS:HB2	1.92	0.41
1:D:1132:TRP:CZ2	1:D:1136:SER:HB2	2.55	0.41
1:A:21:VAL:HG11	1:A:205:ILE:HD13	2.02	0.41
1:A:178:ARG:NE	1:A:194:SER:O	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1092:PHE:HD1	1:A:1202:LEU:HB3	1.85	0.41
1:A:1132:TRP:CZ2	1:A:1136:SER:HB2	2.55	0.41
1:A:1718:ILE:HG22	1:A:1719:HIS:CD2	2.55	0.41
1:A:1749:PRO:HB2	1:A:1755:GLY:C	2.41	0.41
1:A:3018:LEU:HG	1:A:3022:ALA:HB3	2.02	0.41
1:B:360:ALA:HB2	1:B:377:ILE:HG12	2.02	0.41
1:B:372:LEU:HD23	1:B:372:LEU:H	1.85	0.41
1:B:1749:PRO:HB2	1:B:1755:GLY:C	2.41	0.41
1:B:4322:LEU:HD22	1:B:4322:LEU:HA	1.81	0.41
1:B:4907:ASP:HA	1:B:4910:GLU:HB2	2.02	0.41
1:B:4984:ASN:O	1:B:4985:LEU:HG	2.20	0.41
1:C:130:LYS:HE2	1:C:130:LYS:HB2	1.92	0.41
1:C:4003:LEU:HA	1:C:4009:GLN:HE21	1.85	0.41
1:C:4690:GLU:OE1	1:C:4690:GLU:N	2.52	0.41
1:C:4984:ASN:O	1:C:4985:LEU:HG	2.20	0.41
1:D:1479:GLU:O	1:D:1563:GLN:NE2	2.52	0.41
1:D:3274:LEU:N	1:D:3275:PRO:HD2	2.35	0.41
1:D:4631:PHE:HE2	1:D:4640:GLU:HA	1.84	0.41
1:A:350:HIS:CE1	1:A:352:ALA:HB3	2.56	0.41
1:A:1101:ARG:HB3	1:A:1123:VAL:CG2	2.50	0.41
1:A:1969:LEU:HD21	1:A:2009:LEU:HD23	2.02	0.41
1:A:4884:LEU:HD12	1:A:4884:LEU:HA	1.94	0.41
1:B:1101:ARG:HB3	1:B:1123:VAL:CG2	2.50	0.41
1:B:1479:GLU:O	1:B:1563:GLN:NE2	2.52	0.41
1:B:2138:LEU:N	1:B:2139:PRO:HD2	2.36	0.41
1:B:3789:GLU:OE1	1:B:3789:GLU:N	2.50	0.41
1:B:4060:LYS:HD2	1:B:4060:LYS:HA	1.77	0.41
1:C:103:TYR:CD1	1:C:163:VAL:HG22	2.55	0.41
1:C:834:PRO:HD2	1:C:838:HIS:HE1	1.85	0.41
1:C:2138:LEU:N	1:C:2139:PRO:HD2	2.36	0.41
1:C:2332:LEU:HD22	1:C:2432:LEU:HD22	2.01	0.41
1:C:4060:LYS:HD2	1:C:4060:LYS:HA	1.77	0.41
1:D:661:LYS:HB3	1:D:808:TYR:HD1	1.84	0.41
1:D:4702:ASP:O	1:D:4705:VAL:HG12	2.20	0.41
1:A:3300:ALA:HB3	1:A:3301:PRO:HD3	2.02	0.41
1:A:4101:LYS:HA	1:A:4101:LYS:HD3	1.77	0.41
1:A:4572:ALA:O	1:A:4576:ILE:HG12	2.20	0.41
1:B:130:LYS:HE2	1:B:130:LYS:HB2	1.92	0.41
1:B:3188:PRO:HA	1:B:3232:LEU:HD21	2.02	0.41
1:B:4024:VAL:HG23	1:B:4146:LEU:HD22	2.01	0.41
1:C:37:LEU:HD12	1:C:38:ALA:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:179:TYR:HB2	1:C:196:MET:O	2.20	0.41
1:C:350:HIS:CE1	1:C:352:ALA:HB3	2.56	0.41
1:C:1657:LEU:HD23	1:C:1657:LEU:O	2.21	0.41
1:C:2009:LEU:HD12	1:C:2009:LEU:HA	1.79	0.41
1:D:320:LYS:HE3	1:D:384:MET:SD	2.60	0.41
1:D:350:HIS:CE1	1:D:352:ALA:HB3	2.56	0.41
1:D:3789:GLU:OE1	1:D:3789:GLU:N	2.50	0.41
1:A:320:LYS:HE3	1:A:384:MET:SD	2.60	0.41
1:A:2417:HIS:CE1	1:A:2492:ALA:HB1	2.56	0.41
1:A:4702:ASP:O	1:A:4705:VAL:HG12	2.20	0.41
1:A:4984:ASN:O	1:A:4985:LEU:HG	2.20	0.41
1:B:21:VAL:HG11	1:B:205:ILE:HD13	2.02	0.41
1:B:320:LYS:HE3	1:B:384:MET:SD	2.60	0.41
1:B:397:GLU:HA	1:B:400:ALA:HB3	2.02	0.41
1:B:645:ARG:HG2	1:B:826:ILE:HG23	2.03	0.41
1:B:2495:VAL:HG12	1:B:2497:ASP:H	1.85	0.41
1:B:3599:VAL:O	1:B:3603:LEU:HG	2.21	0.41
1:C:870:ILE:HD12	1:C:873:LYS:HB2	2.02	0.41
1:C:4702:ASP:O	1:C:4705:VAL:HG12	2.20	0.41
1:A:2495:VAL:HG12	1:A:2497:ASP:H	1.85	0.41
1:A:2641:LEU:HA	1:A:2641:LEU:HD23	1.86	0.41
1:A:3293:PRO:HB2	1:A:3296:LEU:HB2	2.03	0.41
1:B:1476:MET:HG2	1:B:1574:PRO:HB3	2.02	0.41
1:B:2417:HIS:CE1	1:B:2492:ALA:HB1	2.56	0.41
1:C:1148:VAL:HG21	1:C:1212:ARG:HG3	2.03	0.41
1:C:1718:ILE:HG22	1:C:1719:HIS:CD2	2.55	0.41
1:C:3599:VAL:O	1:C:3603:LEU:HG	2.21	0.41
1:D:179:TYR:HB2	1:D:196:MET:O	2.20	0.41
1:D:215:THR:OG1	1:D:272:SER:O	2.38	0.41
1:D:220:LEU:HD21	1:D:262:LEU:HD21	2.03	0.41
1:D:252:VAL:HG21	1:D:257:ARG:HH21	1.84	0.41
1:D:560:ILE:HA	1:D:563:VAL:HG12	2.02	0.41
1:D:708:GLY:HA3	1:D:722:TRP:HB3	2.03	0.41
1:D:1775:HIS:CE1	1:D:1851:MET:HG3	2.55	0.41
1:D:3599:VAL:O	1:D:3603:LEU:HG	2.21	0.41
1:A:372:LEU:H	1:A:372:LEU:HD23	1.85	0.41
1:A:516:LYS:HE3	1:A:516:LYS:HB2	1.88	0.41
1:A:662:TRP:HZ3	1:A:812:HIS:H	1.69	0.41
1:A:701:GLY:HA3	1:A:725:HIS:CE1	2.56	0.41
1:A:1022:VAL:H	1:A:1027:LEU:HD21	1.86	0.41
1:A:1148:VAL:HG21	1:A:1212:ARG:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2003:GLN:NE2	1:A:3652:MET:SD	2.93	0.41
1:A:3274:LEU:N	1:A:3275:PRO:HD2	2.35	0.41
1:A:4544:LEU:HB3	1:A:4548:ARG:HH12	1.84	0.41
1:B:2967:MET:H	1:B:2967:MET:HG3	1.70	0.41
1:B:4550:LYS:HZ3	1:B:4550:LYS:HG2	1.65	0.41
1:C:424:LYS:HE2	1:C:424:LYS:HB2	1.80	0.41
1:C:661:LYS:HB3	1:C:808:TYR:HD1	1.84	0.41
1:C:747:CYS:HB2	1:C:756:SER:HB3	2.03	0.41
1:C:1969:LEU:HD21	1:C:2009:LEU:HD23	2.02	0.41
1:C:2347:GLU:HA	1:C:2350:ALA:HB3	2.02	0.41
1:D:870:ILE:HD12	1:D:873:LYS:HB2	2.02	0.41
1:A:1765:VAL:HG22	1:A:1766:GLY:N	2.36	0.41
1:B:560:ILE:HA	1:B:563:VAL:HG12	2.02	0.41
1:B:1259:ARG:HH22	1:B:1593:PRO:HA	1.86	0.41
1:B:1775:HIS:CE1	1:B:1851:MET:HG3	2.55	0.41
1:B:4541:TRP:CD2	1:B:4541:TRP:N	2.85	0.41
1:C:708:GLY:HA3	1:C:722:TRP:HB3	2.03	0.41
1:C:1773:PRO:HA	1:C:1774:PRO:HD3	1.91	0.41
1:C:3300:ALA:HB3	1:C:3301:PRO:HD3	2.02	0.41
1:C:3338:LEU:HB2	1:C:3343:GLN:NE2	2.36	0.41
1:C:4702:ASP:OD1	1:C:4702:ASP:N	2.52	0.41
1:D:21:VAL:HG11	1:D:205:ILE:HD13	2.02	0.41
1:D:360:ALA:HB2	1:D:377:ILE:HG12	2.02	0.41
1:D:1657:LEU:O	1:D:1657:LEU:HD23	2.21	0.41
1:D:1718:ILE:HG22	1:D:1719:HIS:CD2	2.55	0.41
1:D:2332:LEU:HD22	1:D:2432:LEU:HD22	2.01	0.41
1:D:2417:HIS:CE1	1:D:2492:ALA:HB1	2.56	0.41
1:D:2538:THR:OG1	1:D:2539:ALA:N	2.52	0.41
1:A:649:PHE:HB3	1:A:776:LEU:HD22	2.03	0.41
1:A:688:LEU:HD23	1:A:688:LEU:H	1.85	0.41
1:A:834:PRO:HD2	1:A:838:HIS:HE1	1.85	0.41
1:A:1476:MET:HG2	1:A:1574:PRO:HB3	2.02	0.41
1:A:1775:HIS:CE1	1:A:1851:MET:HG3	2.55	0.41
1:A:2515:GLN:O	1:A:2518:LEU:HG	2.21	0.41
1:A:2967:MET:H	1:A:2967:MET:HG3	1.70	0.41
1:A:3272:ILE:HG23	1:A:3275:PRO:HG2	2.03	0.41
1:A:3599:VAL:O	1:A:3603:LEU:HG	2.21	0.41
1:B:179:TYR:HB2	1:B:196:MET:O	2.20	0.41
1:B:834:PRO:HD2	1:B:838:HIS:HE1	1.85	0.41
1:B:1132:TRP:CZ2	1:B:1136:SER:HB2	2.55	0.41
1:B:1148:VAL:HG21	1:B:1212:ARG:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2123:LEU:HD12	1:B:2123:LEU:HA	1.93	0.41
1:B:3274:LEU:N	1:B:3275:PRO:HD2	2.35	0.41
1:B:3293:PRO:HB2	1:B:3296:LEU:HB2	2.03	0.41
