



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 30, 2024 – 08:58 pm BST

PDB ID : 1E0J  
Title : gp4d helicase from phage T7 ADPNP complex  
Authors : Singleton, M.R.; Sawaya, M.R.; Ellenberger, T.; Wigley, D.B.  
Deposited on : 2000-03-30  
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

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>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36.2  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

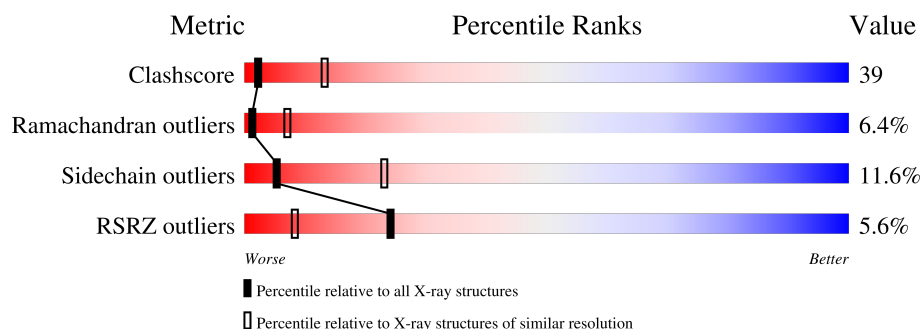
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	289	<div> <div>8%</div> <div>39% 49% 10% ..</div> </div>
1	B	289	<div> <div>3%</div> <div>41% 47% 11% .</div> </div>
1	C	289	<div> <div>6%</div> <div>38% 50% 11%</div> </div>
1	D	289	<div> <div>6%</div> <div>42% 48% 9% .</div> </div>
1	E	289	<div> <div>5%</div> <div>38% 49% 11% .</div> </div>
1	F	289	<div> <div>6%</div> <div>41% 49% 9% .</div> </div>

## 2 Entry composition [i](#)

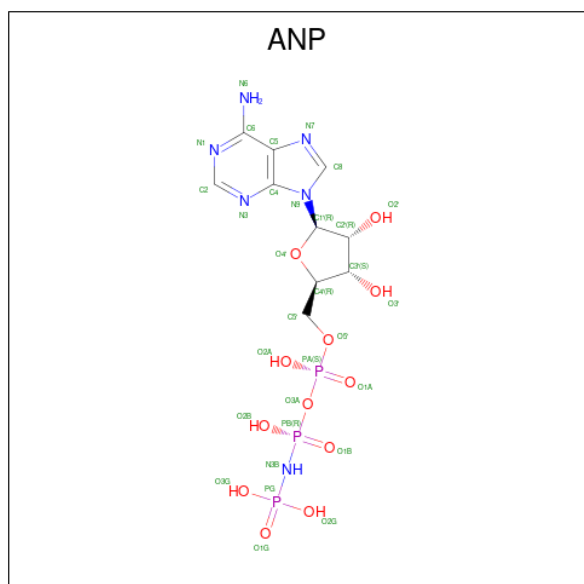
There are 3 unique types of molecules in this entry. The entry contains 13392 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 DNA HELICASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	287	Total	C	N	O	S	0	0	0
			2204	1374	389	428	13			
1	B	288	Total	C	N	O	S	0	0	0
			2214	1378	390	433	13			
1	C	288	Total	C	N	O	S	0	0	0
			2214	1378	390	433	13			
1	D	287	Total	C	N	O	S	0	0	0
			2204	1374	389	428	13			
1	E	288	Total	C	N	O	S	0	0	0
			2214	1378	390	433	13			
1	F	288	Total	C	N	O	S	0	0	0
			2214	1378	390	433	13			

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula:  $C_{10}H_{17}N_6O_{12}P_3$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	D	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	E	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

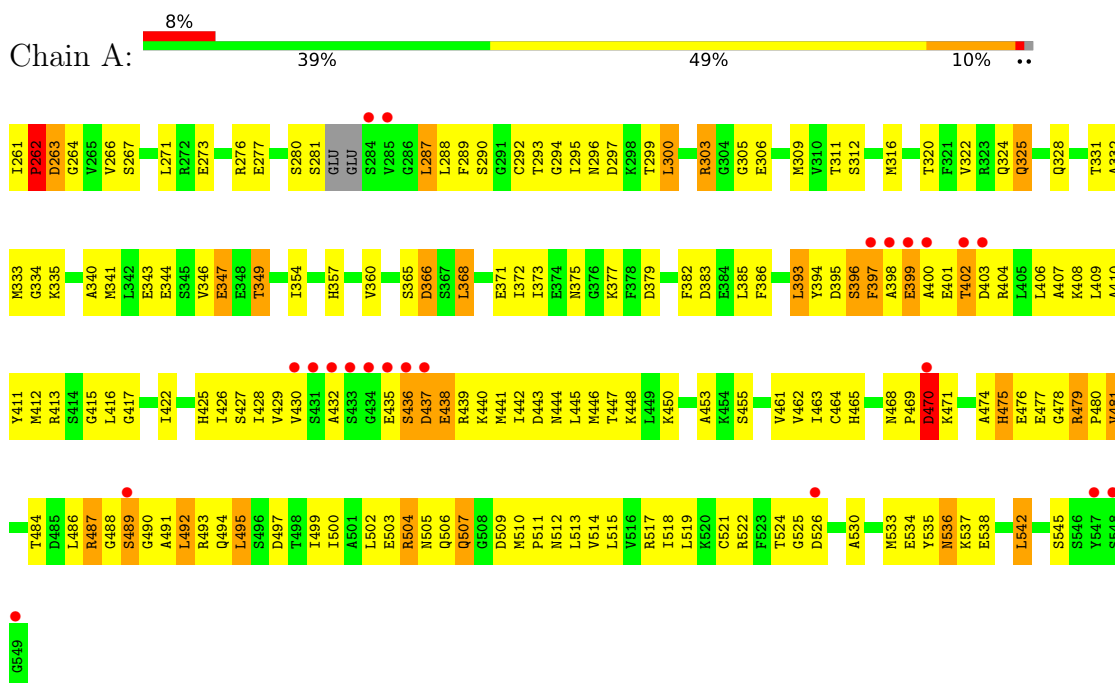
- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		
3	E	1	Total	Mg	0	0
			1	1		

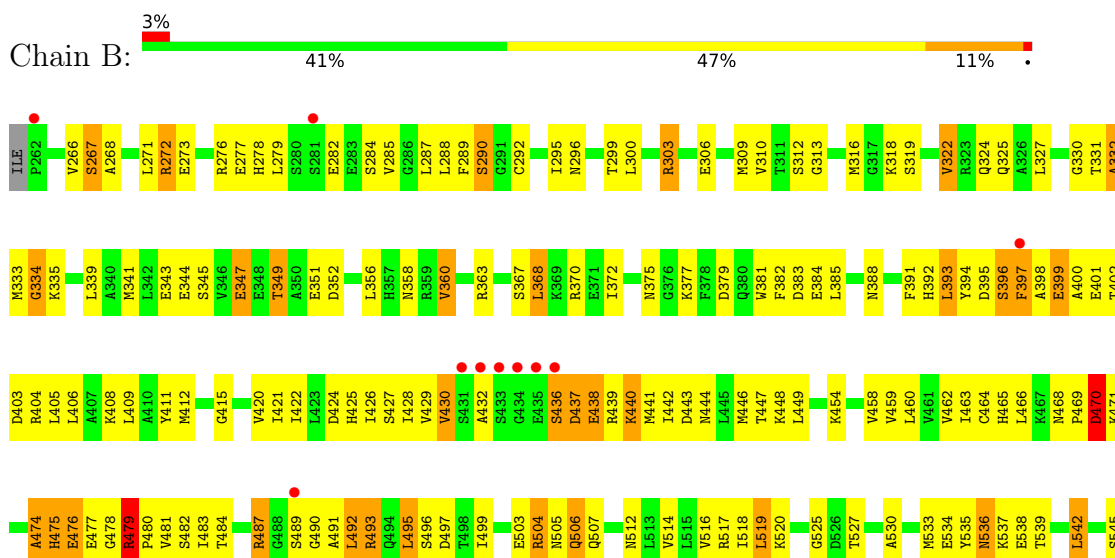
### 3 Residue-property plots

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 electron 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 dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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: DNA HELICASE

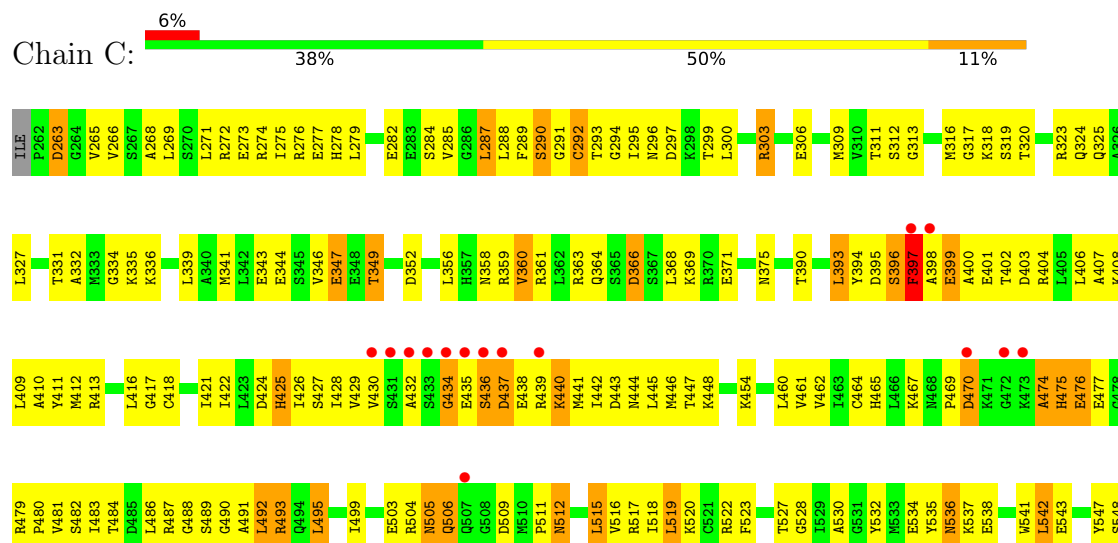


#### • Molecule 1: DNA HELICASE

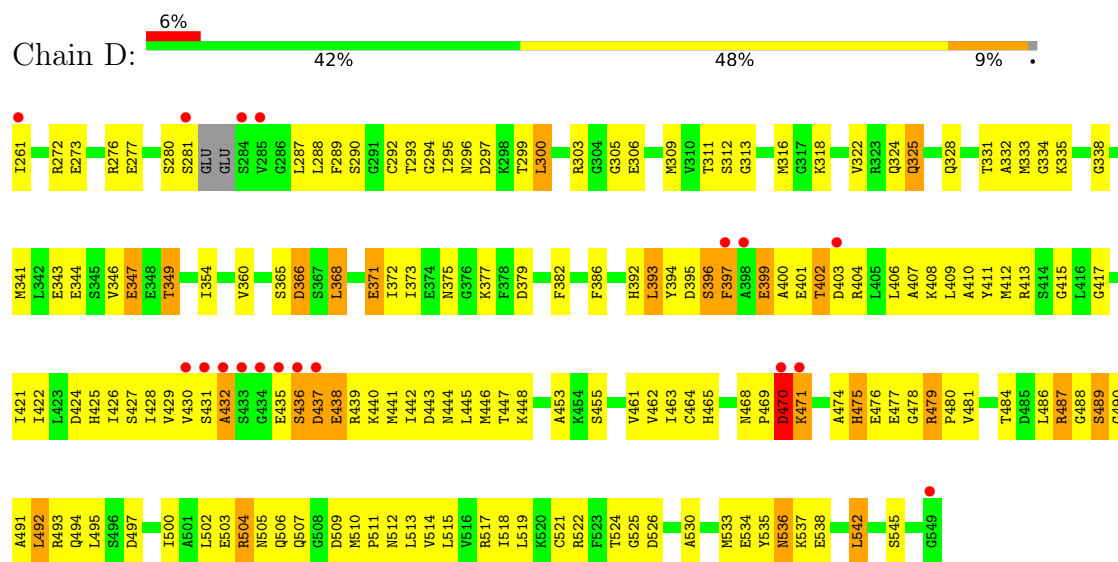




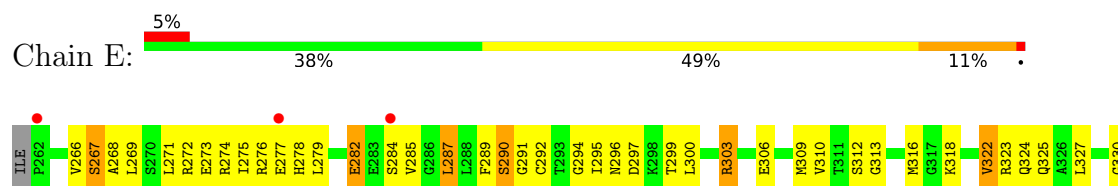
• Molecule 1: DNA HELICASE

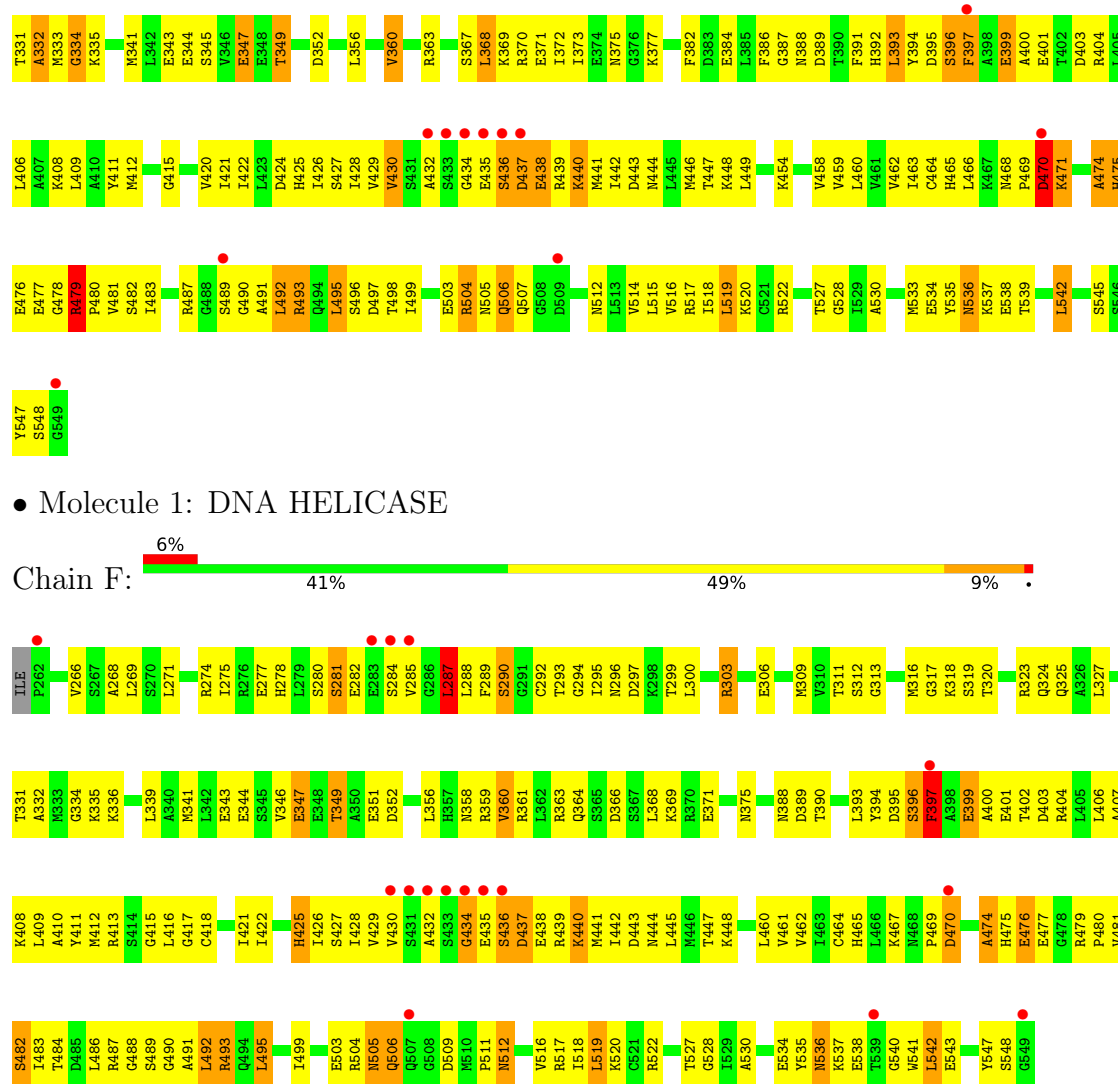


• Molecule 1: DNA HELICASE



• Molecule 1: DNA HELICASE





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	119.18Å 119.18Å 283.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 19.98 – 3.00	Depositor EDS
% Data completeness (in resolution range)	96.7 (20.00-3.00) 97.9 (19.98-3.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.55 (at 2.98Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.253 , 0.304 0.245 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	72.3	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 45.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	13392	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.45% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 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: ANP, MG

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	0.42	0/2233	0.72	3/2999 (0.1%)
1	B	0.41	0/2244	0.73	1/3014 (0.0%)
1	C	0.42	0/2244	0.72	1/3014 (0.0%)
1	D	0.41	0/2233	0.68	1/2999 (0.0%)
1	E	0.40	0/2244	0.72	1/3014 (0.0%)
1	F	0.42	0/2244	0.72	1/3014 (0.0%)
All	All	0.41	0/13442	0.71	8/18054 (0.0%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	262	PRO	N-CA-C	6.27	128.40	112.10
1	C	474	ALA	N-CA-C	6.06	127.36	111.00
1	F	474	ALA	N-CA-C	5.93	127.02	111.00
1	A	474	ALA	N-CA-C	5.91	126.95	111.00
1	A	264	GLY	N-CA-C	5.67	127.27	113.10
1	D	474	ALA	N-CA-C	5.64	126.22	111.00
1	E	474	ALA	N-CA-C	5.60	126.11	111.00
1	B	474	ALA	N-CA-C	5.44	125.69	111.00

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	2204	0	2214	173	0
1	B	2214	0	2216	211	0
1	C	2214	0	2217	187	0
1	D	2204	0	2214	172	0
1	E	2214	0	2217	208	0
1	F	2214	0	2217	162	0
2	A	31	0	13	2	0
2	B	31	0	13	3	0
2	D	31	0	13	2	0
2	E	31	0	13	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
All	All	13392	0	13347	1040	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 39.