1:B:4702:ASP:O	1:B:4705:VAL:HG12	2.20	0.41
1:C:1092:PHE:HD1	1:C:1202:LEU:HB3	1.85	0.41
1:C:1749:PRO:HB2	1:C:1755:GLY:C	2.41	0.41
1:C:1775:HIS:CE1	1:C:1851:MET:HG3	2.55	0.41
1:C:3018:LEU:HG	1:C:3022:ALA:HB3	2.02	0.41
1:C:3368:ARG:O	1:C:3372:VAL:N	2.48	0.41
1:C:4907:ASP:HA	1:C:4910:GLU:HB2	2.02	0.41
1:D:662:TRP:HZ3	1:D:812:HIS:H	1.69	0.41
1:D:675:LEU:HD12	1:D:675:LEU:HA	1.92	0.41
1:D:688:LEU:H	1:D:688:LEU:HD23	1.85	0.41
1:D:1259:ARG:HH22	1:D:1593:PRO:HA	1.86	0.41
1:D:1731:LEU:HD12	1:D:1731:LEU:HA	1.95	0.41
1:D:2347:GLU:HA	1:D:2350:ALA:HB3	2.02	0.41
1:D:3427:PRO:HA	1:D:3430:ASN:HB2	2.03	0.41
1:D:4003:LEU:HA	1:D:4009:GLN:HE21	1.85	0.41
1:D:4543:GLU:O	1:D:4544:LEU:C	2.58	0.41
1:A:708:GLY:HA3	1:A:722:TRP:HB3	2.03	0.41
1:A:870:ILE:HD12	1:A:873:LYS:HB2	2.02	0.41
1:A:1177:THR:O	1:A:1180:ARG:NH1	2.48	0.41
1:A:2039:LEU:HD22	1:A:2131:LEU:HD11	2.03	0.41
1:A:3188:PRO:HA	1:A:3232:LEU:HD21	2.02	0.41
1:A:3789:GLU:OE1	1:A:3789:GLU:N	2.50	0.41
1:B:350:HIS:CE1	1:B:352:ALA:HB3	2.56	0.41
1:B:1022:VAL:H	1:B:1027:LEU:HD21	1.86	0.41
1:B:2009:LEU:HD12	1:B:2009:LEU:HA	1.79	0.41
1:C:222:LEU:HB3	1:C:388:LEU:HD11	2.03	0.41
1:C:560:ILE:HA	1:C:563:VAL:HG12	2.02	0.41
1:C:686:TRP:CE2	1:C:748:LEU:HD21	2.56	0.41
1:C:1132:TRP:CZ2	1:C:1136:SER:HB2	2.55	0.41
1:C:3274:LEU:N	1:C:3275:PRO:HD2	2.35	0.41
1:C:4030:LEU:HD12	1:C:4030:LEU:HA	1.96	0.41
1:D:61:ASP:N	1:D:61:ASP:OD1	2.54	0.41
1:D:701:GLY:HA3	1:D:725:HIS:CE1	2.56	0.41
1:D:834:PRO:HD2	1:D:838:HIS:HE1	1.85	0.41
1:D:1022:VAL:H	1:D:1027:LEU:HD21	1.86	0.41
1:D:1476:MET:HG2	1:D:1574:PRO:HB3	2.02	0.41
1:D:1749:PRO:HB2	1:D:1755:GLY:C	2.41	0.41
1:D:1765:VAL:HG22	1:D:1766:GLY:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1866:ILE:HG23	1:D:1927:LEU:HD22	2.02	0.41
1:D:2380:ILE:HD13	1:D:2380:ILE:HA	1.92	0.41
1:D:3272:ILE:HG23	1:D:3275:PRO:HG2	2.03	0.41
1:A:61:ASP:OD1	1:A:61:ASP:N	2.54	0.40
1:A:1479:GLU:O	1:A:1563:GLN:NE2	2.52	0.40
1:B:37:LEU:HD12	1:B:38:ALA:H	1.85	0.40
1:B:661:LYS:HB3	1:B:808:TYR:HD1	1.84	0.40
1:B:686:TRP:CE2	1:B:748:LEU:HD21	2.56	0.40
1:B:708:GLY:HA3	1:B:722:TRP:HB3	2.03	0.40
1:B:870:ILE:HD12	1:B:873:LYS:HB2	2.02	0.40
1:B:3338:LEU:HB2	1:B:3343:GLN:NE2	2.36	0.40
1:B:3959:LYS:HG3	1:B:4022:ASP:OD2	2.20	0.40
1:B:4572:ALA:O	1:B:4576:ILE:HG12	2.20	0.40
1:B:4702:ASP:OD1	1:B:4702:ASP:N	2.52	0.40
1:C:1259:ARG:HH22	1:C:1593:PRO:HA	1.86	0.40
1:C:2039:LEU:HD22	1:C:2131:LEU:HD11	2.03	0.40
1:C:2515:GLN:O	1:C:2518:LEU:HG	2.21	0.40
1:D:1148:VAL:HG21	1:D:1212:ARG:HG3	2.03	0.40
1:A:220:LEU:HD21	1:A:262:LEU:HD21	2.03	0.40
1:A:560:ILE:HA	1:A:563:VAL:HG12	2.02	0.40
1:A:3427:PRO:HA	1:A:3430:ASN:HB2	2.03	0.40
1:A:4895:GLY:O	1:D:4892:ARG:NH2	2.52	0.40
1:A:4907:ASP:HA	1:A:4910:GLU:HB2	2.02	0.40
1:B:688:LEU:HD23	1:B:688:LEU:H	1.85	0.40
1:B:2515:GLN:O	1:B:2518:LEU:HG	2.21	0.40
1:C:645:ARG:HG2	1:C:826:ILE:HG23	2.03	0.40
1:C:801:LYS:HB2	1:C:801:LYS:HE2	1.77	0.40
1:C:1476:MET:HG2	1:C:1574:PRO:HB3	2.02	0.40
1:D:1969:LEU:HD21	1:D:2009:LEU:HD23	2.02	0.40
1:A:2138:LEU:N	1:A:2139:PRO:HD2	2.36	0.40
1:B:61:ASP:N	1:B:61:ASP:OD1	2.54	0.40
1:B:635:THR:HB	1:B:1693:GLN:HE22	1.87	0.40
1:B:747:CYS:HB2	1:B:756:SER:HB3	2.03	0.40
1:B:1430:THR:O	1:B:1431:THR:OG1	2.37	0.40
1:B:2110:TYR:HD1	1:B:3695:PRO:HD2	1.87	0.40
1:B:2182:ILE:HD13	1:B:2182:ILE:HA	1.98	0.40
1:B:2463:LEU:HD12	1:B:2463:LEU:HA	1.88	0.40
1:B:4557:ARG:HA	1:B:4557:ARG:HD3	1.78	0.40
1:C:308:HIS:O	1:C:309:THR:OG1	2.34	0.40
1:C:537:CYS:SG	1:C:567:VAL:HA	2.62	0.40
1:C:2236:LEU:HB3	1:C:2275:VAL:HG21	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4322:LEU:HA	1:C:4322:LEU:HD22	1.81	0.40
1:C:4873:ASP:OD1	1:C:4873:ASP:N	2.50	0.40
1:D:178:ARG:NH1	1:D:195:PHE:O	2.55	0.40
1:D:397:GLU:HA	1:D:400:ALA:HB3	2.02	0.40
1:D:686:TRP:CE2	1:D:748:LEU:HD21	2.56	0.40
1:D:995:VAL:HG22	1:D:998:ARG:NH1	2.36	0.40
1:D:3293:PRO:HB2	1:D:3296:LEU:HB2	2.03	0.40
1:D:4160:LEU:HD23	1:D:4160:LEU:HA	1.91	0.40
1:A:178:ARG:NH1	1:A:195:PHE:O	2.55	0.40
1:A:397:GLU:HA	1:A:400:ALA:HB3	2.02	0.40
1:A:788:LYS:HG2	1:A:1629:GLN:HA	2.04	0.40
1:A:885:THR:O	1:A:889:GLN:HG2	2.22	0.40
1:A:995:VAL:HG22	1:A:998:ARG:NH1	2.36	0.40
1:A:2110:TYR:HD1	1:A:3695:PRO:HD2	1.87	0.40
1:B:222:LEU:HB3	1:B:388:LEU:HD11	2.03	0.40
1:B:565:TYR:CZ	1:B:569:ILE:HD11	2.57	0.40
1:C:62:LEU:HD23	1:C:62:LEU:HA	1.86	0.40
1:C:178:ARG:NH1	1:C:195:PHE:O	2.55	0.40
1:C:788:LYS:HG2	1:C:1629:GLN:HA	2.04	0.40
1:C:1022:VAL:H	1:C:1027:LEU:HD21	1.86	0.40
1:C:2423:MET:SD	1:C:2498:HIS:ND1	2.80	0.40
1:C:4543:GLU:O	1:C:4544:LEU:C	2.58	0.40
1:D:645:ARG:HG2	1:D:826:ILE:HG23	2.03	0.40
1:D:2138:LEU:N	1:D:2139:PRO:HD2	2.36	0.40
1:D:2558:VAL:HG23	1:D:2560:PRO:HD3	2.04	0.40
1:D:4101:LYS:HA	1:D:4101:LYS:HD3	1.77	0.40
1:D:4984:ASN:O	1:D:4985:LEU:HG	2.20	0.40
1:A:44:ASN:OD1	1:A:44:ASN:N	2.55	0.40
1:A:685:GLY:HA3	1:A:714:TYR:O	2.22	0.40
1:A:1657:LEU:HD23	1:A:1657:LEU:O	2.21	0.40
1:A:1942:LEU:HD12	1:A:1942:LEU:HA	1.96	0.40
1:A:3338:LEU:HB2	1:A:3343:GLN:NE2	2.36	0.40
1:A:3412:LEU:HA	1:A:3415:TYR:HD2	1.87	0.40
1:B:178:ARG:NE	1:B:194:SER:O	2.45	0.40
1:B:1657:LEU:O	1:B:1657:LEU:HD23	2.21	0.40
1:B:2138:LEU:HA	1:B:2138:LEU:HD23	1.88	0.40
1:B:3300:ALA:HB3	1:B:3301:PRO:HD3	2.02	0.40
1:C:157:ARG:NH2	1:C:164:ARG:HH21	2.20	0.40
1:C:2558:VAL:HG23	1:C:2560:PRO:HD3	2.04	0.40
1:D:649:PHE:HB3	1:D:776:LEU:HD22	2.03	0.40
1:D:1704:PRO:O	1:D:1706:PRO:HD2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2515:GLN:O	1:D:2518:LEU:HG	2.21	0.40
1:D:3018:LEU:HG	1:D:3022:ALA:HB3	2.02	0.40
1:D:3657:TYR:HB3	1:D:3661:TRP:HE1	1.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	3938/5037 (78%)	3610 (92%)	325 (8%)	3 (0%)	48	79
1	B	3938/5037 (78%)	3610 (92%)	325 (8%)	3 (0%)	48	79
1	C	3938/5037 (78%)	3610 (92%)	325 (8%)	3 (0%)	48	79
1	D	3938/5037 (78%)	3610 (92%)	325 (8%)	3 (0%)	48	79
All	All	15752/20148 (78%)	14440 (92%)	1300 (8%)	12 (0%)	50	79

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4558	ASN
1	A	4559	PHE
1	A	4560	TYR
1	B	4558	ASN
1	B	4559	PHE
1	B	4560	TYR
1	C	4558	ASN
1	C	4559	PHE
1	C	4560	TYR
1	D	4558	ASN
1	D	4559	PHE
1	D	4560	TYR

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	2909/4276 (68%)	2889 (99%)	20 (1%)	81	86
1	B	2909/4276 (68%)	2889 (99%)	20 (1%)	81	86
1	C	2909/4276 (68%)	2889 (99%)	20 (1%)	81	86
1	D	2909/4276 (68%)	2889 (99%)	20 (1%)	81	86
All	All	11636/17104 (68%)	11556 (99%)	80 (1%)	80	86

All (80) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	275	ARG
1	A	2203	MET
1	A	3773	ARG
1	A	3897	ASN
1	A	3949	ARG
1	A	4085	ARG
1	A	4320	ARG
1	A	4322	LEU
1	A	4323	THR
1	A	4541	TRP
1	A	4544	LEU
1	A	4548	ARG
1	A	4550	LYS
1	A	4551	PHE
1	A	4552	LEU
1	A	4554	TYR
1	A	4555	LEU
1	A	4557	ARG
1	A	4559	PHE
1	A	4561	THR
1	B	275	ARG
1	B	2203	MET
1	B	3773	ARG
1	B	3897	ASN

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Mol	Chain	Res	Type
1	B	3949	ARG
1	B	4085	ARG
1	B	4320	ARG
1	B	4322	LEU
1	B	4323	THR
1	B	4541	TRP
1	B	4544	LEU
1	B	4548	ARG
1	B	4550	LYS
1	B	4551	PHE
1	B	4552	LEU
1	B	4554	TYR
1	B	4555	LEU
1	B	4557	ARG
1	B	4559	PHE
1	B	4561	THR
1	C	275	ARG
1	C	2203	MET
1	C	3773	ARG
1	C	3897	ASN
1	C	3949	ARG
1	C	4085	ARG
1	C	4320	ARG
1	C	4322	LEU
1	C	4323	THR
1	C	4541	TRP
1	C	4544	LEU
1	C	4548	ARG
1	C	4550	LYS
1	C	4551	PHE
1	C	4552	LEU
1	C	4554	TYR
1	C	4555	LEU
1	C	4557	ARG
1	C	4559	PHE
1	C	4561	THR
1	D	275	ARG
1	D	2203	MET
1	D	3773	ARG
1	D	3897	ASN
1	D	3949	ARG
1	D	4085	ARG

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Mol	Chain	Res	Type
1	D	4320	ARG
1	D	4322	LEU
1	D	4323	THR
1	D	4541	TRP
1	D	4544	LEU
1	D	4548	ARG
1	D	4550	LYS
1	D	4551	PHE
1	D	4552	LEU
1	D	4554	TYR
1	D	4555	LEU
1	D	4557	ARG
1	D	4559	PHE
1	D	4561	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1220	GLN
1	A	1970	GLN
1	A	3946	GLN
1	A	3950	ASN
1	B	1220	GLN
1	B	3946	GLN
1	B	3950	ASN
1	C	1220	GLN
1	C	3946	GLN
1	C	3950	ASN
1	D	1220	GLN
1	D	1719	HIS
1	D	1970	GLN
1	D	3946	GLN
1	D	3950	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

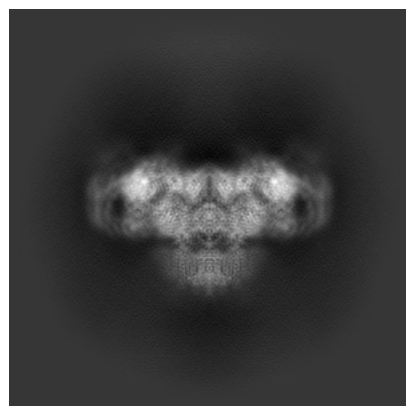
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38044. These allow visual inspection of the internal detail of the map and identification of artifacts.