All (1040) 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:E:290:SER:H	1:E:325:GLN:NE2	1.46	1.14
1:D:476:GLU:HG3	1:E:483:ILE:HD12	1.25	1.10
1:A:290:SER:H	1:A:325:GLN:NE2	1.49	1.08
1:F:327:LEU:HD22	1:F:356:LEU:HD23	1.32	1.07
1:B:290:SER:H	1:B:325:GLN:NE2	1.51	1.05
1:C:327:LEU:HD22	1:C:356:LEU:HD23	1.38	1.03
1:B:476:GLU:HG3	1:C:483:ILE:HD12	1.40	1.03
1:D:290:SER:H	1:D:325:GLN:NE2	1.57	1.02
1:E:324:GLN:HE22	1:E:542:LEU:H	1.07	1.01
1:E:476:GLU:HG3	1:F:483:ILE:HD12	1.43	1.01
1:B:324:GLN:HE22	1:B:542:LEU:H	1.08	0.99
1:E:367:SER:HA	1:E:370:ARG:HH12	1.26	0.99
1:F:344:GLU:HG3	1:F:349:THR:HG22	1.45	0.98
1:B:367:SER:HA	1:B:370:ARG:HH12	1.26	0.98
1:F:290:SER:H	1:F:325:GLN:NE2	1.62	0.98
1:C:344:GLU:HG3	1:C:349:THR:HG22	1.47	0.96
1:A:476:GLU:HG3	1:B:483:ILE:HD12	1.49	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:GLN:HE22	1:A:542:LEU:H	1.08	0.94
1:D:506:GLN:HB2	1:E:527:THR:OG1	1.68	0.94
1:D:324:GLN:HE22	1:D:542:LEU:H	1.01	0.93
1:D:290:SER:H	1:D:325:GLN:HE22	1.08	0.93
1:C:290:SER:H	1:C:325:GLN:NE2	1.66	0.92
1:B:344:GLU:HG3	1:B:349:THR:HG22	1.52	0.92
1:A:506:GLN:HB2	1:B:527:THR:OG1	1.71	0.91
1:D:324:GLN:HE22	1:D:542:LEU:N	1.69	0.90
1:E:344:GLU:HG3	1:E:349:THR:HG22	1.53	0.90
1:E:290:SER:H	1:E:325:GLN:HE22	1.16	0.90
1:E:266:VAL:HG11	1:E:271:LEU:HD21	1.52	0.88
1:E:285:VAL:HG22	1:E:300:LEU:HD22	1.55	0.87
1:A:425:HIS:HE1	1:A:427:SER:HB2	1.40	0.87
1:A:290:SER:H	1:A:325:GLN:HE22	0.91	0.87
1:D:425:HIS:CE1	1:D:427:SER:HB2	2.10	0.87
1:B:266:VAL:HG11	1:B:271:LEU:HD21	1.55	0.86
1:D:324:GLN:NE2	1:D:542:LEU:H	1.73	0.86
1:D:425:HIS:HE1	1:D:427:SER:HB2	1.40	0.86
1:A:425:HIS:CE1	1:A:427:SER:HB2	2.11	0.86
1:A:290:SER:N	1:A:325:GLN:HE22	1.74	0.85
1:A:518:ILE:CD1	1:A:530:ALA:HB2	2.08	0.84
1:A:324:GLN:HE22	1:A:542:LEU:N	1.74	0.84
1:F:429:VAL:HG23	1:F:430:VAL:H	1.41	0.84
1:C:425:HIS:CE1	1:C:427:SER:HB2	2.12	0.83
1:C:491:ALA:O	1:C:495:LEU:HD22	1.77	0.83
1:A:429:VAL:HG23	1:A:430:VAL:H	1.44	0.82
1:E:425:HIS:HE1	1:E:427:SER:HB2	1.43	0.82
1:B:370:ARG:HH11	1:B:370:ARG:HB3	1.44	0.82
1:D:429:VAL:HG23	1:D:430:VAL:H	1.44	0.82
1:F:425:HIS:CE1	1:F:427:SER:HB2	2.13	0.82
1:F:491:ALA:O	1:F:495:LEU:HD22	1.80	0.82
1:E:440:LYS:HZ2	1:E:444:ASN:HB2	1.44	0.82
1:C:404:ARG:NH1	1:C:408:LYS:HE3	1.95	0.82
1:C:429:VAL:HG23	1:C:430:VAL:H	1.43	0.81
1:D:477:GLU:OE2	1:E:482:SER:HB2	1.80	0.81
1:B:290:SER:H	1:B:325:GLN:HE21	1.28	0.81
1:A:324:GLN:NE2	1:A:542:LEU:H	1.78	0.81
1:D:518:ILE:CD1	1:D:530:ALA:HB2	2.11	0.81
1:F:401:GLU:HA	1:F:430:VAL:O	1.80	0.81
1:B:425:HIS:HE1	1:B:427:SER:HB2	1.44	0.80
1:B:477:GLU:HA	1:B:505:ASN:HD22	1.46	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:290:SER:N	1:B:325:GLN:NE2	2.29	0.80
1:E:534:GLU:HG3	1:E:545:SER:HB2	1.63	0.80
1:E:477:GLU:HA	1:E:505:ASN:HD22	1.45	0.80
1:C:536:ASN:HD21	1:C:538:GLU:HB2	1.47	0.80
1:B:399:GLU:HB3	1:B:430:VAL:HG21	1.64	0.79
1:C:401:GLU:HA	1:C:430:VAL:O	1.81	0.79
1:E:399:GLU:HB3	1:E:430:VAL:HG21	1.64	0.79
1:B:440:LYS:HZ2	1:B:444:ASN:HB2	1.48	0.79
1:A:484:THR:HA	1:A:493:ARG:NH2	1.98	0.79
1:F:404:ARG:NH1	1:F:408:LYS:HE3	1.97	0.79
1:D:468:ASN:HD21	1:E:493:ARG:HD2	1.48	0.78
1:A:477:GLU:OE2	1:B:482:SER:HB2	1.84	0.78
1:C:425:HIS:HE1	1:C:427:SER:HB2	1.48	0.78
1:D:289:PHE:H	1:D:296:ASN:HD21	1.32	0.78
1:E:370:ARG:HH11	1:E:370:ARG:HB3	1.48	0.78
1:C:440:LYS:HZ2	1:C:444:ASN:HB2	1.48	0.77
1:E:536:ASN:HD22	1:E:538:GLU:H	1.32	0.77
1:F:425:HIS:HE1	1:F:427:SER:HB2	1.49	0.77
1:B:534:GLU:HG3	1:B:545:SER:HB2	1.67	0.77
1:B:429:VAL:HG23	1:B:430:VAL:H	1.50	0.77
1:A:468:ASN:HD21	1:B:493:ARG:HD2	1.50	0.76
1:E:425:HIS:CE1	1:E:427:SER:HB2	2.20	0.76
1:E:429:VAL:HG23	1:E:430:VAL:H	1.50	0.76
1:E:406:LEU:HD21	1:E:448:LYS:HB3	1.66	0.75
1:B:266:VAL:HG11	1:B:271:LEU:CD2	2.15	0.75
1:B:285:VAL:HG22	1:B:300:LEU:HD22	1.68	0.75
1:B:425:HIS:CE1	1:B:427:SER:HB2	2.22	0.75
1:A:290:SER:N	1:A:325:GLN:NE2	2.31	0.75
1:B:406:LEU:HD21	1:B:448:LYS:HB3	1.68	0.74
1:C:285:VAL:HG22	1:C:300:LEU:HD22	1.68	0.74
1:F:440:LYS:O	1:F:440:LYS:HD3	1.87	0.74
1:B:536:ASN:HD22	1:B:538:GLU:H	1.36	0.74
1:D:484:THR:HA	1:D:493:ARG:NH2	2.03	0.74
1:C:289:PHE:H	1:C:296:ASN:HD21	1.36	0.73
1:C:440:LYS:O	1:C:440:LYS:HD3	1.88	0.73
1:D:290:SER:N	1:D:325:GLN:HE22	1.84	0.73
1:C:404:ARG:HH12	1:C:408:LYS:CE	2.02	0.73
1:E:367:SER:HA	1:E:370:ARG:NH1	2.04	0.73
1:C:309:MET:HE1	1:C:464:CYS:HB3	1.70	0.73
1:C:404:ARG:HH12	1:C:408:LYS:HE3	1.52	0.73
1:E:536:ASN:ND2	1:E:538:GLU:H	1.87	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:316:MET:HA	1:C:504:ARG:NH1	2.05	0.72
1:C:313:GLY:HA3	1:C:316:MET:SD	2.29	0.72
1:E:536:ASN:ND2	1:E:539:THR:H	1.87	0.72
1:F:404:ARG:HH12	1:F:408:LYS:CE	2.02	0.72
1:B:290:SER:H	1:B:325:GLN:HE22	1.35	0.72
1:B:367:SER:HA	1:B:370:ARG:NH1	2.04	0.72
1:B:476:GLU:O	1:B:506:GLN:HG2	1.89	0.72
1:E:375:ASN:HD21	1:E:377:LYS:CG	2.02	0.72
1:F:518:ILE:HD13	1:F:530:ALA:HB2	1.69	0.72
1:F:316:MET:HA	1:F:504:ARG:NH1	2.05	0.72
1:F:536:ASN:HD21	1:F:538:GLU:HB2	1.54	0.72
1:B:324:GLN:NE2	1:B:542:LEU:H	1.87	0.72
1:F:404:ARG:HH12	1:F:408:LYS:HE3	1.54	0.72
1:C:331:THR:HG22	1:C:332:ALA:N	2.04	0.72
1:B:489:SER:O	1:B:491:ALA:N	2.23	0.71
1:D:438:GLU:HA	1:D:441:MET:HG2	1.72	0.71
1:E:489:SER:O	1:E:491:ALA:N	2.23	0.71
1:C:399:GLU:HB3	1:C:430:VAL:HG21	1.72	0.71
1:F:313:GLY:HA3	1:F:316:MET:SD	2.31	0.71
1:E:476:GLU:O	1:E:506:GLN:HG2	1.91	0.71
1:A:438:GLU:HA	1:A:441:MET:HG2	1.73	0.71
1:B:395:ASP:O	1:B:396:SER:HB2	1.90	0.71
1:F:489:SER:O	1:F:491:ALA:N	2.24	0.70
1:E:284:SER:O	1:E:303:ARG:HD2	1.90	0.70
1:B:536:ASN:ND2	1:B:539:THR:H	1.89	0.70
1:E:393:LEU:N	1:E:393:LEU:HD12	2.06	0.70
1:F:404:ARG:HH12	1:F:408:LYS:NZ	1.89	0.70
1:E:324:GLN:NE2	1:E:542:LEU:H	1.87	0.70
1:B:375:ASN:HD21	1:B:377:LYS:CG	2.04	0.70
1:E:404:ARG:NH1	1:E:408:LYS:HE3	2.08	0.69
1:F:476:GLU:O	1:F:506:GLN:HG2	1.92	0.69
1:D:309:MET:HE1	1:D:464:CYS:HB3	1.73	0.69
1:F:331:THR:HG22	1:F:332:ALA:N	2.07	0.69
1:B:394:TYR:HE1	1:B:408:LYS:HD2	1.58	0.69
1:D:440:LYS:HD3	1:D:440:LYS:O	1.93	0.69
1:F:399:GLU:HB3	1:F:430:VAL:HG21	1.75	0.69
1:A:354:ILE:HD11	1:A:386:PHE:HE2	1.56	0.68
1:B:324:GLN:HE22	1:B:542:LEU:N	1.88	0.68
1:B:404:ARG:NH1	1:B:408:LYS:HE3	2.08	0.68
1:C:311:THR:HG21	1:C:486:LEU:HD21	1.74	0.68
1:C:489:SER:O	1:C:491:ALA:N	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:404:ARG:HH12	1:C:408:LYS:NZ	1.90	0.68
1:C:469:PRO:HG3	1:C:474:ALA:CB	2.23	0.68
1:E:395:ASP:O	1:E:396:SER:HB2	1.93	0.68
1:F:280:SER:O	1:F:281:SER:HB2	1.92	0.68
1:C:518:ILE:HD13	1:C:530:ALA:HB2	1.73	0.68
1:E:536:ASN:HD21	1:E:538:GLU:HB2	1.59	0.68
1:F:440:LYS:HZ2	1:F:444:ASN:HB2	1.59	0.68
1:B:429:VAL:HG23	1:B:430:VAL:N	2.08	0.68
1:E:394:TYR:HE1	1:E:408:LYS:HD2	1.58	0.68
1:E:429:VAL:HG23	1:E:430:VAL:N	2.08	0.68
1:E:290:SER:N	1:E:325:GLN:NE2	2.31	0.68
1:F:509:ASP:O	1:F:511:PRO:HD3	1.94	0.68
1:C:476:GLU:O	1:C:506:GLN:HG2	1.93	0.67
1:C:439:ARG:O	1:C:442:ILE:HG22	1.93	0.67
1:B:394:TYR:CE1	1:B:408:LYS:HD2	2.30	0.67
1:C:343:GLU:HG3	1:C:428:ILE:HD11	1.76	0.67
1:C:484:THR:HA	1:C:493:ARG:NH2	2.09	0.67
1:F:285:VAL:HG22	1:F:300:LEU:HD22	1.75	0.67
1:F:444:ASN:OD1	1:F:448:LYS:HE2	1.95	0.67
1:B:393:LEU:N	1:B:393:LEU:HD12	2.10	0.67
1:F:439:ARG:O	1:F:442:ILE:HG22	1.95	0.67
1:D:375:ASN:HD21	1:D:377:LYS:CG	2.07	0.67
1:B:370:ARG:HB3	1:B:370:ARG:NH1	2.07	0.67
1:A:309:MET:HE1	1:A:464:CYS:HB3	1.77	0.67
1:C:509:ASP:O	1:C:511:PRO:HD3	1.95	0.67
1:D:354:ILE:HD11	1:D:386:PHE:HE2	1.60	0.67
1:F:400:ALA:O	1:F:430:VAL:HB	1.95	0.67
1:A:375:ASN:HD21	1:A:377:LYS:CG	2.08	0.66
1:C:444:ASN:OD1	1:C:448:LYS:HE2	1.94	0.66
1:C:536:ASN:C	1:C:536:ASN:HD22	1.97	0.66
1:A:477:GLU:HA	1:A:505:ASN:HD22	1.61	0.66
1:B:478:GLY:O	1:B:479:ARG:HB3	1.96	0.66
1:B:536:ASN:ND2	1:B:538:GLU:H	1.92	0.66
1:D:468:ASN:HD21	1:E:493:ARG:CD	2.08	0.66
1:F:429:VAL:HG23	1:F:430:VAL:N	2.11	0.66
1:A:534:GLU:HG3	1:A:545:SER:HB2	1.76	0.66
1:B:507:GLN:NE2	1:C:528:GLY:HA2	2.10	0.66
1:E:394:TYR:CE1	1:E:408:LYS:HD2	2.31	0.66
1:E:370:ARG:HB3	1:E:370:ARG:NH1	2.10	0.66
1:A:478:GLY:O	1:A:479:ARG:HB3	1.95	0.66
1:B:506:GLN:HB2	1:C:527:THR:OG1	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:375:ASN:HD21	1:E:377:LYS:HG3	1.60	0.66
1:B:440:LYS:NZ	1:B:444:ASN:HB2	2.09	0.65
1:C:477:GLU:HA	1:C:505:ASN:ND2	2.11	0.65
1:C:429:VAL:HG23	1:C:430:VAL:N	2.11	0.65
1:F:290:SER:H	1:F:325:GLN:HE21	1.41	0.65
1:F:469:PRO:HG3	1:F:474:ALA:CB	2.25	0.65
1:D:492:LEU:C	1:D:494:GLN:H	1.98	0.65
1:E:324:GLN:HE22	1:E:542:LEU:N	1.87	0.65
1:D:477:GLU:HA	1:D:505:ASN:HD22	1.60	0.65
1:E:290:SER:N	1:E:325:GLN:HE22	1.92	0.65
1:A:492:LEU:C	1:A:494:GLN:H	1.98	0.65
1:E:536:ASN:HD22	1:E:536:ASN:C	1.99	0.65
1:F:311:THR:HG21	1:F:486:LEU:HD21	1.78	0.65
1:A:440:LYS:O	1:A:440:LYS:HD3	1.97	0.65
1:B:536:ASN:HD21	1:B:538:GLU:HB2	1.61	0.65
1:B:536:ASN:HD22	1:B:536:ASN:C	2.00	0.64
1:E:477:GLU:OE2	1:F:482:SER:HB2	1.96	0.64
1:E:478:GLY:O	1:E:479:ARG:HB3	1.97	0.64
1:C:422:ILE:HD13	1:C:461:VAL:HB	1.78	0.64
1:B:468:ASN:HD21	1:C:493:ARG:CZ	2.11	0.64
1:D:401:GLU:HA	1:D:430:VAL:O	1.97	0.64
1:A:305:GLY:HA2	1:A:453:ALA:O	1.98	0.64
1:A:429:VAL:HG23	1:A:430:VAL:N	2.12	0.64
1:A:489:SER:O	1:A:491:ALA:N	2.31	0.64
1:C:402:THR:HG23	1:C:445:LEU:HD13	1.79	0.64
1:C:400:ALA:O	1:C:430:VAL:HB	1.98	0.64
1:D:290:SER:N	1:D:325:GLN:NE2	2.39	0.63
1:E:536:ASN:HD22	1:E:538:GLU:N	1.95	0.63
1:B:470:ASP:OD2	1:C:467:LYS:NZ	2.31	0.63
1:D:489:SER:O	1:D:491:ALA:N	2.32	0.63
1:E:290:SER:H	1:E:325:GLN:HE21	1.38	0.63
1:F:343:GLU:HG3	1:F:428:ILE:HD11	1.80	0.63
1:E:476:GLU:CG	1:F:483:ILE:HD12	2.26	0.63
1:E:440:LYS:O	1:E:440:LYS:HD3	1.97	0.63
1:B:382:PHE:HE1	1:C:275:ILE:HD12	1.63	0.63
1:D:429:VAL:HG23	1:D:430:VAL:N	2.12	0.63
1:E:426:ILE:HG12	1:E:426:ILE:O	1.97	0.63
1:E:518:ILE:HD13	1:E:530:ALA:HB2	1.81	0.63
1:C:339:LEU:HB3	1:C:341:MET:HE3	1.81	0.63
1:C:536:ASN:ND2	1:C:538:GLU:H	1.96	0.63
1:F:289:PHE:H	1:F:296:ASN:HD21	1.46	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:383:ASP:CG	1:B:272:ARG:HH22	2.01	0.62
1:A:437:ASP:C	1:A:439:ARG:H	2.03	0.62
1:D:373:ILE:HD11	1:E:279:LEU:HB2	1.80	0.62
1:F:290:SER:N	1:F:325:GLN:NE2	2.42	0.62
1:D:395:ASP:O	1:D:396:SER:HB2	1.98	0.62
1:E:440:LYS:NZ	1:E:444:ASN:HB2	2.13	0.62
1:B:375:ASN:HD21	1:B:377:LYS:HG3	1.63	0.62
1:F:536:ASN:ND2	1:F:538:GLU:H	1.98	0.62
1:D:375:ASN:HD21	1:D:377:LYS:HG3	1.65	0.62
1:A:401:GLU:HA	1:A:430:VAL:O	1.99	0.62
1:F:484:THR:HA	1:F:493:ARG:NH2	2.15	0.62
1:E:444:ASN:OD1	1:E:448:LYS:HE2	1.98	0.62
1:F:406:LEU:HD21	1:F:448:LYS:HB3	1.82	0.62
1:F:292:CYS:SG	1:F:295:ILE:CD1	2.88	0.62
1:D:399:GLU:HB3	1:D:430:VAL:HG21	1.82	0.62
1:E:360:VAL:HG11	1:E:368:LEU:HD11	1.81	0.61
1:A:262:PRO:O	1:A:263:ASP:HB2	1.99	0.61
1:A:344:GLU:OE2	1:A:349:THR:HB	2.00	0.61
1:A:382:PHE:CZ	1:B:272:ARG:HB2	2.34	0.61
1:D:534:GLU:HG3	1:D:545:SER:HB2	1.81	0.61
1:C:395:ASP:O	1:C:396:SER:HB2	2.01	0.61
1:D:468:ASN:ND2	1:E:493:ARG:HD2	2.15	0.61
1:F:395:ASP:O	1:F:396:SER:HB2	2.00	0.61
1:A:395:ASP:O	1:A:396:SER:HB2	1.98	0.61
1:F:443:ASP:O	1:F:447:THR:HG23	2.00	0.61
1:A:294:GLY:HA2	1:A:297:ASP:HB2	1.82	0.61
1:A:426:ILE:HG12	1:A:426:ILE:O	2.00	0.61
1:D:465:HIS:O	1:D:487:ARG:HB2	2.00	0.61
1:F:438:GLU:HA	1:F:441:MET:HG2	1.82	0.61
1:F:477:GLU:HA	1:F:505:ASN:ND2	2.14	0.61
1:F:536:ASN:C	1:F:536:ASN:HD22	2.02	0.61
1:B:273:GLU:OE2	1:B:276:ARG:NH1	2.34	0.61
1:A:289:PHE:HA	1:A:325:GLN:HE21	1.65	0.61
1:C:275:ILE:O	1:C:278:HIS:HB3	2.00	0.61
1:C:438:GLU:HA	1:C:441:MET:HG2	1.83	0.61
1:D:437:ASP:C	1:D:439:ARG:H	2.04	0.61
1:D:392:HIS:ND1	1:E:267:SER:HB2	2.15	0.61
1:B:444:ASN:OD1	1:B:448:LYS:HE2	2.01	0.60
1:A:397:PHE:HZ	1:B:454:LYS:HE3	1.66	0.60
1:A:402:THR:HG23	1:A:445:LEU:HD13	1.83	0.60
1:B:344:GLU:CG	1:B:349:THR:HG22	2.29	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:422:ILE:HD13	1:F:461:VAL:HB	1.82	0.60
1:B:518:ILE:HD13	1:B:530:ALA:HB2	1.83	0.60
1:C:443:ASP:O	1:C:447:THR:HG23	2.01	0.60
1:D:289:PHE:N	1:D:296:ASN:HD21	1.99	0.60
1:D:394:TYR:CE1	1:D:408:LYS:HD2	2.37	0.60
1:E:514:VAL:HG13	1:E:533:MET:HB2	1.81	0.60
1:B:351:GLU:HG3	1:C:279:LEU:HD21	1.83	0.60
1:E:278:HIS:O	1:E:282:GLU:HB3	2.01	0.60
1:F:266:VAL:HG11	1:F:271:LEU:HD21	1.83	0.60
1:B:292:CYS:HB2	1:B:533:MET:HG2	1.83	0.60
1:E:344:GLU:CG	1:E:349:THR:HG22	2.29	0.60
1:E:470:ASP:OD2	1:F:467:LYS:NZ	2.34	0.60
1:B:313:GLY:HA3	1:B:316:MET:SD	2.41	0.60
1:D:375:ASN:ND2	1:D:377:LYS:HG3	2.17	0.60
1:B:440:LYS:O	1:B:440:LYS:HD3	2.01	0.60
1:C:324:GLN:HE22	1:C:542:LEU:H	1.49	0.60
1:A:375:ASN:ND2	1:A:377:LYS:HG3	2.17	0.60
1:A:518:ILE:HD11	1:A:530:ALA:HB2	1.84	0.60
1:B:290:SER:N	1:B:325:GLN:HE22	1.96	0.60
1:B:446:MET:SD	1:B:492:LEU:HB3	2.42	0.60
1:D:426:ILE:HG12	1:D:426:ILE:O	2.01	0.60
1:B:331:THR:O	1:B:334:GLY:N	2.30	0.60
1:B:536:ASN:HD22	1:B:538:GLU:N	2.00	0.60
1:F:402:THR:HG23	1:F:445:LEU:HD13	1.83	0.59
1:C:358:ASN:O	1:C:360:VAL:HG22	2.01	0.59
1:C:290:SER:N	1:C:325:GLN:NE2	2.44	0.59
1:E:375:ASN:ND2	1:E:377:LYS:HG3	2.18	0.59
1:A:492:LEU:C	1:A:494:GLN:N	2.56	0.59
1:C:303:ARG:O	1:C:306:GLU:HB2	2.02	0.59
1:F:358:ASN:O	1:F:360:VAL:HG22	2.02	0.59
1:F:287:LEU:HD11	1:F:335:LYS:HG3	1.84	0.59
1:D:311:THR:HG21	1:D:486:LEU:HD21	1.85	0.59
1:D:492:LEU:C	1:D:494:GLN:N	2.56	0.59
1:E:375:ASN:HD21	1:E:377:LYS:CB	2.15	0.59
1:D:402:THR:HG23	1:D:445:LEU:HD13	1.85	0.59
1:A:439:ARG:O	1:A:442:ILE:HG22	2.03	0.59
1:F:339:LEU:HB3	1:F:341:MET:HE3	1.84	0.59
1:F:343:GLU:C	1:F:397:PHE:HE1	2.06	0.59
1:A:262:PRO:O	1:A:263:ASP:CB	2.50	0.59
1:B:480:PRO:HA	1:B:503:GLU:CD	2.22	0.58
1:E:309:MET:HE1	1:E:464:CYS:HB3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:382:PHE:HE1	1:F:275:ILE:HD12	1.68	0.58
1:A:375:ASN:HD21	1:A:377:LYS:HG3	1.68	0.58
1:A:394:TYR:CE1	1:A:408:LYS:HD2	2.39	0.58
1:A:399:GLU:HB3	1:A:430:VAL:HG21	1.85	0.58
1:D:397:PHE:CZ	1:E:454:LYS:HE3	2.38	0.58
1:E:331:THR:HG22	1:E:332:ALA:N	2.17	0.58
1:E:480:PRO:HA	1:E:503:GLU:CD	2.23	0.58
1:D:477:GLU:HA	1:D:505:ASN:ND2	2.18	0.58
1:D:506:GLN:HB2	1:E:527:THR:HG1	1.67	0.58
1:F:303:ARG:O	1:F:306:GLU:HB2	2.04	0.58
1:A:484:THR:HA	1:A:493:ARG:HH22	1.69	0.58
1:B:469:PRO:HG3	1:B:474:ALA:CB	2.34	0.58
1:F:320:THR:HG22	1:F:324:GLN:HE21	1.69	0.58
1:A:333:MET:O	1:A:335:LYS:HG2	2.03	0.58
1:B:477:GLU:HA	1:B:505:ASN:ND2	2.16	0.58
1:C:278:HIS:O	1:C:282:GLU:HB2	2.03	0.58
1:C:480:PRO:HA	1:C:503:GLU:CD	2.24	0.58
1:C:491:ALA:O	1:C:495:LEU:CD2	2.50	0.58
1:E:309:MET:HE3	1:E:462:VAL:HG12	1.85	0.58
1:A:444:ASN:OD1	1:A:448:LYS:HE2	2.04	0.58
1:E:282:GLU:O	1:E:282:GLU:HG3	2.03	0.58
1:E:477:GLU:HA	1:E:505:ASN:ND2	2.16	0.58
1:B:319:SER:OG	2:B:700:ANP:O1B	2.22	0.57
1:C:406:LEU:HD21	1:C:448:LYS:HB3	1.86	0.57
1:D:305:GLY:HA2	1:D:453:ALA:O	2.03	0.57
1:D:444:ASN:OD1	1:D:448:LYS:HE2	2.04	0.57
1:F:394:TYR:OH	1:F:400:ALA:HB2	2.04	0.57
1:C:394:TYR:OH	1:C:400:ALA:HB2	2.04	0.57
1:E:372:ILE:HA	1:E:375:ASN:OD1	2.03	0.57
1:E:534:GLU:HG3	1:E:545:SER:CB	2.34	0.57
1:E:327:LEU:HD22	1:E:356:LEU:HD23	1.86	0.57
1:E:401:GLU:HA	1:E:430:VAL:O	2.04	0.57
1:A:469:PRO:O	1:A:470:ASP:C	2.43	0.57
1:B:312:SER:OG	1:B:318:LYS:HG3	2.03	0.57
1:B:360:VAL:HG11	1:B:368:LEU:HD11	1.85	0.57
1:C:290:SER:H	1:C:325:GLN:HE21	1.46	0.57
1:A:477:GLU:HA	1:A:505:ASN:ND2	2.19	0.57
1:B:491:ALA:O	1:B:495:LEU:HD22	2.05	0.57
1:E:289:PHE:H	1:E:296:ASN:HD21	1.50	0.57
1:D:443:ASP:O	1:D:447:THR:HG23	2.05	0.57
1:D:331:THR:HG22	1:D:332:ALA:N	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:404:ARG:HH12	1:E:408:LYS:CE	2.17	0.57