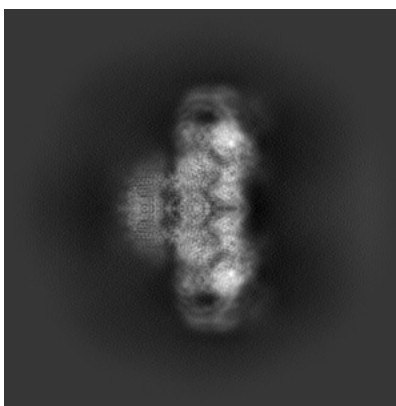
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

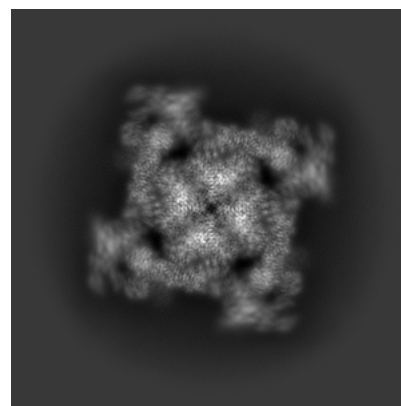
6.1.1 Primary map



X

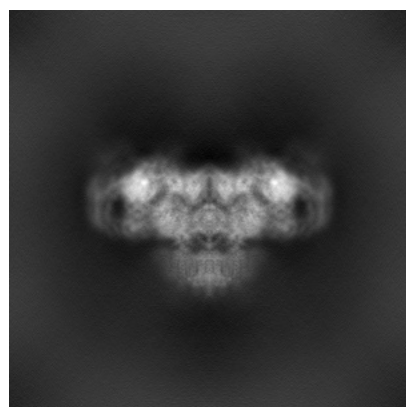


Y

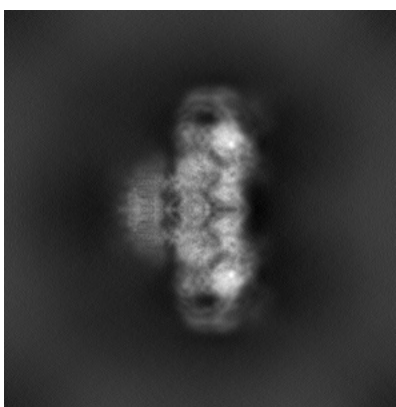


Z

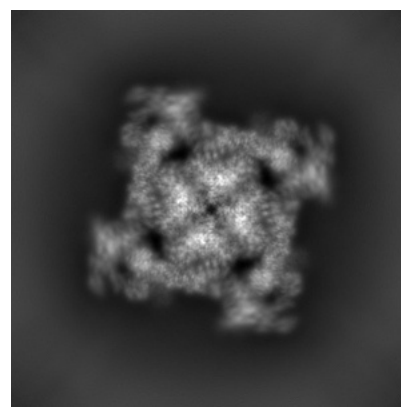
6.1.2 Raw map



X



Y

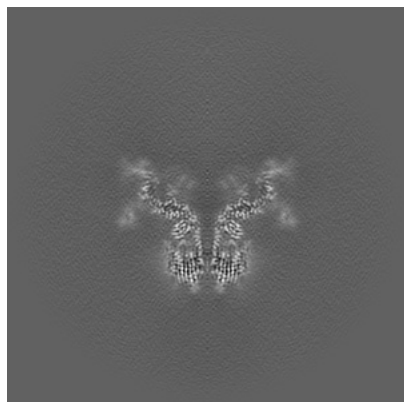


Z

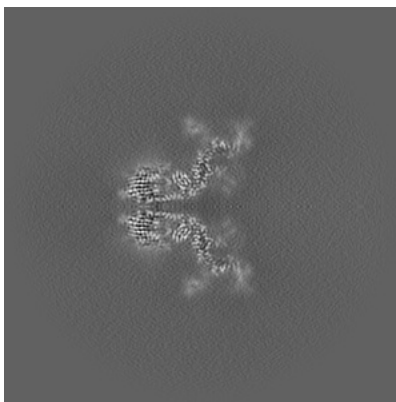
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

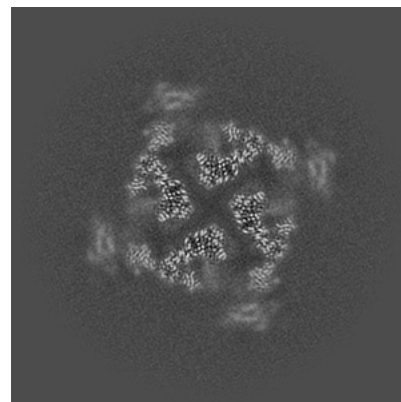
6.2.1 Primary map



X Index: 240

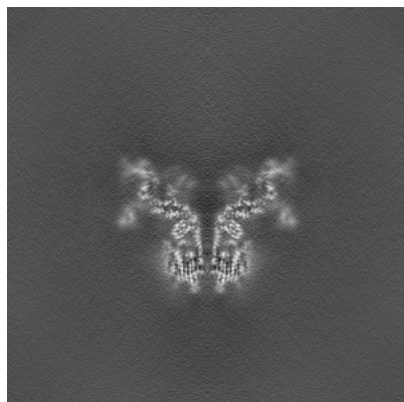


Y Index: 240

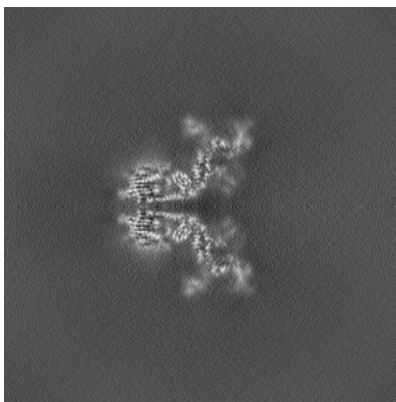


Z Index: 240

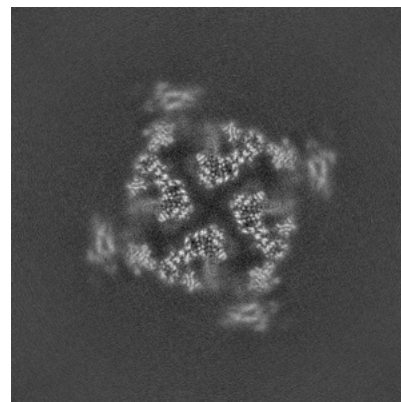
6.2.2 Raw map



X Index: 240



Y Index: 240

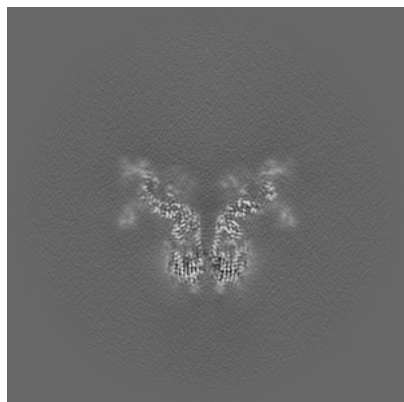


Z Index: 240

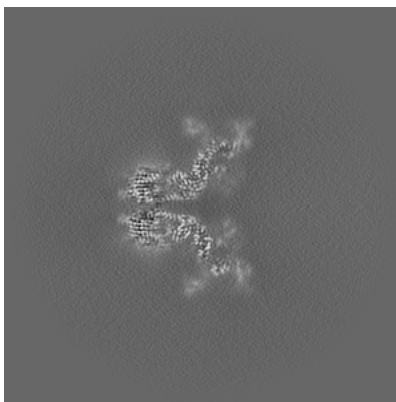
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

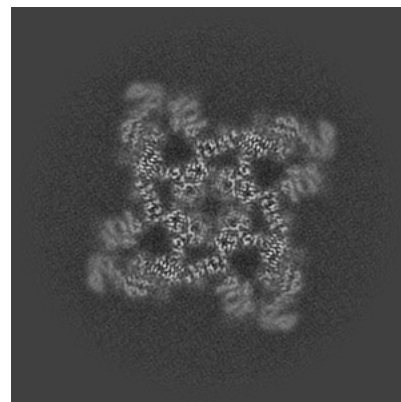
6.3.1 Primary map



X Index: 241

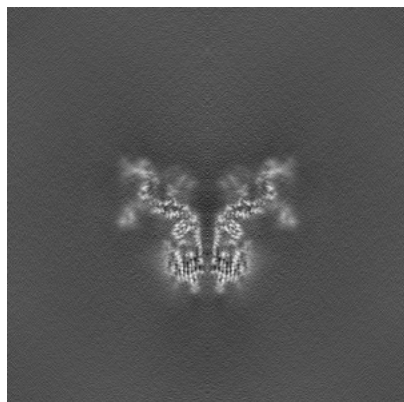


Y Index: 241

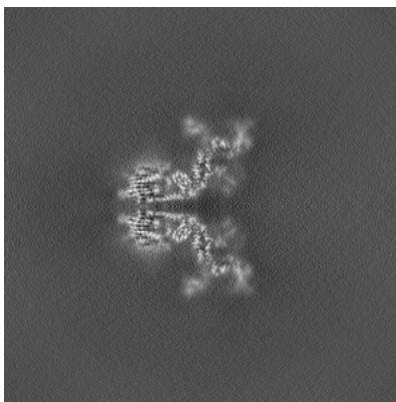


Z Index: 264

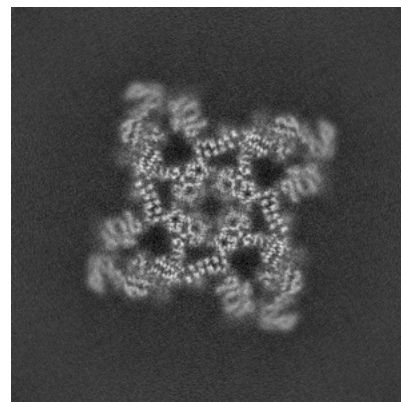
6.3.2 Raw map



X Index: 240



Y Index: 240

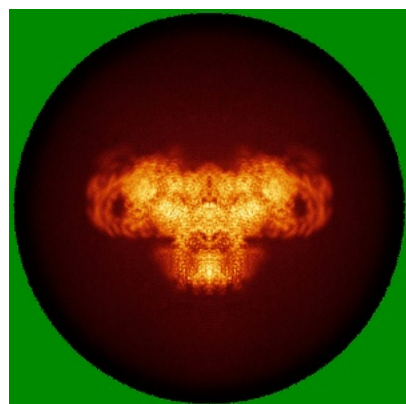


Z Index: 264

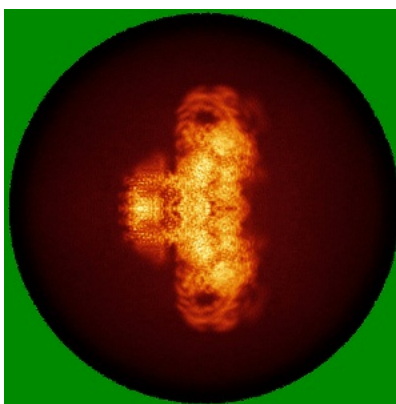
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

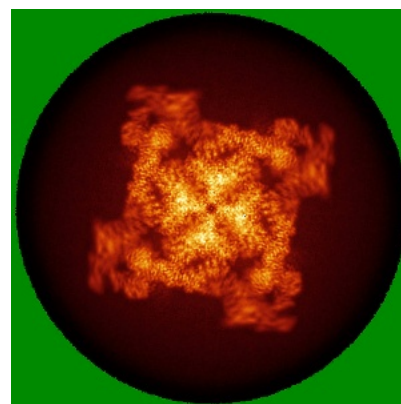
6.4.1 Primary map



X

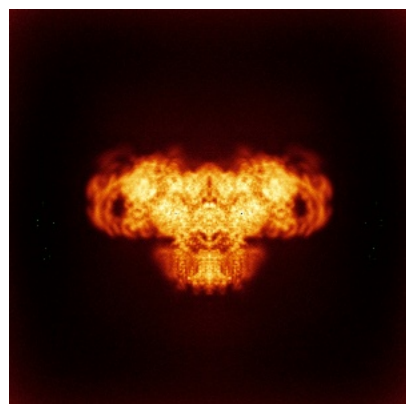


Y

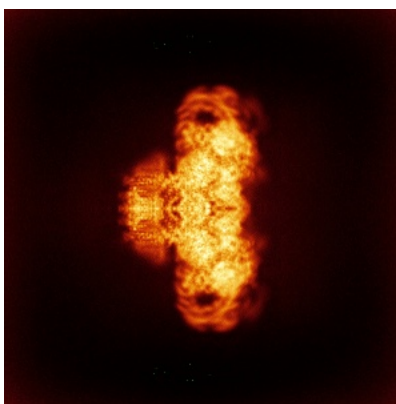


Z

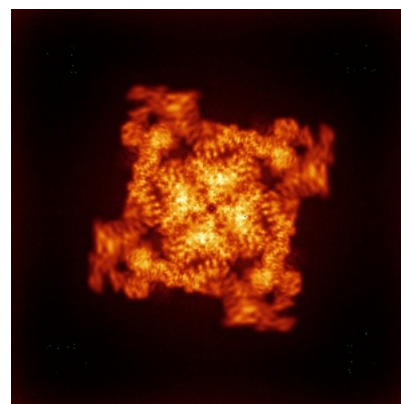
6.4.2 Raw map



X



Y

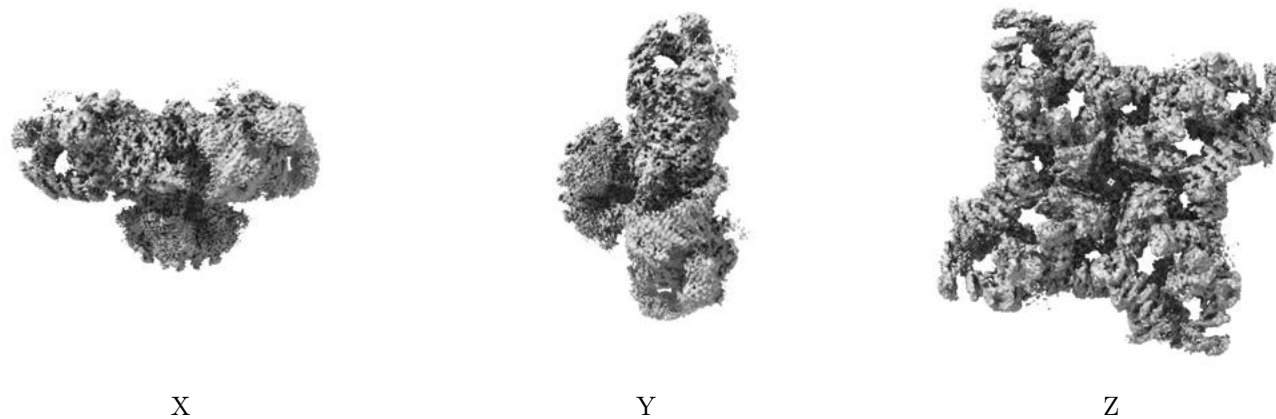


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

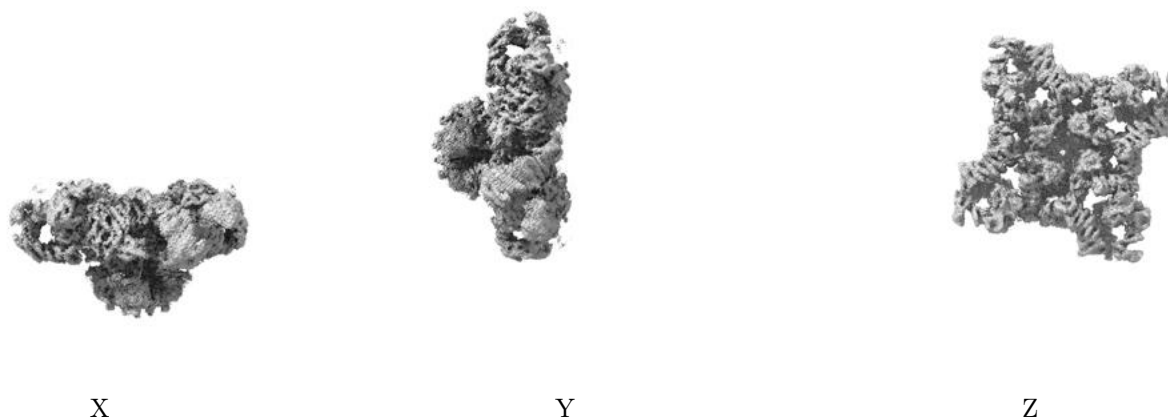
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.254. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