1:A:311:THR:HG21	1:A:486:LEU:HD21	1.87	0.57
1:C:399:GLU:HB3	1:C:430:VAL:CG2	2.34	0.57
1:D:439:ARG:O	1:D:442:ILE:HG22	2.05	0.57
1:E:292:CYS:HB2	1:E:533:MET:HG2	1.86	0.57
1:F:440:LYS:HD3	1:F:440:LYS:C	2.23	0.57
1:A:296:ASN:O	1:A:300:LEU:N	2.31	0.57
1:C:284:SER:HB2	1:C:523:PHE:HZ	1.70	0.57
1:D:509:ASP:C	1:D:511:PRO:HD3	2.24	0.56
1:F:426:ILE:O	1:F:426:ILE:HG23	2.05	0.56
1:A:536:ASN:HD21	1:A:538:GLU:HB2	1.70	0.56
1:C:287:LEU:HD11	1:C:335:LYS:HG3	1.86	0.56
1:C:399:GLU:HB3	1:C:430:VAL:HG11	1.87	0.56
1:C:440:LYS:HD3	1:C:440:LYS:C	2.25	0.56
1:C:536:ASN:ND2	1:C:538:GLU:HB2	2.17	0.56
1:D:478:GLY:O	1:D:479:ARG:HB3	2.04	0.56
1:E:394:TYR:OH	1:E:400:ALA:HB2	2.04	0.56
1:E:399:GLU:HB3	1:E:430:VAL:CG2	2.33	0.56
1:A:379:ASP:OD1	1:B:276:ARG:NH2	2.38	0.56
1:A:507:GLN:HE21	1:B:517:ARG:HH11	1.53	0.56
1:B:375:ASN:HD21	1:B:377:LYS:CB	2.18	0.56
1:B:426:ILE:HG12	1:B:426:ILE:O	2.04	0.56
1:B:468:ASN:HD21	1:C:493:ARG:CD	2.17	0.56
1:C:343:GLU:C	1:C:397:PHE:HE1	2.09	0.56
1:C:512:ASN:O	1:C:534:GLU:HA	2.05	0.56
1:E:420:VAL:HG13	1:E:459:VAL:CG1	2.35	0.56
1:F:512:ASN:O	1:F:534:GLU:HA	2.04	0.56
1:C:407:ALA:O	1:C:410:ALA:HB3	2.05	0.56
1:B:266:VAL:HG12	1:B:267:SER:N	2.20	0.56
1:C:396:SER:O	1:C:397:PHE:CB	2.54	0.56
1:D:294:GLY:HA2	1:D:297:ASP:HB2	1.85	0.56
1:F:399:GLU:HB3	1:F:430:VAL:CG2	2.35	0.56
1:B:375:ASN:ND2	1:B:377:LYS:HG3	2.21	0.56
1:C:273:GLU:OE2	1:C:276:ARG:NH1	2.38	0.56
1:F:290:SER:H	1:F:325:GLN:HE22	1.52	0.56
1:F:492:LEU:HD12	1:F:492:LEU:H	1.70	0.56
1:B:404:ARG:HH12	1:B:408:LYS:CE	2.18	0.56
1:B:468:ASN:HD21	1:C:493:ARG:NE	2.03	0.56
1:D:393:LEU:N	1:D:393:LEU:HD12	2.21	0.56
1:E:331:THR:O	1:E:334:GLY:N	2.29	0.56
1:F:399:GLU:HB3	1:F:430:VAL:HG11	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:399:GLU:HB3	1:A:430:VAL:HG11	1.88	0.56
1:B:289:PHE:H	1:B:296:ASN:HD21	1.53	0.56
1:A:273:GLU:OE1	1:A:276:ARG:NH1	2.39	0.56
1:D:366:ASP:OD1	1:E:284:SER:HB3	2.06	0.56
1:E:477:GLU:CA	1:E:505:ASN:HD22	2.17	0.56
1:B:344:GLU:HG3	1:B:349:THR:CG2	2.33	0.56
1:A:289:PHE:H	1:A:296:ASN:HD21	1.54	0.55
1:B:401:GLU:HB3	1:B:404:ARG:HB2	1.88	0.55
1:D:261:ILE:HG22	1:D:261:ILE:O	2.06	0.55
1:B:394:TYR:OH	1:B:400:ALA:HB2	2.06	0.55
1:D:379:ASP:OD1	1:E:276:ARG:NH2	2.39	0.55
1:E:309:MET:HE3	1:E:462:VAL:C	2.27	0.55
1:A:365:SER:OG	1:A:368:LEU:HB2	2.07	0.55
1:B:309:MET:HE3	1:B:462:VAL:HG12	1.87	0.55
1:B:468:ASN:HD21	1:C:493:ARG:HD2	1.70	0.55
1:D:289:PHE:HA	1:D:325:GLN:HE21	1.70	0.55
1:E:392:HIS:C	1:E:393:LEU:HD12	2.26	0.55
1:C:469:PRO:HG3	1:C:474:ALA:HB1	1.88	0.55
1:E:375:ASN:HD21	1:E:377:LYS:HB2	1.71	0.55
1:A:303:ARG:HB2	1:A:306:GLU:OE2	2.06	0.55
1:A:422:ILE:HD13	1:A:461:VAL:HB	1.89	0.55
1:A:509:ASP:C	1:A:511:PRO:HD3	2.27	0.55
1:D:312:SER:HB2	1:D:502:LEU:O	2.06	0.55
1:E:399:GLU:HB3	1:E:430:VAL:HG11	1.87	0.55
1:C:294:GLY:HA2	1:C:297:ASP:HB2	1.88	0.55
1:C:363:ARG:HA	1:C:369:LYS:HE2	1.89	0.55
1:D:344:GLU:OE2	1:D:349:THR:HB	2.05	0.55
1:D:399:GLU:HB3	1:D:430:VAL:HG11	1.88	0.55
1:A:413:ARG:O	1:A:417:GLY:HA2	2.06	0.55
1:B:401:GLU:HA	1:B:430:VAL:O	2.07	0.55
1:D:469:PRO:O	1:D:470:ASP:C	2.45	0.55
1:F:309:MET:HE1	1:F:464:CYS:HB3	1.88	0.55
1:F:346:VAL:HG23	1:F:347:GLU:N	2.21	0.55
1:B:284:SER:O	1:B:303:ARG:HD2	2.07	0.55
1:B:477:GLU:CA	1:B:505:ASN:HD22	2.15	0.55
1:E:313:GLY:HA3	1:E:316:MET:SD	2.47	0.55
1:F:480:PRO:HA	1:F:503:GLU:CD	2.27	0.55
1:F:536:ASN:ND2	1:F:538:GLU:HB2	2.22	0.55
1:B:351:GLU:OE1	1:C:278:HIS:NE2	2.40	0.55
1:B:399:GLU:HB3	1:B:430:VAL:CG2	2.33	0.55
1:D:536:ASN:HD21	1:D:538:GLU:HB2	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:396:SER:O	1:F:397:PHE:CB	2.55	0.55
1:B:420:VAL:HG13	1:B:459:VAL:CG1	2.37	0.54
1:C:492:LEU:HD12	1:C:492:LEU:H	1.70	0.54
1:D:446:MET:HG3	1:D:492:LEU:HB3	1.89	0.54
1:D:468:ASN:HD21	1:E:493:ARG:CZ	2.19	0.54
1:B:439:ARG:O	1:B:442:ILE:HG22	2.07	0.54
1:D:492:LEU:HD12	1:D:493:ARG:H	1.73	0.54
1:C:426:ILE:HG23	1:C:426:ILE:O	2.07	0.54
1:D:309:MET:HE3	1:D:462:VAL:HG12	1.90	0.54
1:E:446:MET:SD	1:E:492:LEU:HB3	2.48	0.54
1:F:324:GLN:HE22	1:F:542:LEU:H	1.55	0.54
1:F:393:LEU:HD12	1:F:393:LEU:N	2.22	0.54
1:A:309:MET:HE3	1:A:462:VAL:HG12	1.90	0.54
1:A:393:LEU:HD12	1:A:393:LEU:N	2.23	0.54
1:D:413:ARG:O	1:D:417:GLY:HA2	2.07	0.54
1:B:400:ALA:O	1:B:430:VAL:HB	2.08	0.54
1:D:536:ASN:ND2	1:D:538:GLU:HB2	2.23	0.54
1:E:345:SER:OG	1:E:347:GLU:HG2	2.08	0.54
1:E:439:ARG:O	1:E:442:ILE:HG22	2.07	0.54
1:E:469:PRO:HG3	1:E:474:ALA:CB	2.37	0.54
1:B:534:GLU:HG3	1:B:545:SER:CB	2.37	0.54
1:C:547:TYR:CG	1:C:548:SER:N	2.76	0.54
1:E:506:GLN:HB2	1:F:527:THR:OG1	2.08	0.54
1:A:536:ASN:ND2	1:A:538:GLU:HB2	2.23	0.54
1:C:426:ILE:O	1:C:426:ILE:HG12	2.08	0.54
1:D:518:ILE:HD11	1:D:530:ALA:HB2	1.90	0.54
1:E:303:ARG:O	1:E:306:GLU:HB2	2.07	0.54
1:E:273:GLU:OE1	1:E:276:ARG:NH1	2.40	0.54
1:B:331:THR:HG22	1:B:332:ALA:N	2.22	0.53
1:B:425:HIS:NE2	1:B:465:HIS:NE2	2.56	0.53
1:B:514:VAL:HG13	1:B:533:MET:HB2	1.90	0.53
1:D:288:LEU:HD12	1:D:288:LEU:H	1.73	0.53
1:E:437:ASP:C	1:E:439:ARG:H	2.12	0.53
1:F:324:GLN:HE22	1:F:542:LEU:HB2	1.71	0.53
1:A:266:VAL:HG11	1:A:271:LEU:HD21	1.89	0.53
1:A:300:LEU:HD12	1:A:524:THR:CG2	2.38	0.53
1:B:443:ASP:O	1:B:447:THR:HG23	2.08	0.53
1:F:344:GLU:CG	1:F:349:THR:HG22	2.31	0.53
1:A:303:ARG:HB2	1:A:306:GLU:CD	2.28	0.53
1:B:303:ARG:O	1:B:306:GLU:HB2	2.08	0.53
1:B:370:ARG:NH1	1:B:370:ARG:CB	2.71	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:268:ALA:HA	1:C:271:LEU:HD12	1.90	0.53
1:D:470:ASP:OD1	1:E:493:ARG:NH2	2.41	0.53
1:A:288:LEU:H	1:A:288:LEU:HD12	1.73	0.53
1:B:327:LEU:HD22	1:B:356:LEU:HD23	1.90	0.53
1:B:399:GLU:HB3	1:B:430:VAL:HG11	1.89	0.53
1:D:386:PHE:CD1	1:E:268:ALA:HB1	2.44	0.53
1:F:413:ARG:O	1:F:417:GLY:HA2	2.09	0.53
1:B:379:ASP:OD2	1:C:276:ARG:NH2	2.41	0.53
1:E:401:GLU:HB3	1:E:404:ARG:HB2	1.90	0.53
1:E:536:ASN:ND2	1:E:538:GLU:N	2.53	0.53
1:F:278:HIS:O	1:F:282:GLU:HB2	2.08	0.53
1:A:446:MET:HG3	1:A:492:LEU:HB3	1.90	0.53
1:D:300:LEU:HD12	1:D:524:THR:CG2	2.39	0.53
1:E:278:HIS:O	1:E:282:GLU:CB	2.56	0.53
1:E:491:ALA:O	1:E:495:LEU:HD22	2.09	0.53
1:A:524:THR:C	1:A:526:ASP:H	2.10	0.53
1:A:324:GLN:HE22	1:A:542:LEU:HB2	1.74	0.53
1:C:271:LEU:O	1:C:275:ILE:HG13	2.08	0.53
1:E:344:GLU:HG3	1:E:349:THR:CG2	2.32	0.53
1:A:506:GLN:CB	1:B:527:THR:OG1	2.53	0.53
1:B:437:ASP:C	1:B:439:ARG:H	2.13	0.53
1:B:493:ARG:O	1:B:493:ARG:HG3	2.09	0.53
1:C:411:TYR:OH	1:C:416:LEU:HD21	2.09	0.53
1:D:343:GLU:HG3	1:D:428:ILE:HD11	1.89	0.53
1:B:397:PHE:CE1	1:C:454:LYS:HE3	2.43	0.52
1:D:303:ARG:HB2	1:D:306:GLU:CD	2.29	0.52
1:D:311:THR:O	1:D:312:SER:HB3	2.09	0.52
1:A:292:CYS:HB2	1:A:533:MET:HG2	1.90	0.52
1:C:344:GLU:CG	1:C:349:THR:HG22	2.32	0.52
1:F:363:ARG:HA	1:F:369:LYS:HE2	1.91	0.52
1:D:375:ASN:HD21	1:D:377:LYS:CB	2.23	0.52
1:E:312:SER:OG	1:E:318:LYS:HG3	2.10	0.52
1:F:351:GLU:OE2	1:F:363:ARG:HG3	2.09	0.52
1:D:382:PHE:CE1	1:E:272:ARG:HA	2.45	0.52
1:A:401:GLU:HB3	1:A:404:ARG:HB2	1.90	0.52
1:C:440:LYS:HZ2	1:C:444:ASN:CB	2.20	0.52
1:D:401:GLU:HB3	1:D:404:ARG:HB2	1.92	0.52
1:B:375:ASN:HD21	1:B:377:LYS:HB2	1.73	0.52
1:B:478:GLY:O	1:B:479:ARG:CB	2.57	0.52
1:B:535:TYR:HD1	1:B:542:LEU:HD13	1.75	0.52
1:D:422:ILE:HD13	1:D:461:VAL:HB	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:292:CYS:SG	1:F:295:ILE:HD12	2.50	0.52
1:A:331:THR:HG22	1:A:332:ALA:N	2.24	0.52
1:A:343:GLU:HG3	1:A:428:ILE:HD11	1.92	0.52
1:F:407:ALA:O	1:F:410:ALA:HB3	2.10	0.52
1:F:469:PRO:HG3	1:F:474:ALA:HB1	1.91	0.52
1:F:547:TYR:CG	1:F:548:SER:N	2.77	0.52
1:A:515:LEU:HD23	1:A:515:LEU:C	2.30	0.52
1:B:372:ILE:HA	1:B:375:ASN:OD1	2.09	0.52
1:C:324:GLN:HE22	1:C:542:LEU:N	2.07	0.52
1:D:524:THR:C	1:D:526:ASP:H	2.12	0.52
1:F:491:ALA:O	1:F:495:LEU:CD2	2.54	0.52
1:A:396:SER:O	1:A:397:PHE:CB	2.58	0.52
1:B:392:HIS:C	1:B:393:LEU:HD12	2.31	0.52
1:C:394:TYR:HE2	1:C:408:LYS:HD2	1.75	0.52
1:C:476:GLU:H	1:C:476:GLU:CD	2.11	0.52
1:D:280:SER:O	1:D:281:SER:HB2	2.09	0.52
1:B:404:ARG:HH12	1:B:408:LYS:HE3	1.75	0.51
1:D:303:ARG:HB2	1:D:306:GLU:OE2	2.11	0.51
1:E:370:ARG:NH1	1:E:370:ARG:CB	2.74	0.51
1:A:300:LEU:HD12	1:A:524:THR:HG21	1.92	0.51
1:E:468:ASN:HD21	1:F:493:ARG:CZ	2.23	0.51
1:A:346:VAL:HG23	1:A:347:GLU:N	2.25	0.51
1:B:425:HIS:CE1	1:B:465:HIS:CD2	2.98	0.51
1:C:324:GLN:HE22	1:C:542:LEU:HB2	1.75	0.51
1:F:411:TYR:OH	1:F:416:LEU:HD21	2.11	0.51
1:A:366:ASP:OD1	1:B:284:SER:HB3	2.11	0.51
1:B:285:VAL:HG22	1:B:300:LEU:CD2	2.37	0.51
1:B:347:GLU:OE1	1:C:274:ARG:HD2	2.11	0.51
1:C:290:SER:H	1:C:325:GLN:HE22	1.56	0.51
1:A:443:ASP:O	1:A:447:THR:HG23	2.11	0.51
1:D:300:LEU:HD12	1:D:524:THR:HG21	1.93	0.51
1:E:352:ASP:OD2	1:E:363:ARG:NH2	2.44	0.51
1:F:396:SER:O	1:F:397:PHE:HB2	2.10	0.51
1:C:396:SER:O	1:C:397:PHE:HB2	2.10	0.51
1:C:536:ASN:HD22	1:C:538:GLU:H	1.57	0.51
1:A:492:LEU:HD12	1:A:493:ARG:H	1.76	0.51
1:C:440:LYS:NZ	1:C:444:ASN:HB2	2.23	0.51
1:D:292:CYS:HB2	1:D:533:MET:HG2	1.92	0.51
1:D:322:VAL:CG1	1:D:422:ILE:HG21	2.41	0.51
1:A:426:ILE:O	1:A:426:ILE:HG23	2.11	0.50
1:B:309:MET:HE3	1:B:462:VAL:C	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:290:SER:OG	1:D:328:GLN:HG2	2.11	0.50
1:D:468:ASN:HD21	1:E:493:ARG:NE	2.09	0.50
1:E:478:GLY:O	1:E:479:ARG:CB	2.58	0.50
1:A:290:SER:OG	1:A:328:GLN:HG2	2.11	0.50
1:D:372:ILE:HA	1:D:375:ASN:OD1	2.11	0.50
1:D:536:ASN:HD22	1:D:538:GLU:H	1.59	0.50
1:E:333:MET:O	1:E:335:LYS:HG2	2.11	0.50
1:A:517:ARG:HD2	1:A:519:LEU:HD11	1.94	0.50
1:B:306:GLU:HA	1:B:497:ASP:OD2	2.12	0.50
1:B:352:ASP:OD2	1:B:363:ARG:NH2	2.44	0.50
1:E:299:THR:O	1:E:300:LEU:HB2	2.11	0.50
1:A:397:PHE:CZ	1:B:454:LYS:HE3	2.45	0.50
1:E:469:PRO:O	1:E:470:ASP:C	2.50	0.50
1:C:320:THR:HG22	1:C:324:GLN:HE21	1.77	0.50
1:D:346:VAL:HG23	1:D:347:GLU:N	2.27	0.50
1:D:394:TYR:OH	1:D:400:ALA:HB2	2.12	0.50
1:E:404:ARG:HH12	1:E:408:LYS:HE3	1.75	0.50
1:F:426:ILE:O	1:F:426:ILE:HG12	2.11	0.50
1:F:483:ILE:HG12	1:F:519:LEU:HG	1.94	0.50
1:A:465:HIS:O	1:A:487:ARG:HB2	2.11	0.50
1:E:341:MET:HB3	1:E:344:GLU:HG2	1.92	0.50
1:F:404:ARG:HH12	1:F:408:LYS:HZ1	1.58	0.50
1:F:492:LEU:HD12	1:F:492:LEU:N	2.27	0.50
1:A:373:ILE:HD11	1:B:279:LEU:HB2	1.93	0.50
1:A:375:ASN:HD21	1:A:377:LYS:CB	2.25	0.50
1:D:411:TYR:O	1:D:415:GLY:N	2.45	0.50
1:A:468:ASN:ND2	1:B:493:ARG:HD2	2.24	0.50
1:C:536:ASN:C	1:C:536:ASN:ND2	2.65	0.50
1:D:426:ILE:O	1:D:426:ILE:HG23	2.12	0.50
1:A:437:ASP:C	1:A:439:ARG:N	2.66	0.49
1:D:476:GLU:CG	1:E:483:ILE:HD12	2.18	0.49
1:E:404:ARG:HG3	1:E:404:ARG:HH11	1.77	0.49
1:E:449:LEU:HD22	1:E:460:LEU:HD21	1.94	0.49
1:F:425:HIS:CD2	1:F:465:HIS:NE2	2.80	0.49
1:F:476:GLU:H	1:F:476:GLU:CD	2.13	0.49
1:E:440:LYS:HD3	1:E:440:LYS:C	2.33	0.49
1:E:493:ARG:O	1:E:493:ARG:HG3	2.12	0.49
1:D:303:ARG:O	1:D:306:GLU:HB2	2.12	0.49
1:A:509:ASP:O	1:A:511:PRO:HD3	2.13	0.49
1:C:331:THR:HG22	1:C:332:ALA:H	1.76	0.49
1:C:346:VAL:HG23	1:C:347:GLU:N	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:296:ASN:O	1:D:300:LEU:N	2.34	0.49
1:E:395:ASP:OD2	1:F:274:ARG:NH2	2.36	0.49
1:E:266:VAL:HG11	1:E:271:LEU:CD2	2.33	0.49
1:E:400:ALA:O	1:E:430:VAL:HB	2.12	0.49
1:C:266:VAL:HG11	1:C:271:LEU:HD21	1.95	0.49
1:C:413:ARG:O	1:C:417:GLY:HA2	2.12	0.49
1:C:499:ILE:HG13	1:C:520:LYS:HB3	1.95	0.49
1:A:404:ARG:O	1:A:408:LYS:HG3	2.12	0.49
1:A:475:HIS:H	1:A:479:ARG:HD2	1.77	0.49
1:B:409:LEU:HA	1:B:412:MET:CE	2.43	0.49
1:E:425:HIS:CE1	1:E:465:HIS:CD2	3.00	0.49
1:C:469:PRO:CG	1:C:474:ALA:CB	2.91	0.49
1:D:394:TYR:HE1	1:D:408:LYS:HD2	1.73	0.49
1:D:404:ARG:NH1	1:D:408:LYS:HE3	2.28	0.49
2:A:700:ANP:O4'	1:B:525:GLY:HA3	2.12	0.49
1:B:383:ASP:CG	1:C:272:ARG:HH22	2.16	0.49
1:B:469:PRO:O	1:B:470:ASP:C	2.50	0.49
1:D:309:MET:CE	1:D:464:CYS:HB3	2.43	0.49
1:F:483:ILE:HD11	1:F:519:LEU:O	2.13	0.49
1:A:372:ILE:HA	1:A:375:ASN:OD1	2.12	0.49
1:A:404:ARG:NH1	1:A:408:LYS:HE3	2.28	0.49
1:D:484:THR:HA	1:D:493:ARG:HH22	1.74	0.49
1:F:294:GLY:HA2	1:F:297:ASP:HB2	1.95	0.49
1:F:499:ILE:HG13	1:F:520:LYS:HB3	1.96	0.48
1:B:339:LEU:HB3	1:B:341:MET:HE2	1.95	0.48
1:E:285:VAL:CG2	1:E:300:LEU:HD22	2.34	0.48
1:E:476:GLU:CD	1:E:476:GLU:H	2.16	0.48
1:A:312:SER:HB2	1:A:502:LEU:O	2.13	0.48
2:B:700:ANP:O3G	1:C:522:ARG:NH1	2.46	0.48
1:C:313:GLY:CA	1:C:316:MET:SD	2.99	0.48
1:E:306:GLU:HA	1:E:497:ASP:OD2	2.14	0.48
1:E:420:VAL:HG13	1:E:459:VAL:HG12	1.95	0.48
1:C:309:MET:HE3	1:C:462:VAL:HG12	1.95	0.48
1:C:536:ASN:HB2	1:C:543:GLU:OE1	2.13	0.48
1:D:316:MET:HA	1:D:504:ARG:NH1	2.28	0.48
1:D:396:SER:O	1:D:397:PHE:CB	2.61	0.48
1:D:437:ASP:C	1:D:439:ARG:N	2.67	0.48
1:F:399:GLU:HB3	1:F:430:VAL:CG1	2.44	0.48
1:A:411:TYR:OH	1:A:416:LEU:HD21	2.12	0.48
1:A:470:ASP:OD1	1:B:493:ARG:NH2	2.46	0.48
1:B:383:ASP:OD1	1:C:272:ARG:NH2	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:411:TYR:O	1:B:415:GLY:N	2.46	0.48
1:D:299:THR:O	1:D:300:LEU:HB2	2.14	0.48
1:B:536:ASN:ND2	1:B:538:GLU:N	2.59	0.48
1:C:483:ILE:HG12	1:C:519:LEU:HG	1.96	0.48
1:D:402:THR:HG23	1:D:445:LEU:CD1	2.44	0.48
1:E:492:LEU:HD12	1:E:493:ARG:H	1.79	0.48
1:F:289:PHE:HA	1:F:325:GLN:HE21	1.79	0.48
1:F:434:GLY:O	1:F:435:GLU:HG3	2.13	0.48
1:C:312:SER:OG	1:C:318:LYS:CG	2.61	0.48
1:C:492:LEU:HD12	1:C:492:LEU:N	2.29	0.48
1:E:387:GLY:O	1:E:389:ASP:N	2.47	0.48
1:A:316:MET:HA	1:A:504:ARG:NH1	2.29	0.48
1:A:402:THR:HG23	1:A:445:LEU:CD1	2.43	0.48
1:D:517:ARG:HD2	1:D:519:LEU:HD11	1.96	0.48
1:E:396:SER:O	1:E:397:PHE:CB	2.62	0.48
1:F:312:SER:OG	1:F:318:LYS:CG	2.62	0.48
1:A:394:TYR:HE1	1:A:408:LYS:HD2	1.78	0.47
1:B:404:ARG:NH1	1:B:408:LYS:CE	2.77	0.47
1:B:449:LEU:HD22	1:B:460:LEU:HD21	1.96	0.47
1:C:393:LEU:HD12	1:C:393:LEU:N	2.29	0.47
1:C:434:GLY:O	1:C:435:GLU:HG3	2.14	0.47
1:D:509:ASP:O	1:D:511:PRO:HD3	2.13	0.47
1:B:440:LYS:HD3	1:B:440:LYS:C	2.34	0.47
1:C:469:PRO:O	1:C:470:ASP:C	2.52	0.47
1:D:535:TYR:HD1	1:D:542:LEU:HD13	1.78	0.47
1:E:474:ALA:HA	1:E:479:ARG:HD2	1.96	0.47
1:F:299:THR:O	1:F:300:LEU:HB2	2.13	0.47
1:A:309:MET:CE	1:A:464:CYS:HB3	2.42	0.47
1:A:536:ASN:HD22	1:A:538:GLU:H	1.62	0.47
1:B:345:SER:OG	1:B:347:GLU:HG2	2.14	0.47
1:B:474:ALA:HA	1:B:479:ARG:HD2	1.94	0.47
1:C:292:CYS:SG	1:C:295:ILE:CD1	3.02	0.47
1:F:394:TYR:HE2	1:F:408:LYS:HD2	1.79	0.47
1:F:356:LEU:HG	1:F:541:TRP:NE1	2.29	0.47
1:F:469:PRO:O	1:F:470:ASP:C	2.51	0.47
1:F:536:ASN:ND2	1:F:536:ASN:C	2.68	0.47
1:B:396:SER:O	1:B:397:PHE:CB	2.62	0.47
2:B:700:ANP:O3G	1:C:522:ARG:CZ	2.62	0.47
1:C:343:GLU:HG3	1:C:428:ILE:CD1	2.44	0.47
1:E:271:LEU:O	1:E:275:ILE:HG13	2.14	0.47
1:E:425:HIS:NE2	1:E:465:HIS:NE2	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:361:ARG:NH1	1:F:535:TYR:OH	2.48	0.47
1:B:492:LEU:HD12	1:B:493:ARG:H	1.79	0.47
1:B:506:GLN:CB	1:C:527:THR:OG1	2.63	0.47
1:D:429:VAL:CG2	1:D:430:VAL:H	2.23	0.47
1:E:443:ASP:O	1:E:447:THR:HG23	2.13	0.47
1:F:536:ASN:HD22	1:F:538:GLU:H	1.62	0.47
1:A:322:VAL:CG1	1:A:422:ILE:HG21	2.44	0.47
1:A:324:GLN:NE2	1:A:542:LEU:HB2	2.30	0.47
1:B:429:VAL:CG2	1:B:430:VAL:H	2.22	0.47
1:B:476:GLU:CD	1:B:476:GLU:H	2.18	0.47
1:D:292:CYS:SG	1:D:295:ILE:CD1	3.03	0.47
1:E:426:ILE:HD12	1:E:446:MET:CE	2.43	0.47
1:E:496:SER:O	1:E:520:LYS:HE2	2.14	0.47
1:F:309:MET:HE3	1:F:462:VAL:HG12	1.97	0.47
1:F:434:GLY:C	1:F:435:GLU:HG3	2.35	0.47
1:F:492:LEU:HD12	1:F:493:ARG:H	1.80	0.47
1:A:311:THR:O	1:A:312:SER:HB3	2.14	0.47
1:C:361:ARG:NH1	1:C:535:TYR:OH	2.48	0.47
1:C:434:GLY:C	1:C:435:GLU:HG3	2.35	0.47
1:D:538:GLU:HA	1:D:538:GLU:OE1	2.13	0.47
1:F:421:ILE:HB	1:F:460:LEU:HD12	1.97	0.47
1:B:426:ILE:O	1:B:426:ILE:HG23	2.14	0.47
1:D:475:HIS:H	1:D:479:ARG:HD2	1.80	0.47
1:B:309:MET:CE	1:B:462:VAL:HG12	2.44	0.46
1:B:469:PRO:HG3	1:B:474:ALA:HB1	1.96	0.46
1:C:344:GLU:OE2	1:C:349:THR:HB	2.14	0.46
1:E:436:SER:O	1:E:437:ASP:O	2.32	0.46
1:E:537:LYS:HE2	1:E:537:LYS:HB3	1.72	0.46
1:D:306:GLU:HG2	1:D:497:ASP:HB2	1.97	0.46
1:D:515:LEU:HD23	1:D:515:LEU:C	2.36	0.46
1:E:393:LEU:N	1:E:393:LEU:CD1	2.77	0.46
1:E:411:TYR:O	1:E:415:GLY:N	2.47	0.46
1:E:535:TYR:HD1	1:E:542:LEU:HD13	1.80	0.46
1:A:357:HIS:CG	1:A:385:LEU:HD13	2.50	0.46
1:B:343:GLU:HG3	1:B:428:ILE:HD11	1.97	0.46
1:D:407:ALA:O	1:D:410:ALA:HB3	2.14	0.46
1:D:425:HIS:NE2	1:D:465:HIS:NE2	2.62	0.46
1:D:502:LEU:HD23	1:D:514:VAL:HG21	1.97	0.46
1:E:399:GLU:OE1	1:E:430:VAL:HG22	2.16	0.46
1:E:404:ARG:NH1	1:E:408:LYS:CE	2.76	0.46
1:F:313:GLY:CA	1:F:316:MET:SD	3.02	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:399:GLU:HB3	1:C:430:VAL:CG1	2.45	0.46
1:C:483:ILE:HD11	1:C:519:LEU:O	2.15	0.46
1:D:365:SER:OG	1:D:368:LEU:HB2	2.15	0.46
1:F:395:ASP:O	1:F:396:SER:CB	2.64	0.46
1:A:394:TYR:OH	1:A:400:ALA:HB2	2.15	0.46
1:B:436:SER:O	1:B:437:ASP:O	2.33	0.46
1:C:263:ASP:OD1	1:C:263:ASP:N	2.46	0.46
1:D:468:ASN:OD1	1:E:493:ARG:CZ	2.63	0.46
1:E:309:MET:HE3	1:E:462:VAL:O	2.15	0.46
1:F:537:LYS:HB3	1:F:537:LYS:HE2	1.70	0.46
1:B:309:MET:HE1	1:B:464:CYS:HB3	1.98	0.46
1:B:429:VAL:CG2	1:B:430:VAL:N	2.78	0.46
1:C:492:LEU:HD12	1:C:493:ARG:H	1.81	0.46
1:E:273:GLU:OE2	1:E:276:ARG:NH1	2.48	0.46
1:A:306:GLU:HG2	1:A:497:ASP:HB2	1.97	0.46
1:A:309:MET:HB3	1:A:499:ILE:HG12	1.98	0.46
1:A:386:PHE:CD1	1:B:268:ALA:HB1	2.50	0.46
1:D:324:GLN:HE22	1:D:542:LEU:HB2	1.81	0.46
1:E:429:VAL:CG2	1:E:430:VAL:N	2.77	0.46
1:C:442:ILE:HG23	1:C:443:ASP:OD1	2.16	0.46
1:F:295:ILE:HD11	1:F:516:VAL:HG11	1.97	0.46
1:A:346:VAL:CG2	1:A:347:GLU:N	2.79	0.46
1:A:524:THR:C	1:A:526:ASP:N	2.70	0.46
1:E:429:VAL:CG2	1:E:430:VAL:H	2.22	0.46
1:A:292:CYS:O	1:A:295:ILE:HD13	2.16	0.46
1:A:537:LYS:HB3	1:A:537:LYS:HE2	1.74	0.46
1:C:289:PHE:HB3	1:C:325:GLN:NE2	2.30	0.46
1:F:409:LEU:HA	1:F:412:MET:HE3	1.96	0.46
1:A:289:PHE:N	1:A:296:ASN:HD21	2.13	0.45
1:D:404:ARG:O	1:D:408:LYS:HG3	2.16	0.45
1:C:285:VAL:HG22	1:C:300:LEU:CD2	2.43	0.45
1:E:295:ILE:HG13	1:E:516:VAL:HG11	1.97	0.45
1:E:542:LEU:HD12	1:E:542:LEU:HA	1.88	0.45
1:A:320:THR:OG1	2:A:700:ANP:H8	2.16	0.45
1:C:395:ASP:O	1:C:396:SER:CB	2.64	0.45
1:D:476:GLU:O	1:D:506:GLN:HG2	2.16	0.45
1:E:409:LEU:HD23	1:E:412:MET:CE	2.46	0.45
1:E:409:LEU:HA	1:E:412:MET:CE	2.46	0.45
1:F:440:LYS:NZ	1:F:444:ASN:HB2	2.28	0.45
1:F:442:ILE:HG23	1:F:443:ASP:OD1	2.16	0.45
1:D:392:HIS:HA	1:E:267:SER:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:421:ILE:HG12	1:E:458:VAL:HG21	1.99	0.45
1:A:411:TYR:O	1:A:415:GLY:N	2.49	0.45
1:B:316:MET:HA	1:B:504:ARG:NH1	2.32	0.45
1:C:312:SER:OG	1:C:318:LYS:HG2	2.16	0.45
1:C:324:GLN:NE2	1:C:542:LEU:H	2.15	0.45
1:C:425:HIS:CD2	1:C:465:HIS:NE2	2.85	0.45
1:D:399:GLU:HB3	1:D:430:VAL:CG2	2.47	0.45
1:D:425:HIS:H	1:D:463:ILE:HB	1.81	0.45
1:A:510:MET:SD	1:A:513:LEU:HD22	2.56	0.45
1:B:404:ARG:HG3	1:B:404:ARG:HH11	1.82	0.45
1:C:295:ILE:HD11	1:C:516:VAL:HG11	1.99	0.45
1:C:436:SER:O	1:C:437:ASP:O	2.35	0.45
1:D:401:GLU:O	1:D:404:ARG:HB3	2.16	0.45
1:E:438:GLU:HA	1:E:441:MET:HG2	1.99	0.45
1:E:480:PRO:HA	1:E:503:GLU:OE2	2.17	0.45
1:F:440:LYS:HZ2	1:F:444:ASN:CB	2.28	0.45
1:A:292:CYS:HB3	1:A:295:ILE:HD13	1.98	0.45
1:A:401:GLU:O	1:A:404:ARG:HB3	2.16	0.45
1:B:480:PRO:HB3	1:B:517:ARG:NH2	2.32	0.45
1:C:352:ASP:OD2	1:C:363:ARG:NH2	2.50	0.45
1:C:477:GLU:HA	1:C:505:ASN:HD22	1.80	0.45
1:D:311:THR:HG21	1:D:486:LEU:CD2	2.46	0.45
1:D:318:LYS:NZ	2:D:700:ANP:O1G	2.40	0.45
1:D:510:MET:SD	1:D:513:LEU:HD22	2.57	0.45
1:A:425:HIS:H	1:A:463:ILE:HB	1.81	0.45
1:F:436:SER:O	1:F:437:ASP:O	2.35	0.45
1:A:538:GLU:OE1	1:A:538:GLU:HA	2.17	0.45
1:B:292:CYS:O	1:B:295:ILE:HD13	2.16	0.45
1:B:310:VAL:O	1:B:463:ILE:HA	2.17	0.45
1:B:399:GLU:OE1	1:B:430:VAL:HG22	2.16	0.45
1:B:295:ILE:HG13	1:B:516:VAL:HG11	1.99	0.45
1:C:319:SER:O	1:C:323:ARG:HB2	2.17	0.45
1:E:292:CYS:O	1:E:295:ILE:HD13	2.17	0.45
1:A:407:ALA:O	1:A:410:ALA:HB3	2.16	0.44
1:A:436:SER:O	1:A:437:ASP:O	2.35	0.44
1:B:440:LYS:HZ2	1:B:444:ASN:HD22	1.63	0.44
1:D:333:MET:O	1:D:335:LYS:HG2	2.16	0.44
1:D:521:CYS:O	1:D:525:GLY:N	2.43	0.44
1:A:273:GLU:OE2	1:A:276:ARG:NH1	2.50	0.44
1:D:375:ASN:HD21	1:D:377:LYS:HB2	1.81	0.44
1:E:515:LEU:C	1:E:515:LEU:HD23	2.37	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:469:PRO:CG	1:F:474:ALA:CB	2.93	0.44
1:D:542:LEU:HD12	1:D:542:LEU:HA	1.89	0.44
1:E:469:PRO:HG3	1:E:474:ALA:HB1	1.98	0.44
1:E:471:LYS:O	1:E:471:LYS:HD3	2.18	0.44
1:A:299:THR:O	1:A:300:LEU:HB2	2.17	0.44
1:D:346:VAL:CG2	1:D:347:GLU:N	2.81	0.44
1:E:273:GLU:CD	1:E:276:ARG:NH1	2.70	0.44
1:E:387:GLY:O	1:F:269:LEU:HD11	2.16	0.44
1:F:429:VAL:CG2	1:F:430:VAL:H	2.21	0.44
1:B:471:LYS:HD3	1:B:471:LYS:O	2.18	0.44
1:C:289:PHE:CD1	1:C:295:ILE:HG21	2.53	0.44
1:C:299:THR:O	1:C:300:LEU:HB2	2.17	0.44
1:C:359:ARG:HD3	1:C:541:TRP:NE1	2.33	0.44
1:C:547:TYR:CD2	1:C:548:SER:N	2.86	0.44
1:E:404:ARG:O	1:E:408:LYS:HG3	2.17	0.44
1:E:498:THR:HA	1:E:520:LYS:O	2.18	0.44
1:A:287:LEU:HD11	1:A:335:LYS:HG3	1.98	0.44
1:A:289:PHE:CA	1:A:325:GLN:HE21	2.30	0.44
1:C:289:PHE:N	1:C:296:ASN:HD21	2.11	0.44
1:E:424:ASP:O	1:E:425:HIS:CB	2.66	0.44
1:D:273:GLU:OE2	1:D:276:ARG:NH1	2.50	0.44
1:D:382:PHE:HE1	1:E:275:ILE:HD12	1.82	0.44
1:D:436:SER:O	1:D:437:ASP:O	2.36	0.44
1:D:537:LYS:HE2	1:D:537:LYS:HB3	1.75	0.44
1:F:547:TYR:CD2	1:F:548:SER:N	2.86	0.44
1:A:273:GLU:CD	1:A:276:ARG:NH1	2.71	0.44
1:A:303:ARG:O	1:A:306:GLU:HB2	2.18	0.44
1:B:438:GLU:HA	1:B:441:MET:HG2	2.00	0.44
1:B:466:LEU:HD13	1:B:475:HIS:CE1	2.53	0.44
1:D:292:CYS:O	1:D:295:ILE:HD13	2.18	0.44
1:A:396:SER:OG	1:A:398:ALA:HB3	2.18	0.43
1:A:480:PRO:HA	1:A:503:GLU:CD	2.37	0.43
1:A:491:ALA:O	1:A:494:GLN:HB2	2.17	0.43
1:A:502:LEU:HD23	1:A:514:VAL:HG21	1.99	0.43
1:B:442:ILE:HG23	1:B:443:ASP:N	2.32	0.43
1:B:517:ARG:HD2	1:B:519:LEU:CD1	2.48	0.43
1:C:291:GLY:O	1:C:292:CYS:HB2	2.18	0.43
1:E:310:VAL:O	1:E:463:ILE:HA	2.18	0.43
1:E:387:GLY:C	1:E:389:ASP:H	2.22	0.43
1:A:436:SER:O	1:A:437:ASP:C	2.55	0.43
1:C:289:PHE:CD1	1:C:295:ILE:CG2	3.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:386:PHE:O	1:E:269:LEU:HG	2.17	0.43
1:E:442:ILE:HG23	1:E:443:ASP:N	2.33	0.43
2:E:700:ANP:O3G	1:F:522:ARG:NH1	2.50	0.43
1:F:406:LEU:CD2	1:F:448:LYS:HB3	2.48	0.43
1:B:339:LEU:HD22	1:B:341:MET:HE3	2.00	0.43
1:D:400:ALA:O	1:D:430:VAL:HB	2.17	0.43
1:F:312:SER:OG	1:F:318:LYS:HG2	2.18	0.43
1:D:480:PRO:HA	1:D:503:GLU:CD	2.39	0.43
1:F:319:SER:O	1:F:323:ARG:HB2	2.18	0.43
1:B:358:ASN:O	1:B:360:VAL:HG22	2.18	0.43
1:B:536:ASN:ND2	1:B:536:ASN:C	2.70	0.43
1:D:436:SER:O	1:D:437:ASP:C	2.56	0.43
1:E:294:GLY:HA2	1:E:297:ASP:HB2	2.00	0.43
1:A:375:ASN:HD21	1:A:377:LYS:HB2	1.82	0.43
1:B:324:GLN:HE22	1:B:542:LEU:HB2	1.84	0.43
1:B:426:ILE:HD12	1:B:446:MET:CE	2.48	0.43
1:E:322:VAL:HG12	1:E:323:ARG:N	2.33	0.43
1:F:493:ARG:O	1:F:493:ARG:HG3	2.17	0.43
1:A:425:HIS:NE2	1:A:465:HIS:NE2	2.67	0.43
1:C:289:PHE:CA	1:C:325:GLN:HE21	2.32	0.43
1:E:426:ILE:CD1	1:E:446:MET:HE2	2.49	0.43
1:F:292:CYS:C	1:F:293:THR:O	2.49	0.43
1:F:317:GLY:O	1:F:318:LYS:C	2.57	0.43
1:F:344:GLU:OE2	1:F:349:THR:HB	2.18	0.43
1:A:280:SER:O	1:A:281:SER:HB2	2.19	0.43
1:B:468:ASN:ND2	1:C:493:ARG:HD2	2.33	0.43
1:B:537:LYS:HE2	1:B:537:LYS:HB3	1.70	0.43
2:D:700:ANP:O3G	1:E:522:ARG:NH2	2.51	0.43
1:F:359:ARG:HD3	1:F:541:TRP:NE1	2.33	0.43
1:D:408:LYS:O	1:D:412:MET:HG3	2.19	0.43
1:E:536:ASN:ND2	1:E:536:ASN:C	2.70	0.43
1:A:399:GLU:HB3	1:A:430:VAL:CG2	2.49	0.43
1:A:437:ASP:O	1:A:439:ARG:N	2.52	0.43
1:A:476:GLU:O	1:A:506:GLN:HG2	2.19	0.43
1:C:475:HIS:C	1:C:477:GLU:N	2.72	0.43
1:D:475:HIS:C	1:D:477:GLU:N	2.72	0.43
1:D:524:THR:C	1:D:526:ASP:N	2.72	0.43
1:A:266:VAL:HG12	1:A:267:SER:N	2.34	0.42
1:A:450:LYS:HB2	1:A:495:LEU:HB3	2.01	0.42
1:A:480:PRO:HB3	1:A:517:ARG:NH2	2.34	0.42
1:B:480:PRO:HB3	1:B:517:ARG:HH21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:289:PHE:HA	1:C:325:GLN:HE21	1.84	0.42
1:C:356:LEU:HG	1:C:541:TRP:NE1	2.33	0.42
1:C:421:ILE:HB	1:C:460:LEU:HD12	2.01	0.42
1:D:313:GLY:HA3	1:D:316:MET:SD	2.59	0.42
1:D:435:GLU:O	1:D:436:SER:O	2.37	0.42
1:D:480:PRO:HB3	1:D:517:ARG:NH2	2.34	0.42
1:A:408:LYS:O	1:A:412:MET:HG3	2.20	0.42
1:C:394:TYR:CE2	1:C:408:LYS:HD2	2.53	0.42
1:C:426:ILE:CD1	1:C:446:MET:HE2	2.49	0.42
1:E:369:LYS:NZ	1:F:282:GLU:HG3	2.33	0.42
1:A:396:SER:O	1:A:397:PHE:HB3	2.19	0.42
1:A:475:HIS:C	1:A:477:GLU:N	2.73	0.42
1:A:542:LEU:HD12	1:A:542:LEU:HA	1.88	0.42
1:B:266:VAL:CG1	1:B:267:SER:N	2.81	0.42
1:B:341:MET:HB3	1:B:344:GLU:HG2	2.00	0.42
1:D:491:ALA:O	1:D:494:GLN:HB2	2.19	0.42
1:E:399:GLU:HB3	1:E:430:VAL:CG1	2.49	0.42
1:A:404:ARG:HG3	1:A:404:ARG:HH11	1.84	0.42
1:B:446:MET:HE2	1:B:446:MET:HA	2.01	0.42
1:C:537:LYS:HB3	1:C:537:LYS:HE2	1.69	0.42
1:E:463:ILE:HG22	1:E:464:CYS:N	2.33	0.42
1:F:320:THR:HG22	1:F:324:GLN:NE2	2.33	0.42
1:B:424:ASP:O	1:B:425:HIS:CB	2.68	0.42
1:B:484:THR:HA	1:B:493:ARG:NH2	2.34	0.42
1:C:273:GLU:OE1	1:C:273:GLU:HA	2.19	0.42
1:D:409:LEU:HD23	1:D:412:MET:HE2	2.00	0.42
1:D:507:GLN:NE2	1:E:528:GLY:HA2	2.35	0.42
1:F:359:ARG:CZ	1:F:541:TRP:CZ2	3.02	0.42
1:A:409:LEU:HD23	1:A:412:MET:HE2	2.01	0.42
1:E:309:MET:CE	1:E:462:VAL:HG12	2.50	0.42
1:F:344:GLU:HA	1:F:397:PHE:CE1	2.55	0.42
1:B:404:ARG:O	1:B:408:LYS:HG3	2.20	0.42
1:B:507:GLN:NE2	1:C:528:GLY:CA	2.80	0.42
1:C:404:ARG:HG3	1:C:404:ARG:HH11	1.84	0.42
1:E:426:ILE:O	1:E:426:ILE:HG23	2.19	0.42
1:F:477:GLU:HA	1:F:505:ASN:HD22	1.82	0.42
1:F:509:ASP:C	1:F:511:PRO:HD3	2.40	0.42
1:A:261:ILE:HA	1:A:262:PRO:HD2	1.84	0.42
1:A:521:CYS:O	1:A:525:GLY:N	2.43	0.42
1:B:309:MET:HE3	1:B:462:VAL:O	2.20	0.42
1:B:496:SER:OG	1:B:499:ILE:HD11	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:278:HIS:O	1:C:282:GLU:CB	2.66	0.42
1:D:475:HIS:C	1:D:477:GLU:H	2.23	0.42
1:A:311:THR:HG21	1:A:486:LEU:CD2	2.48	0.42
1:B:401:GLU:HB3	1:B:404:ARG:CB	2.49	0.42
1:B:405:LEU:O	1:B:408:LYS:N	2.53	0.42
1:C:344:GLU:HA	1:C:397:PHE:CE1	2.55	0.42
1:E:343:GLU:HG3	1:E:428:ILE:HD11	2.00	0.42
1:E:517:ARG:HD2	1:E:519:LEU:CD1	2.50	0.42
1:F:336:LYS:HB3	1:F:418:CYS:HA	2.02	0.42
1:F:388:ASN:O	1:F:389:ASP:C	2.57	0.42
1:F:399:GLU:CB	1:F:430:VAL:HG11	2.49	0.42
1:B:322:VAL:CG1	1:B:422:ILE:HG21	2.50	0.41
1:B:420:VAL:HG13	1:B:459:VAL:HG12	2.02	0.41
1:C:269:LEU:HA	1:C:269:LEU:HD23	1.84	0.41
1:C:536:ASN:HD22	1:C:537:LYS:N	2.18	0.41
1:D:506:GLN:HG2	1:D:506:GLN:H	1.68	0.41
1:A:535:TYR:HD1	1:A:542:LEU:HD13	1.84	0.41
1:B:383:ASP:O	1:B:385:LEU:N	2.53	0.41
1:B:401:GLU:OE1	1:B:404:ARG:N	2.36	0.41
1:B:405:LEU:O	1:B:406:LEU:C	2.58	0.41
1:C:317:GLY:O	1:C:318:LYS:C	2.58	0.41
1:C:336:LYS:HB3	1:C:418:CYS:HA	2.02	0.41
1:D:368:LEU:O	1:D:371:GLU:HB2	2.20	0.41
1:E:322:VAL:CG1	1:E:422:ILE:HG21	2.50	0.41
1:F:343:GLU:HG3	1:F:428:ILE:CD1	2.48	0.41
1:F:411:TYR:O	1:F:415:GLY:N	2.49	0.41
1:B:322:VAL:HG13	1:B:422:ILE:HG21	2.01	0.41
1:B:465:HIS:O	1:B:487:ARG:HB2	2.20	0.41
1:C:424:ASP:O	1:C:425:HIS:CB	2.68	0.41
1:C:515:LEU:HB2	1:C:532:TYR:CE2	2.55	0.41
1:C:515:LEU:HD12	1:C:532:TYR:CE2	2.55	0.41
1:C:517:ARG:HD2	1:C:519:LEU:CD1	2.50	0.41
1:E:330:GLY:HA3	1:E:391:PHE:CZ	2.56	0.41
1:E:506:GLN:HG2	1:E:506:GLN:H	1.54	0.41
1:E:536:ASN:HD21	1:E:538:GLU:CB	2.32	0.41
1:B:299:THR:O	1:B:300:LEU:HB2	2.20	0.41
1:B:333:MET:O	1:B:335:LYS:HG2	2.20	0.41
1:B:358:ASN:ND2	1:B:381:TRP:CE2	2.88	0.41
1:B:496:SER:O	1:B:520:LYS:HE2	2.20	0.41
1:D:492:LEU:HD12	1:D:493:ARG:N	2.35	0.41
1:E:466:LEU:HD13	1:E:475:HIS:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:496:SER:OG	1:E:499:ILE:HD11	2.20	0.41
1:F:346:VAL:CG2	1:F:347:GLU:N	2.83	0.41
1:F:401:GLU:OE1	1:F:404:ARG:N	2.43	0.41
1:F:536:ASN:HB2	1:F:543:GLU:OE1	2.20	0.41
1:A:481:VAL:HG12	1:A:503:GLU:HG2	2.01	0.41
1:C:404:ARG:HH12	1:C:408:LYS:HZ1	1.68	0.41
1:D:404:ARG:HG3	1:D:404:ARG:HH11	1.86	0.41
1:D:437:ASP:O	1:D:439:ARG:N	2.54	0.41
1:E:480:PRO:HB3	1:E:517:ARG:NH2	2.35	0.41
1:F:437:ASP:C	1:F:439:ARG:H	2.22	0.41
1:F:535:TYR:HE1	1:F:540:GLY:O	2.03	0.41
1:B:282:GLU:O	1:B:282:GLU:HG3	2.20	0.41
1:B:443:ASP:OD1	1:B:491:ALA:HB2	2.21	0.41
1:B:468:ASN:ND2	1:C:493:ARG:CZ	2.82	0.41
1:E:316:MET:HA	1:E:504:ARG:NH1	2.35	0.41
1:E:386:PHE:CD1	1:F:268:ALA:HB1	2.55	0.41
1:F:352:ASP:OD2	1:F:363:ARG:NH2	2.53	0.41
1:B:483:ILE:CG2	1:B:493:ARG:HB2	2.50	0.41
1:E:434:GLY:C	1:E:435:GLU:HG3	2.41	0.41
1:A:435:GLU:O	1:A:436:SER:O	2.39	0.41
1:A:517:ARG:HD2	1:A:519:LEU:CD1	2.50	0.41
1:B:278:HIS:O	1:B:282:GLU:CB	2.69	0.41
1:C:359:ARG:CZ	1:C:541:TRP:CZ2	3.04	0.41
1:D:471:LYS:O	1:D:471:LYS:HD3	2.21	0.41
1:E:476:GLU:HB3	1:E:506:GLN:NE2	2.36	0.41
1:A:340:ALA:N	1:A:341:MET:HE2	2.36	0.41
1:A:475:HIS:C	1:A:477:GLU:H	2.24	0.41
1:B:295:ILE:HD12	1:B:295:ILE:N	2.35	0.41
1:B:330:GLY:HA3	1:B:391:PHE:CZ	2.55	0.41
1:B:476:GLU:CG	1:C:483:ILE:HD12	2.28	0.41
1:B:506:GLN:HG2	1:B:506:GLN:H	1.52	0.41
1:C:265:VAL:O	1:C:265:VAL:HG12	2.21	0.41
1:C:313:GLY:H	1:C:316:MET:HE2	1.86	0.41
1:D:324:GLN:NE2	1:D:542:LEU:HB2	2.35	0.41
1:D:406:LEU:HD21	1:D:448:LYS:HB3	2.02	0.41
1:E:442:ILE:HG23	1:E:443:ASP:OD1	2.20	0.41
1:E:507:GLN:NE2	1:F:528:GLY:HA2	2.35	0.41
1:F:339:LEU:O	1:F:393:LEU:HA	2.21	0.41
1:A:429:VAL:CG2	1:A:430:VAL:H	2.23	0.41
1:C:437:ASP:C	1:C:439:ARG:H	2.24	0.41
1:E:291:GLY:HA2	1:E:542:LEU:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:547:TYR:CG	1:E:548:SER:N	2.89	0.41
1:A:306:GLU:HG2	1:A:497:ASP:CB	2.51	0.40
1:A:396:SER:HB3	1:A:397:PHE:H	1.72	0.40
1:A:400:ALA:O	1:A:430:VAL:HB	2.21	0.40
1:B:480:PRO:HA	1:B:503:GLU:OE2	2.21	0.40
1:C:292:CYS:C	1:C:293:THR:O	2.53	0.40
1:C:399:GLU:CB	1:C:430:VAL:HG11	2.49	0.40
1:B:421:ILE:HG12	1:B:458:VAL:HG21	2.03	0.40
1:D:396:SER:O	1:D:397:PHE:HB3	2.22	0.40
1:D:399:GLU:HB3	1:D:430:VAL:CG1	2.51	0.40
1:E:316:MET:O	1:E:504:ARG:NH1	2.53	0.40
1:B:411:TYR:CD1	1:B:415:GLY:HA3	2.56	0.40
1:B:442:ILE:HG23	1:B:443:ASP:OD1	2.21	0.40
1:D:368:LEU:HD23	1:D:368:LEU:HA	1.86	0.40
1:E:373:ILE:HD13	1:F:280:SER:HB3	2.03	0.40
1:F:309:MET:CE	1:F:464:CYS:HB3	2.50	0.40
1:F:404:ARG:HH11	1:F:404:ARG:HG3	1.86	0.40
1:F:538:GLU:HA	1:F:538:GLU:OE1	2.21	0.40
1:A:536:ASN:ND2	1:A:538:GLU:H	2.19	0.40
1:B:398:ALA:O	1:B:399:GLU:C	2.60	0.40
1:B:492:LEU:HD12	1:B:493:ARG:N	2.36	0.40
1:C:309:MET:CE	1:C:464:CYS:HB3	2.45	0.40
1:C:398:ALA:O	1:C:399:GLU:C	2.60	0.40
1:C:401:GLU:OE1	1:C:404:ARG:N	2.42	0.40
1:C:409:LEU:HA	1:C:412:MET:HE3	2.04	0.40
1:C:509:ASP:C	1:C:511:PRO:HD3	2.41	0.40
1:D:341:MET:HA	1:D:424:ASP:HB3	2.03	0.40
1:D:431:SER:O	1:D:432:ALA:C	2.59	0.40
1:E:292:CYS:HB3	1:E:295:ILE:HD13	2.02	0.40
1:E:426:ILE:CD1	1:E:446:MET:CE	2.98	0.40
1:F:437:ASP:C	1:F:439:ARG:N	2.75	0.40
1:A:411:TYR:CD1	1:A:415:GLY:HA3	2.57	0.40
1:B:426:ILE:CD1	1:B:446:MET:HE2	2.52	0.40
1:C:313:GLY:H	1:C:316:MET:CE	2.34	0.40
1:C:366:ASP:N	1:C:366:ASP:OD1	2.54	0.40
1:D:338:GLY:HA3	1:D:421:ILE:HD13	2.04	0.40
1:D:425:HIS:CE1	1:D:465:HIS:CD2	3.10	0.40
1:F:324:GLN:HE22	1:F:542:LEU:N	2.17	0.40
1:F:517:ARG:HD2	1:F:519:LEU:CD1	2.50	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	283/289 (98%)	231 (82%)	32 (11%)	20 (7%)	1	5
1	B	286/289 (99%)	242 (85%)	26 (9%)	18 (6%)	1	7
1	C	286/289 (99%)	234 (82%)	35 (12%)	17 (6%)	1	9
1	D	283/289 (98%)	231 (82%)	34 (12%)	18 (6%)	1	7
1	E	286/289 (99%)	243 (85%)	24 (8%)	19 (7%)	1	6
1	F	286/289 (99%)	232 (81%)	37 (13%)	17 (6%)	1	9
All	All	1710/1734 (99%)	1413 (83%)	188 (11%)	109 (6%)	1	7