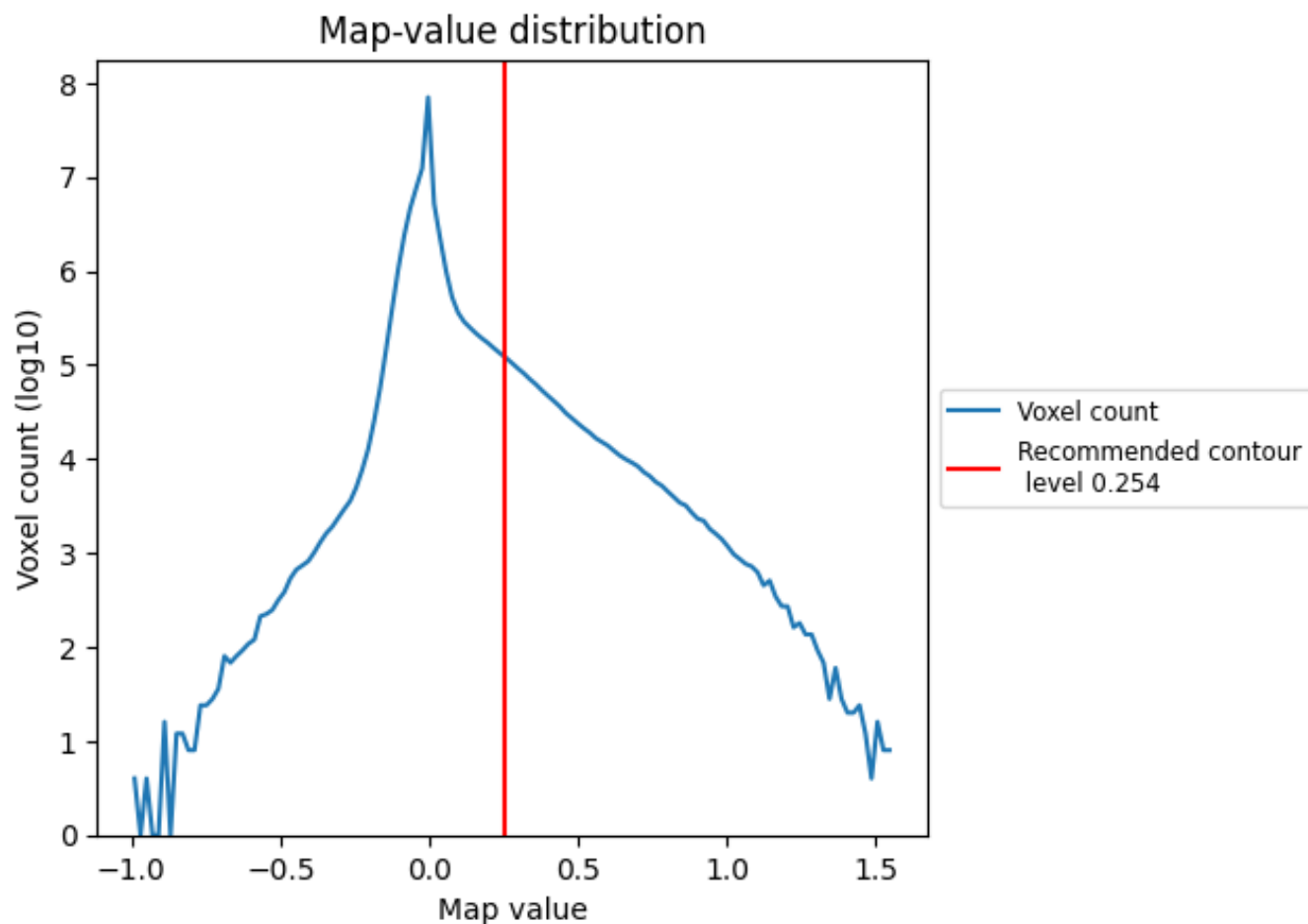
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

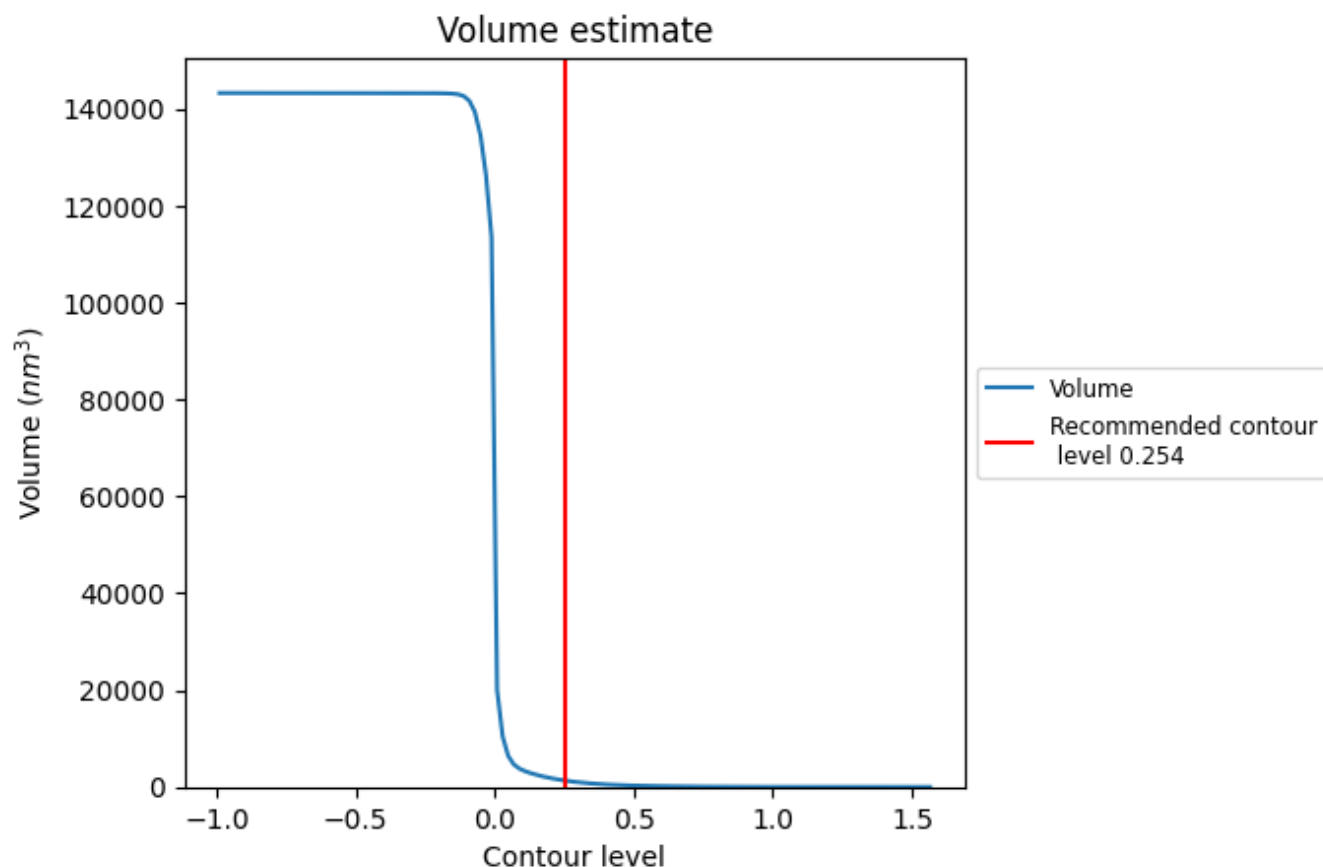
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

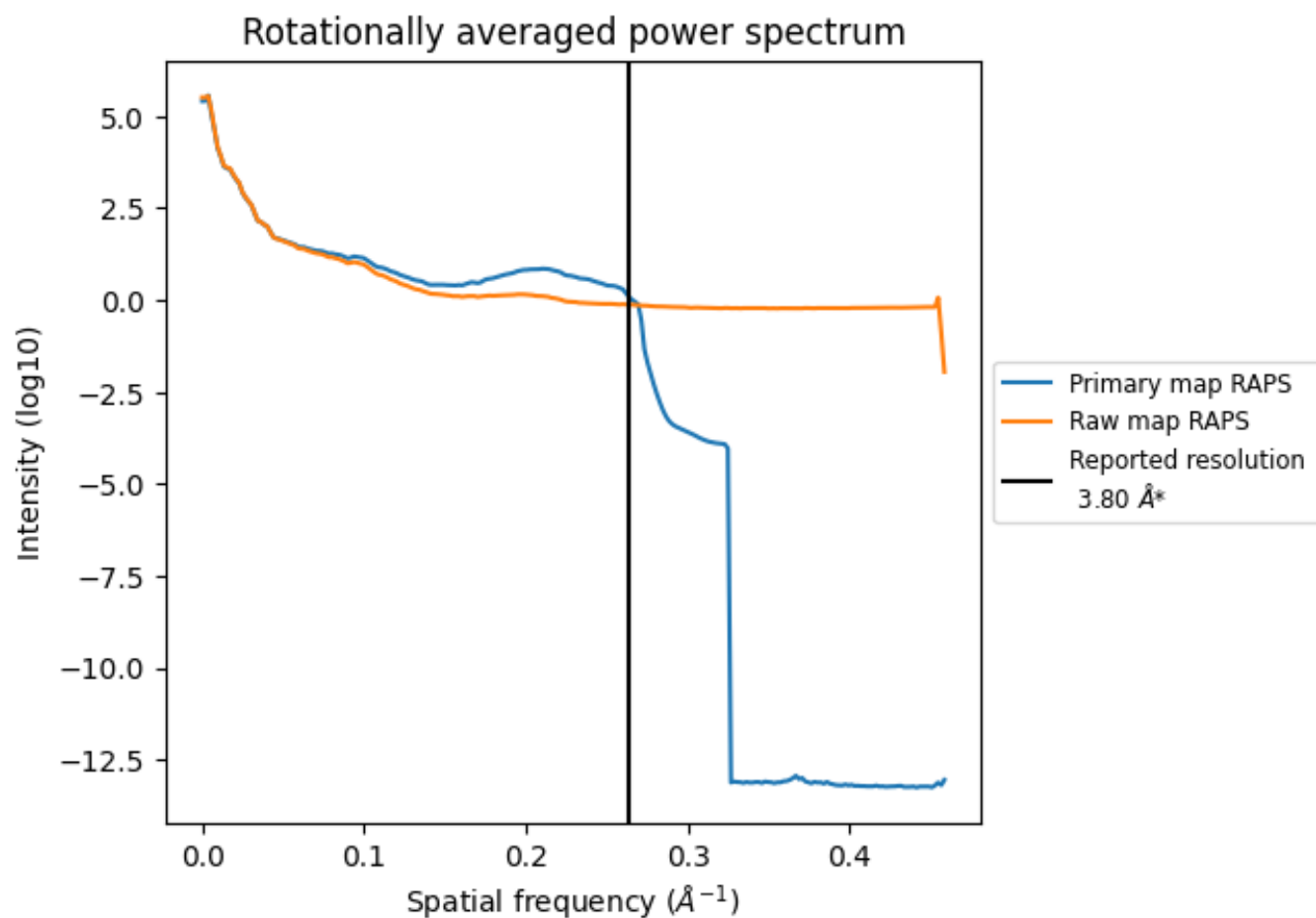
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1304 nm³; this corresponds to an approximate mass of 1178 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

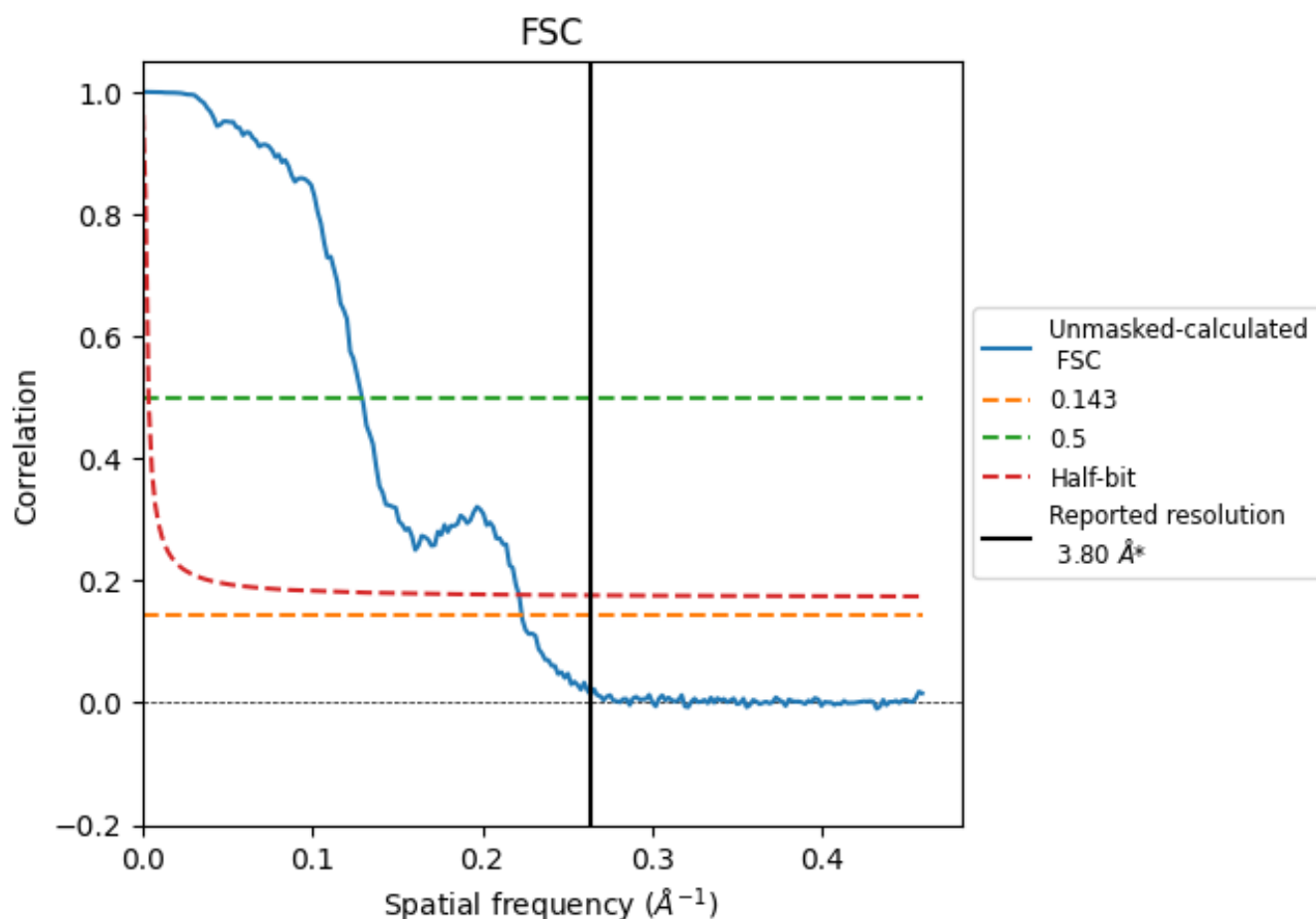


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 \AA^{-1}

8.2 Resolution estimates [i](#)

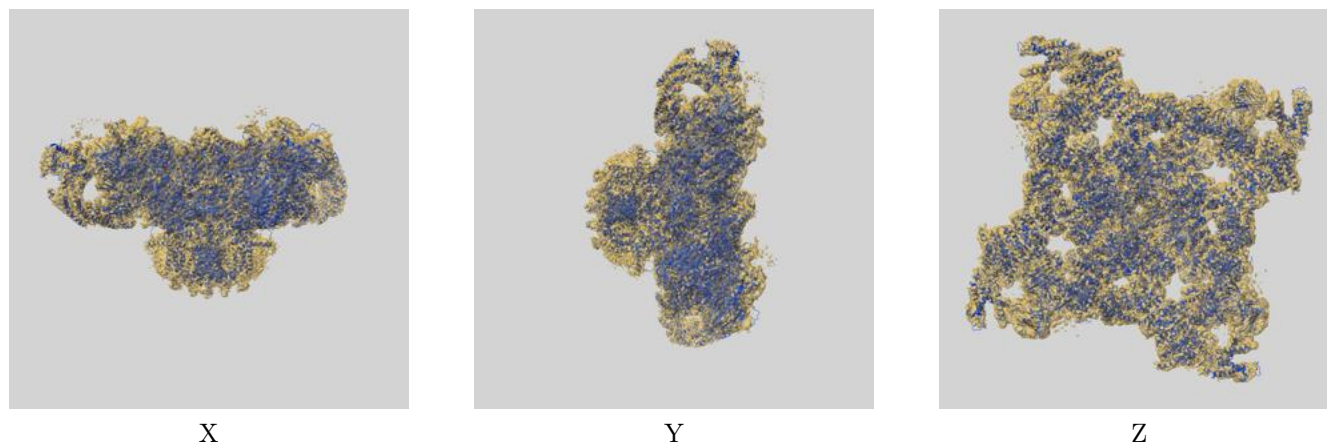
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.48	7.75	4.51