All (109) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	262	PRO
1	A	263	ASP
1	A	396	SER
1	A	436	SER
1	A	437	ASP
1	A	475	HIS
1	A	490	GLY
1	B	396	SER
1	B	436	SER
1	B	437	ASP
1	B	475	HIS
1	B	490	GLY
1	C	396	SER
1	C	436	SER
1	C	437	ASP
1	C	475	HIS
1	C	490	GLY
1	D	396	SER
1	D	436	SER
1	D	437	ASP

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Mol	Chain	Res	Type
1	D	475	HIS
1	D	490	GLY
1	E	388	ASN
1	E	396	SER
1	E	436	SER
1	E	437	ASP
1	E	475	HIS
1	E	490	GLY
1	F	396	SER
1	F	436	SER
1	F	437	ASP
1	F	475	HIS
1	F	490	GLY
1	A	287	LEU
1	A	397	PHE
1	A	399	GLU
1	A	432	ALA
1	A	488	GLY
1	A	489	SER
1	B	334	GLY
1	B	388	ASN
1	B	397	PHE
1	B	399	GLU
1	B	432	ALA
1	C	334	GLY
1	C	397	PHE
1	D	397	PHE
1	D	399	GLU
1	D	432	ALA
1	D	488	GLY
1	D	489	SER
1	E	334	GLY
1	E	397	PHE
1	E	399	GLU
1	E	432	ALA
1	F	287	LEU
1	F	334	GLY
1	F	371	GLU
1	F	397	PHE
1	A	334	GLY
1	A	438	GLU
1	B	384	GLU

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Mol	Chain	Res	Type
1	B	479	ARG
1	C	287	LEU
1	C	292	CYS
1	C	399	GLU
1	C	432	ALA
1	D	287	LEU
1	E	479	ARG
1	F	399	GLU
1	F	432	ALA
1	F	479	ARG
1	A	470	ASP
1	A	471	LYS
1	A	479	ARG
1	B	287	LEU
1	B	438	GLU
1	C	364	GLN
1	C	371	GLU
1	C	425	HIS
1	C	479	ARG
1	D	334	GLY
1	D	371	GLU
1	D	438	GLU
1	D	471	LYS
1	D	479	ARG
1	E	332	ALA
1	E	384	GLU
1	E	438	GLU
1	F	281	SER
1	F	364	GLN
1	F	425	HIS
1	A	371	GLU
1	A	402	THR
1	B	332	ALA
1	B	470	ASP
1	D	402	THR
1	D	470	ASP
1	E	287	LEU
1	E	470	ASP
1	E	471	LYS
1	F	488	GLY
1	B	402	THR
1	C	488	GLY

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Mol	Chain	Res	Type
1	E	371	GLU
1	F	434	GLY
1	C	434	GLY
1	B	430	VAL
1	E	430	VAL

### 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 X-ray entries followed by that with respect to entries of similar resolution.