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.48 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

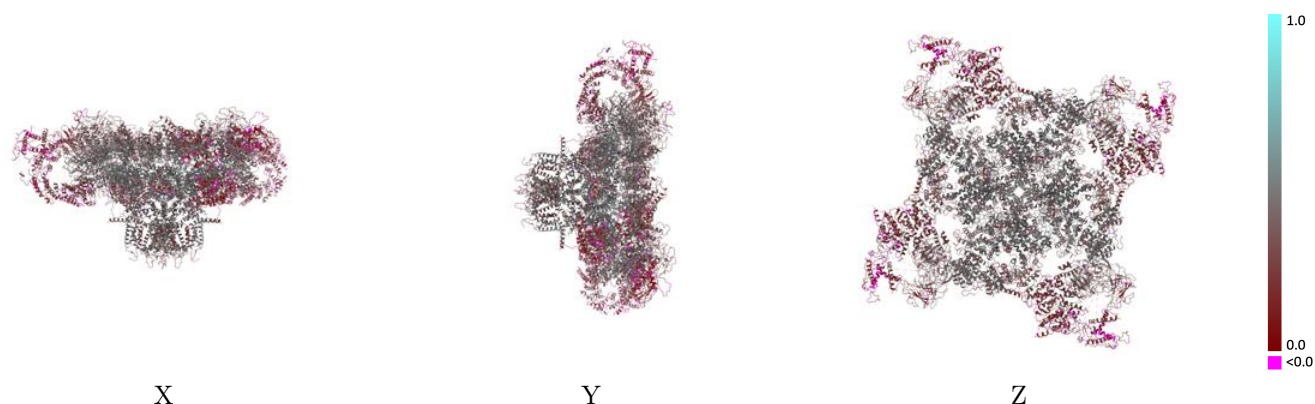
This section contains information regarding the fit between EMDB map EMD-38044 and PDB model 8X4A. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



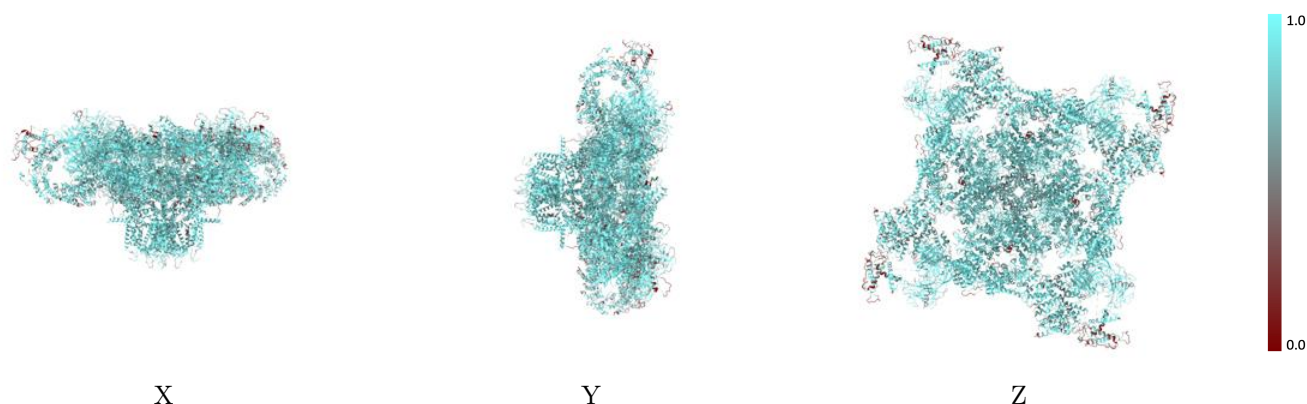
The images above show the 3D surface view of the map at the recommended contour level 0.254 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



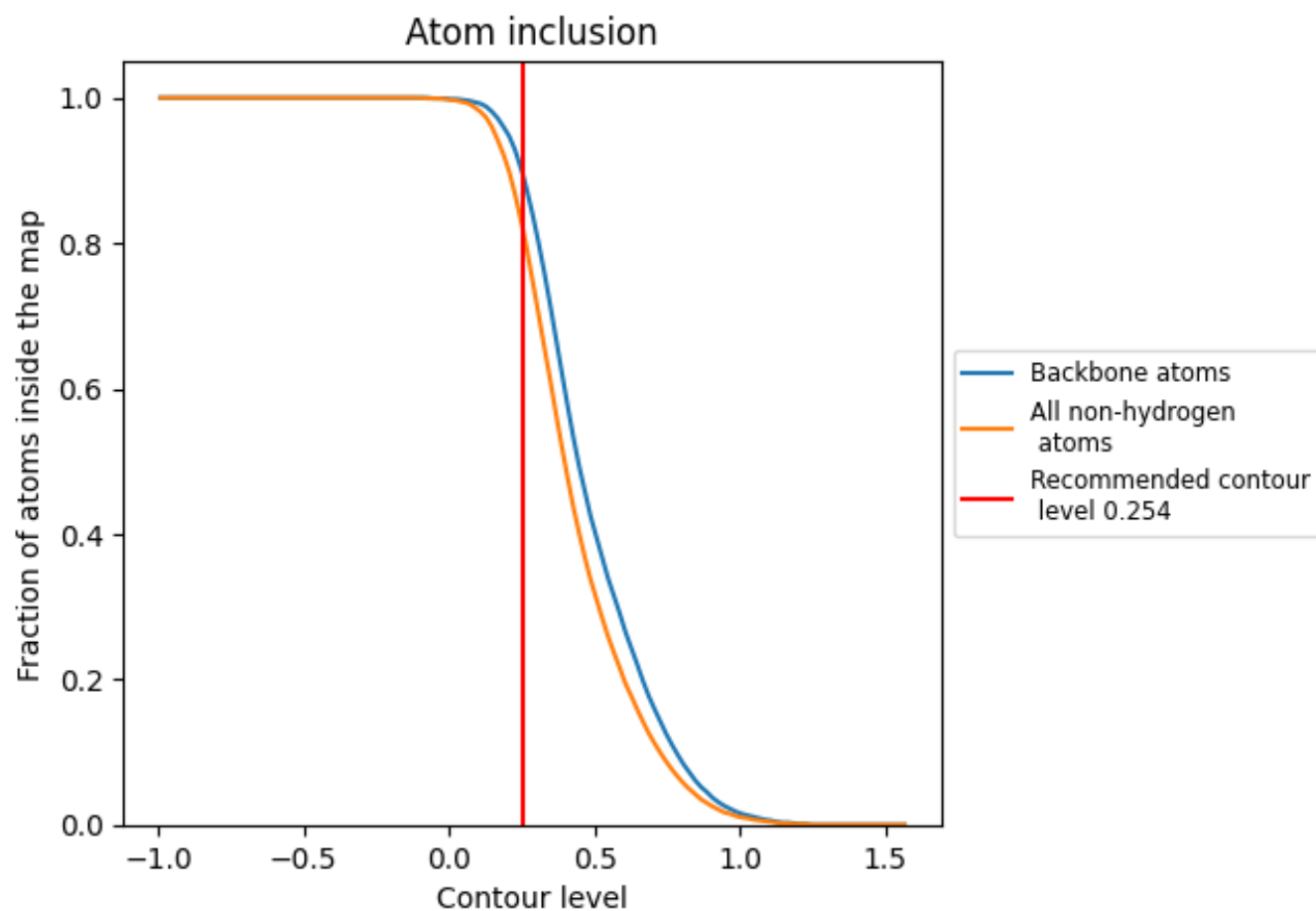
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.254).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.254) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8200	<div></div> 0.3500
A	<div></div> 0.8200	<div></div> 0.3510
B	<div></div> 0.8210	<div></div> 0.3510
C	<div></div> 0.8200	<div></div> 0.3500
D	<div></div> 0.8210	<div></div> 0.3500