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	240/242 (99%)	214 (89%)	26 (11%)	6	26
1	B	241/242 (100%)	213 (88%)	28 (12%)	5	23
1	C	241/242 (100%)	210 (87%)	31 (13%)	4	19
1	D	240/242 (99%)	216 (90%)	24 (10%)	7	29
1	E	241/242 (100%)	213 (88%)	28 (12%)	5	23
1	F	241/242 (100%)	211 (88%)	30 (12%)	4	20
All	All	1444/1452 (99%)	1277 (88%)	167 (12%)	5	23

All (167) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	277	GLU
1	A	293	THR
1	A	300	LEU
1	A	303	ARG
1	A	325	GLN
1	A	347	GLU
1	A	349	THR
1	A	360	VAL
1	A	366	ASP
1	A	368	LEU
1	A	393	LEU
1	A	403	ASP
1	A	406	LEU

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Mol	Chain	Res	Type
1	A	455	SER
1	A	470	ASP
1	A	481	VAL
1	A	487	ARG
1	A	492	LEU
1	A	495	LEU
1	A	500	ILE
1	A	504	ARG
1	A	507	GLN
1	A	512	ASN
1	A	522	ARG
1	A	536	ASN
1	A	542	LEU
1	B	267	SER
1	B	272	ARG
1	B	277	GLU
1	B	288	LEU
1	B	290	SER
1	B	303	ARG
1	B	322	VAL
1	B	347	GLU
1	B	349	THR
1	B	360	VAL
1	B	368	LEU
1	B	393	LEU
1	B	403	ASP
1	B	440	LYS
1	B	470	ASP
1	B	476	GLU
1	B	479	ARG
1	B	481	VAL
1	B	487	ARG
1	B	492	LEU
1	B	493	ARG
1	B	495	LEU
1	B	504	ARG
1	B	506	GLN
1	B	512	ASN
1	B	519	LEU
1	B	536	ASN
1	B	542	LEU
1	C	263	ASP

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Mol	Chain	Res	Type
1	C	277	GLU
1	C	288	LEU
1	C	290	SER
1	C	303	ARG
1	C	347	GLU
1	C	349	THR
1	C	360	VAL
1	C	366	ASP
1	C	368	LEU
1	C	375	ASN
1	C	390	THR
1	C	393	LEU
1	C	397	PHE
1	C	403	ASP
1	C	440	LYS
1	C	470	ASP
1	C	476	GLU
1	C	481	VAL
1	C	482	SER
1	C	487	ARG
1	C	492	LEU
1	C	493	ARG
1	C	495	LEU
1	C	505	ASN
1	C	506	GLN
1	C	512	ASN
1	C	515	LEU
1	C	519	LEU
1	C	536	ASN
1	C	542	LEU
1	D	272	ARG
1	D	277	GLU
1	D	293	THR
1	D	300	LEU
1	D	325	GLN
1	D	347	GLU
1	D	349	THR
1	D	360	VAL
1	D	366	ASP
1	D	368	LEU
1	D	393	LEU
1	D	403	ASP

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Mol	Chain	Res	Type
1	D	455	SER
1	D	470	ASP
1	D	481	VAL
1	D	487	ARG
1	D	492	LEU
1	D	495	LEU
1	D	500	ILE
1	D	504	ARG
1	D	512	ASN
1	D	522	ARG
1	D	536	ASN
1	D	542	LEU
1	E	267	SER
1	E	274	ARG
1	E	277	GLU
1	E	282	GLU
1	E	287	LEU
1	E	290	SER
1	E	303	ARG
1	E	322	VAL
1	E	347	GLU
1	E	349	THR
1	E	360	VAL
1	E	368	LEU
1	E	393	LEU
1	E	403	ASP
1	E	440	LYS
1	E	470	ASP
1	E	479	ARG
1	E	481	VAL
1	E	487	ARG
1	E	492	LEU
1	E	493	ARG
1	E	495	LEU
1	E	504	ARG
1	E	506	GLN
1	E	512	ASN
1	E	519	LEU
1	E	536	ASN
1	E	542	LEU
1	F	277	GLU
1	F	284	SER

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Mol	Chain	Res	Type
1	F	287	LEU
1	F	288	LEU
1	F	290	SER
1	F	303	ARG
1	F	347	GLU
1	F	349	THR
1	F	360	VAL
1	F	366	ASP
1	F	368	LEU
1	F	375	ASN
1	F	390	THR
1	F	397	PHE
1	F	403	ASP
1	F	440	LYS
1	F	470	ASP
1	F	476	GLU
1	F	481	VAL
1	F	482	SER
1	F	487	ARG
1	F	492	LEU
1	F	493	ARG
1	F	495	LEU
1	F	505	ASN
1	F	506	GLN
1	F	512	ASN
1	F	519	LEU
1	F	536	ASN
1	F	542	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (60) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	296	ASN
1	A	324	GLN
1	A	325	GLN
1	A	358	ASN
1	A	375	ASN
1	A	392	HIS
1	A	475	HIS
1	A	494	GLN
1	A	505	ASN
1	A	507	GLN

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Mol	Chain	Res	Type
1	A	536	ASN
1	B	296	ASN
1	B	324	GLN
1	B	325	GLN
1	B	358	ASN
1	B	375	ASN
1	B	392	HIS
1	B	468	ASN
1	B	475	HIS
1	B	505	ASN
1	B	507	GLN
1	B	536	ASN
1	C	296	ASN
1	C	324	GLN
1	C	325	GLN
1	C	358	ASN
1	C	375	ASN
1	C	425	HIS
1	C	494	GLN
1	C	505	ASN
1	C	536	ASN
1	D	296	ASN
1	D	324	GLN
1	D	325	GLN
1	D	375	ASN
1	D	475	HIS
1	D	494	GLN
1	D	505	ASN
1	D	507	GLN
1	D	536	ASN
1	E	296	ASN
1	E	324	GLN
1	E	325	GLN
1	E	358	ASN
1	E	375	ASN
1	E	475	HIS
1	E	505	ASN
1	E	506	GLN
1	E	507	GLN
1	E	536	ASN
1	F	296	ASN
1	F	324	GLN

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Mol	Chain	Res	Type
1	F	325	GLN
1	F	358	ASN
1	F	375	ASN
1	F	392	HIS
1	F	425	HIS
1	F	494	GLN
1	F	505	ASN
1	F	536	ASN

### 5.3.3 RNA [i](#)

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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	ANP	A	700	3	29,33,33	1.54	4 (13%)	31,52,52	1.89	4 (12%)
2	ANP	D	700	3	29,33,33	1.56	4 (13%)	31,52,52	1.86	5 (16%)
2	ANP	E	700	3	29,33,33	1.49	3 (10%)	31,52,52	1.87	4 (12%)
2	ANP	B	700	3	29,33,33	1.22	5 (17%)	31,52,52	1.81	4 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ANP	A	700	3	-	3/14/38/38	0/3/3/3
2	ANP	D	700	3	-	3/14/38/38	0/3/3/3
2	ANP	E	700	3	-	3/14/38/38	0/3/3/3
2	ANP	B	700	3	-	3/14/38/38	0/3/3/3

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	700	ANP	PB-O1B	5.60	1.55	1.46
2	E	700	ANP	PB-O1B	5.05	1.54	1.46
2	A	700	ANP	PB-O1B	4.40	1.53	1.46
2	B	700	ANP	PB-O1B	2.86	1.50	1.46
2	A	700	ANP	PG-N3B	-2.85	1.55	1.63
2	D	700	ANP	PB-O2B	-2.79	1.49	1.56
2	B	700	ANP	PB-O2B	-2.74	1.49	1.56
2	A	700	ANP	PB-O2B	-2.69	1.49	1.56
2	A	700	ANP	O4'-C1'	2.66	1.44	1.41
2	E	700	ANP	PB-O2B	-2.63	1.49	1.56
2	D	700	ANP	PG-N3B	-2.35	1.57	1.63
2	B	700	ANP	PG-N3B	-2.26	1.57	1.63
2	D	700	ANP	PG-O2G	-2.16	1.50	1.56
2	B	700	ANP	O4'-C1'	2.10	1.44	1.41
2	B	700	ANP	PG-O2G	-2.05	1.51	1.56
2	E	700	ANP	C4-N3	2.03	1.38	1.35

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	700	ANP	O1G-PG-N3B	-7.78	100.31	111.77
2	A	700	ANP	O1G-PG-N3B	-7.71	100.41	111.77
2	D	700	ANP	O1G-PG-N3B	-7.61	100.56	111.77
2	B	700	ANP	O1G-PG-N3B	-7.35	100.94	111.77
2	A	700	ANP	O2B-PB-O1B	4.85	120.09	109.92
2	E	700	ANP	O2B-PB-O1B	4.73	119.84	109.92
2	B	700	ANP	O2B-PB-O1B	4.70	119.77	109.92
2	D	700	ANP	O2B-PB-O1B	4.70	119.77	109.92
2	D	700	ANP	O2G-PG-O3G	2.49	114.27	107.64
2	B	700	ANP	O2G-PG-O3G	2.48	114.25	107.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	700	ANP	O2G-PG-O3G	2.46	114.19	107.64
2	A	700	ANP	C5-C6-N6	2.41	124.01	120.35
2	E	700	ANP	O2G-PG-O3G	2.37	113.94	107.64
2	B	700	ANP	C5-C6-N6	2.23	123.75	120.35
2	E	700	ANP	C5-C6-N6	2.23	123.74	120.35
2	D	700	ANP	C5-C6-N6	2.17	123.64	120.35
2	D	700	ANP	O3A-PB-N3B	-2.10	100.78	106.59

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	700	ANP	PB-N3B-PG-O1G
2	A	700	ANP	PG-N3B-PB-O1B
2	A	700	ANP	PG-N3B-PB-O3A
2	B	700	ANP	PB-N3B-PG-O1G
2	B	700	ANP	PG-N3B-PB-O1B
2	B	700	ANP	PG-N3B-PB-O3A
2	D	700	ANP	PB-N3B-PG-O1G
2	D	700	ANP	PG-N3B-PB-O1B
2	D	700	ANP	PG-N3B-PB-O3A
2	E	700	ANP	PB-N3B-PG-O1G
2	E	700	ANP	PG-N3B-PB-O1B
2	E	700	ANP	PG-N3B-PB-O3A

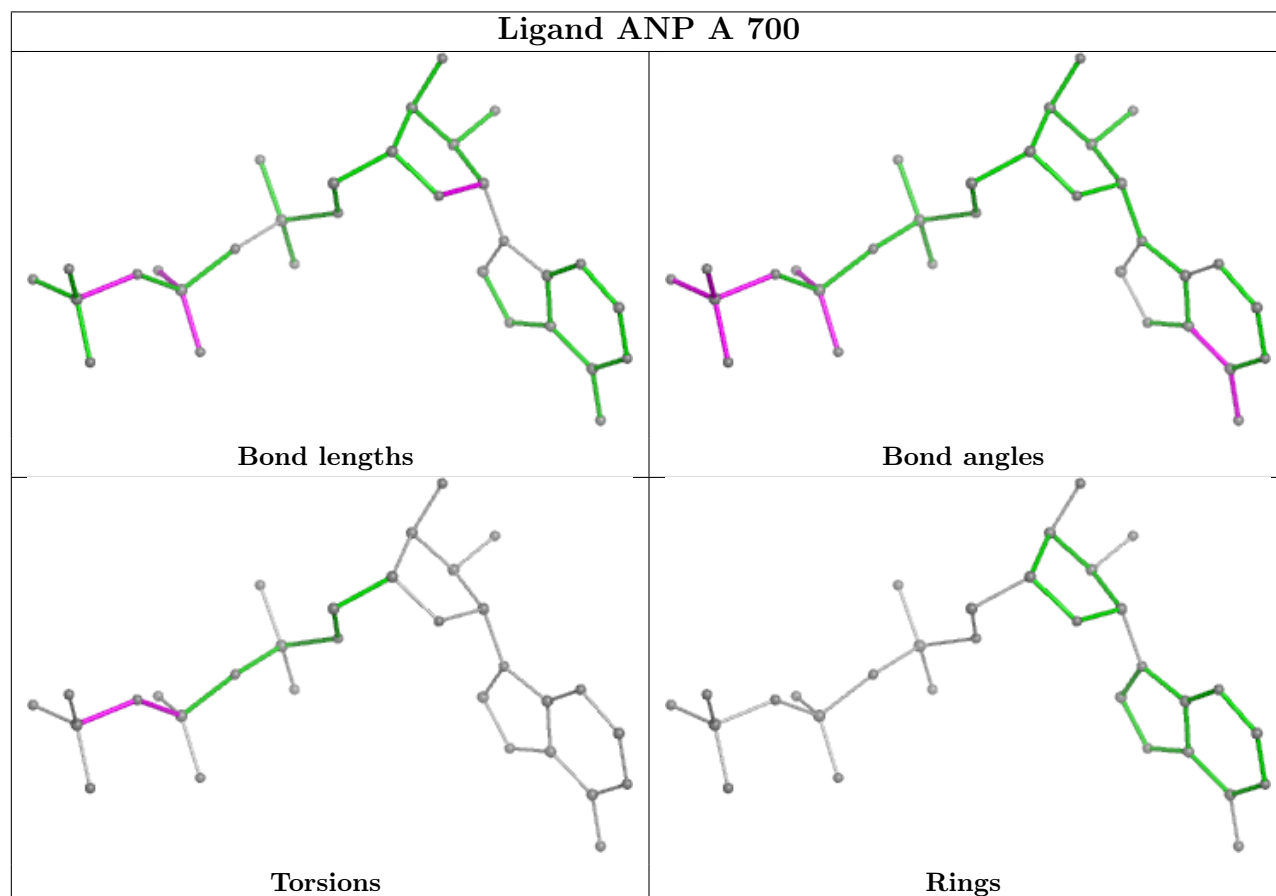
There are no ring outliers.

4 monomers are involved in 8 short contacts:

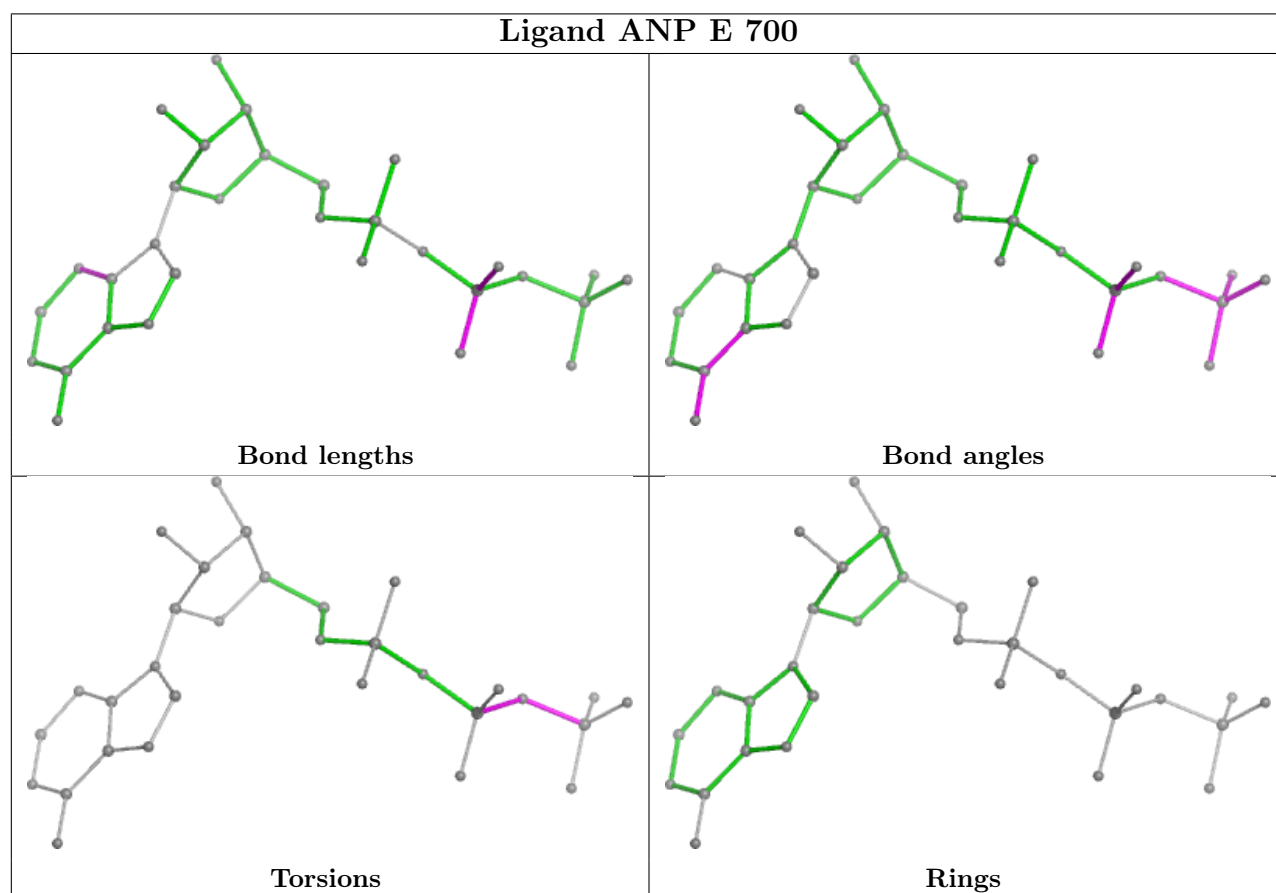
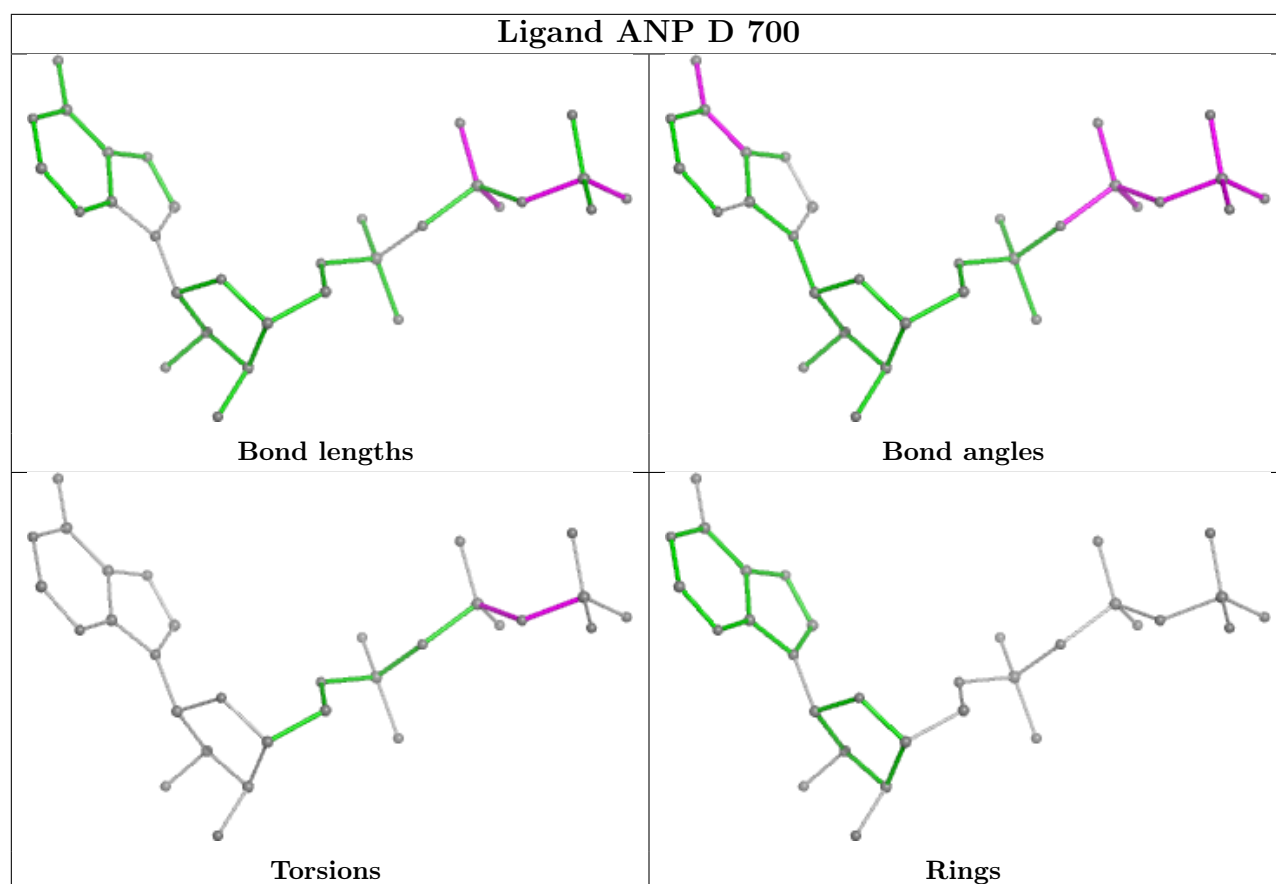
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	700	ANP	2	0
2	D	700	ANP	2	0
2	E	700	ANP	1	0
2	B	700	ANP	3	0

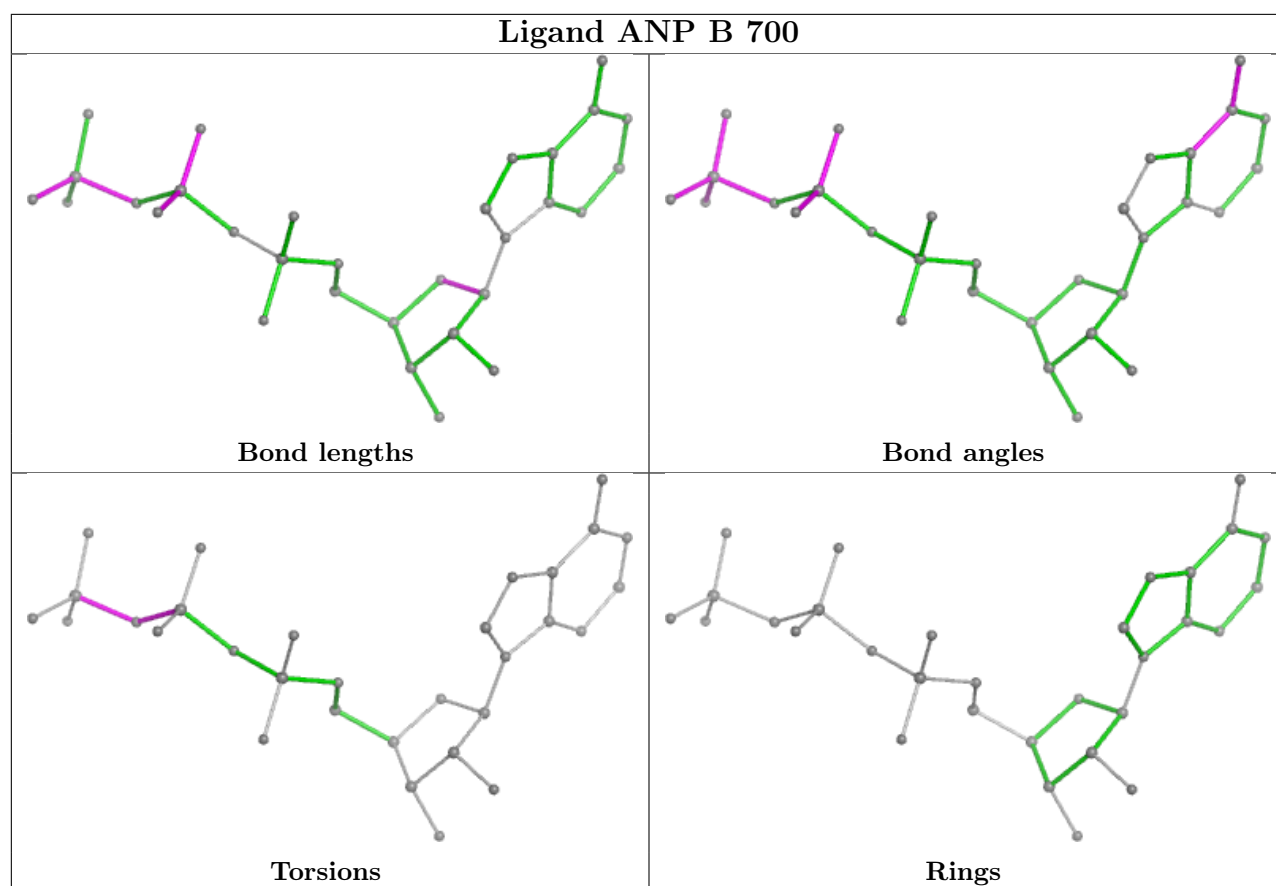
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the

average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









## 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 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	287/289 (99%)	0.14	22 (7%) 13 4	40, 67, 132, 169	0
1	B	288/289 (99%)	-0.22	10 (3%) 44 18	33, 58, 124, 159	0
1	C	288/289 (99%)	-0.17	16 (5%) 24 8	34, 60, 126, 155	0
1	D	287/289 (99%)	0.04	18 (6%) 20 6	44, 69, 135, 166	0
1	E	288/289 (99%)	-0.20	14 (4%) 29 11	37, 62, 124, 161	0
1	F	288/289 (99%)	-0.02	16 (5%) 24 8	38, 62, 128, 158	0
All	All	1726/1734 (99%)	-0.07	96 (5%) 24 8	33, 64, 131, 169	0

All (96) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	284	SER	17.3
1	B	433	SER	10.3
1	A	433	SER	10.2
1	D	432	ALA	10.1
1	F	433	SER	9.8
1	A	434	GLY	9.4
1	A	432	ALA	9.3
1	A	435	GLU	8.8
1	D	434	GLY	8.7
1	D	431	SER	8.6
1	F	434	GLY	8.5
1	A	285	VAL	8.4
1	D	433	SER	8.1
1	D	284	SER	7.7
1	F	432	ALA	7.4
1	E	434	GLY	7.3
1	D	436	SER	7.3
1	D	435	GLU	6.7
1	F	431	SER	6.6

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Mol	Chain	Res	Type	RSRZ
1	B	434	GLY	6.3
1	F	262	PRO	5.9
1	E	397	PHE	5.8
1	A	436	SER	5.7
1	E	436	SER	5.7
1	A	431	SER	5.3
1	E	435	GLU	5.2
1	E	433	SER	5.1
1	A	548	SER	5.0
1	C	436	SER	4.9
1	C	431	SER	4.8
1	A	549	GLY	4.7
1	F	549	GLY	4.7
1	D	437	ASP	4.7
1	C	470	ASP	4.3
1	B	432	ALA	4.3
1	F	436	SER	4.2
1	D	397	PHE	4.1
1	C	397	PHE	4.1
1	C	435	GLU	4.0
1	F	430	VAL	4.0
1	C	432	ALA	4.0
1	B	397	PHE	4.0
1	A	399	GLU	3.9
1	D	430	VAL	3.9
1	E	437	ASP	3.8
1	C	433	SER	3.7
1	B	435	GLU	3.7
1	A	430	VAL	3.7
1	E	284	SER	3.5
1	C	472	GLY	3.5
1	D	549	GLY	3.4
1	C	437	ASP	3.3
1	D	261	ILE	3.3
1	C	434	GLY	3.2
1	A	547	TYR	3.2
1	C	473	LYS	3.2
1	F	435	GLU	3.1
1	F	470	ASP	3.0
1	E	262	PRO	3.0
1	A	397	PHE	2.9
1	A	398	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	549	GLY	2.9
1	D	470	ASP	2.8
1	D	398	ALA	2.8
1	D	285	VAL	2.8
1	D	471	LYS	2.8
1	D	281	SER	2.8
1	B	262	PRO	2.8
1	B	436	SER	2.7
1	F	283	GLU	2.7
1	E	470	ASP	2.7
1	F	507	GLN	2.7
1	E	432	ALA	2.7
1	A	403	ASP	2.7
1	A	400	ALA	2.6
1	A	526	ASP	2.6
1	F	539	THR	2.5
1	F	284	SER	2.5
1	E	489	SER	2.4
1	A	470	ASP	2.4
1	E	277	GLU	2.4
1	B	431	SER	2.4
1	F	397	PHE	2.4
1	A	489	SER	2.3
1	D	403	ASP	2.3
1	C	439	ARG	2.2
1	C	430	VAL	2.2
1	A	437	ASP	2.2
1	A	402	THR	2.2
1	E	549	GLY	2.1
1	B	281	SER	2.1
1	B	489	SER	2.1
1	F	285	VAL	2.1
1	E	509	ASP	2.1
1	C	507	GLN	2.0
1	C	398	ALA	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

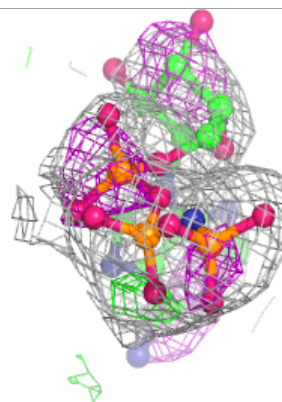
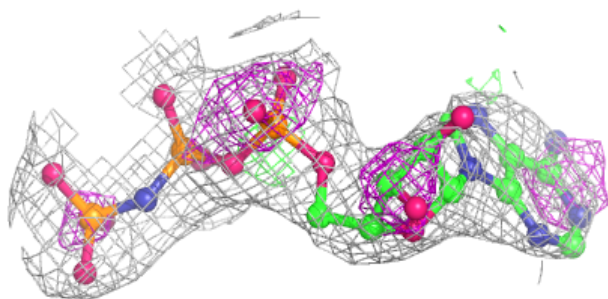
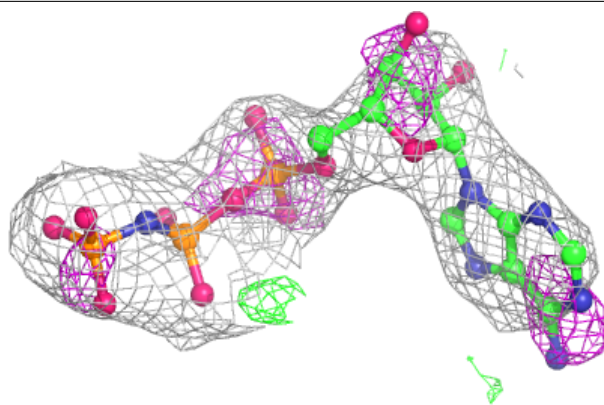
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	MG	E	701	1/1	0.73	0.16	43,43,43,43	0
3	MG	D	701	1/1	0.90	0.13	43,43,43,43	0
3	MG	A	701	1/1	0.92	0.11	38,38,38,38	0
2	ANP	A	700	31/31	0.94	0.23	32,39,51,55	0
2	ANP	D	700	31/31	0.95	0.18	30,38,52,59	0
3	MG	B	701	1/1	0.96	0.19	38,38,38,38	0
2	ANP	E	700	31/31	0.96	0.13	33,36,53,55	0
2	ANP	B	700	31/31	0.96	0.13	32,36,49,57	0

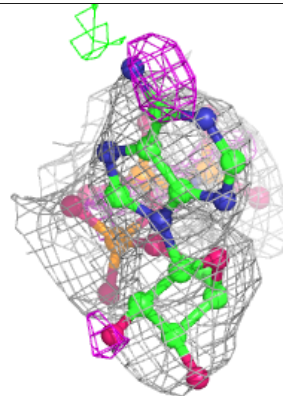
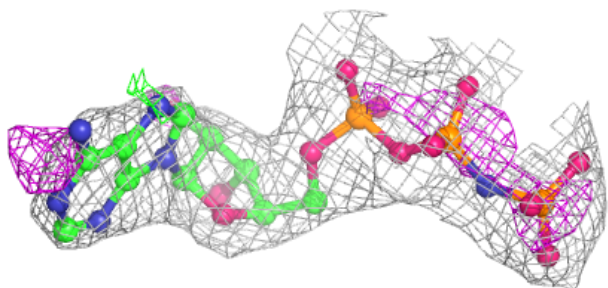
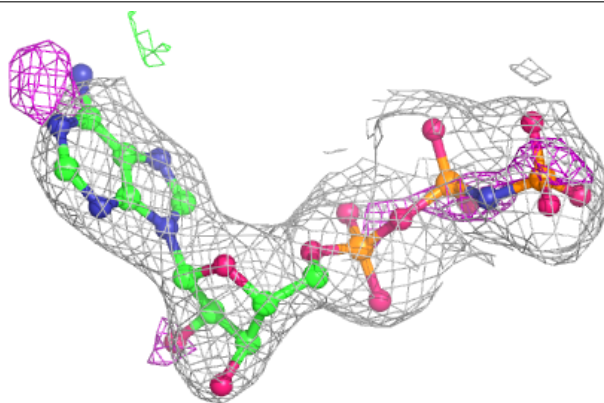
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around ANP A 700:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around ANP D 700:**

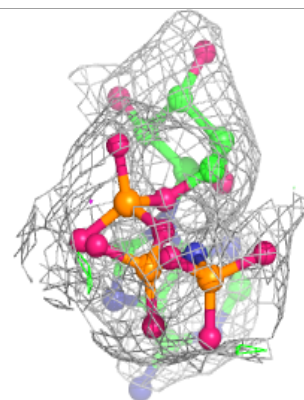
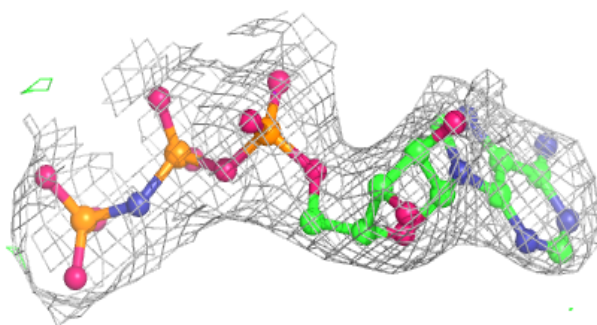
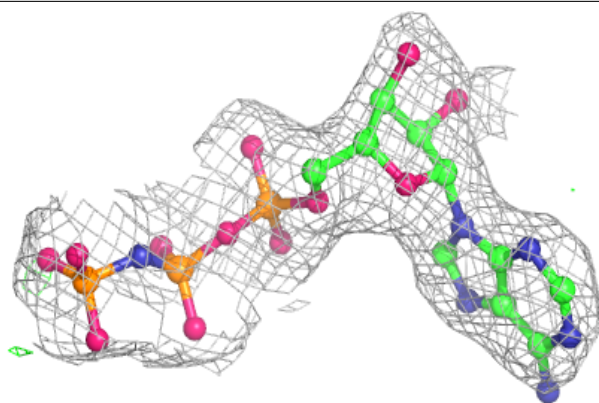
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



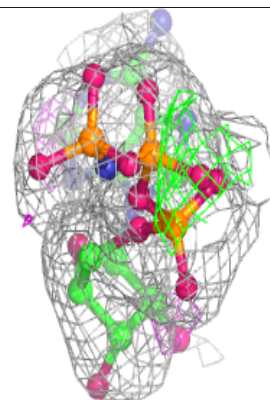
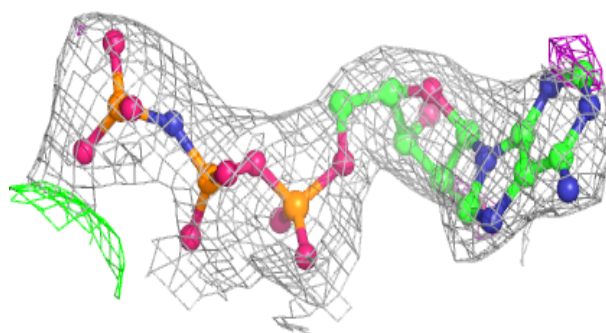
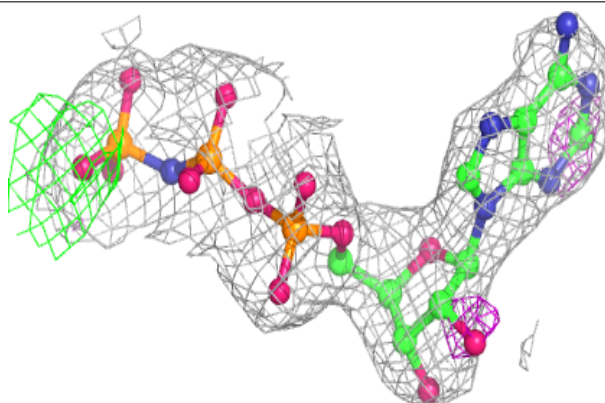


**Electron density around ANP E 700:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around ANP B 700:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.