



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 11:52 am BST

PDB ID : 5AJ3
EMDB ID : EMD-2913
Title : Structure of the small subunit of the mammalian mitoribosome
Authors : Greber, B.J.; Bieri, P.; Leibundgut, M.; Leitner, A.; Aebersold, R.; Boehringer, D.; Ban, N.
Deposited on : 2015-02-20
Resolution : 3.60 Å(reported)

This is a wwPDB EM Validation Summary 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.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
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) : 2.39

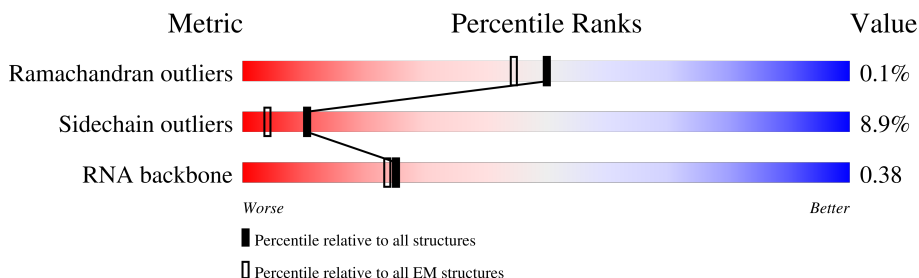
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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.









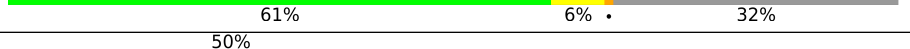
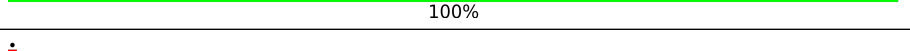

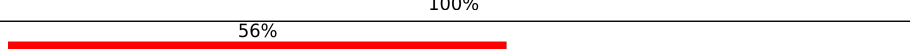
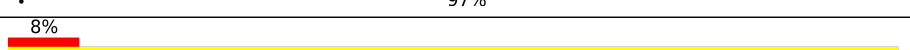
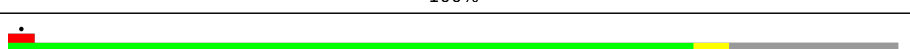
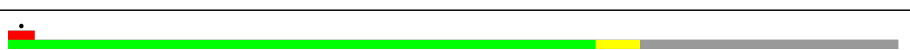

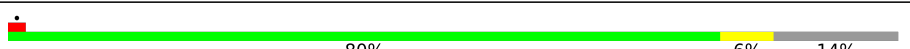
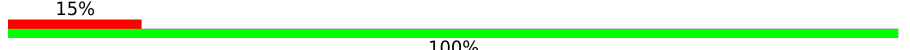
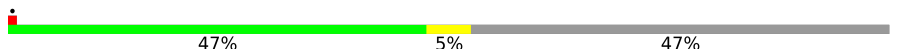



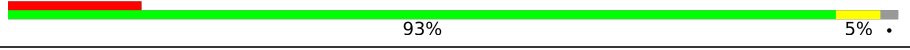
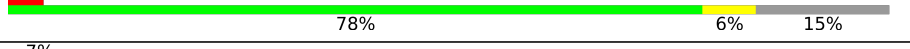



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	962	
2	B	289	
3	C	167	
4	E	430	
5	F	124	
6	G	242	
7	I	397	
8	J	201	

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Mol	Chain	Length	Quality of chain
9	K	196	
10	L	139	
11	N	128	
12	O	239	
13	P	135	
14	Q	130	
15	R	143	
16	T	14	
17	U	87	
18	V	64	
18	Y	64	
19	X	13	
20	a	360	
21	b	190	
22	c	173	
23	d	205	
24	e	336	
25	f	188	
26	g	397	
27	h	387	
28	i	106	
29	j	218	
30	k	325	
31	m	118	
32	n	199	

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Mol	Chain	Length	Quality of chain
33	o	692	<div><div>53%</div><div>68%</div><div>31%</div></div>
34	p	258	<div><div>66%</div><div>7%</div><div>27%</div></div>
35	s	16	<div><div>100%</div><div>100%</div></div>
36	z	17	<div><div>24%</div><div>100%</div></div>

2 Entry composition

There are 40 unique types of molecules in this entry. The entry contains 66363 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 RNA chain called MITORIBOSOMAL 12S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	960	Total	C	N	O	P	0	0
			20411	9162	3708	6581	960		

- Molecule 2 is a protein called MITORIBOSOMAL PROTEIN US2M, MRPS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	220	Total	C	N	O	S	0	0
			1762	1126	326	304	6		

- Molecule 3 is a protein called MITORIBOSOMAL PROTEIN US3M, MRPS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	132	Total	C	N	O	S	0	0
			1075	695	195	181	4		

- Molecule 4 is a protein called MITORIBOSOMAL PROTEIN US5M, MRPS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	328	Total	C	N	O	S	0	0
			2621	1641	498	471	11		

- Molecule 5 is a protein called MITORIBOSOMAL PROTEIN BS6M, MRPS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	123	Total	C	N	O	S	0	0
			990	626	180	178	6		

- Molecule 6 is a protein called MITORIBOSOMAL PROTEIN US7M, MRPS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	208	Total	C	N	O	S	0	0
			1721	1097	314	299	11		

- Molecule 7 is a protein called MITORIBOSOMAL PROTEIN US9M, MRPS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	311	Total	C	N	O	S	0	0
			2498	1586	450	449	13		

- Molecule 8 is a protein called MITORIBOSOMAL PROTEIN US10M, MRPS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	129	Total	C	N	O	S	0	0
			1067	690	182	192	3		

- Molecule 9 is a protein called MITORIBOSOMAL PROTEIN US11M, MRPS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	136	Total	C	N	O	S	0	0
			1001	628	192	178	3		

- Molecule 10 is a protein called MITORIBOSOMAL PROTEIN US12M, MRPS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	109	Total	C	N	O	S	0	0
			840	524	172	138	6		

- Molecule 11 is a protein called MITORIBOSOMAL PROTEIN US14M, MRPS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	101	Total	C	N	O	S	0	0
			858	534	174	144	6		

- Molecule 12 is a protein called MITORIBOSOMAL PROTEIN US15M, MRPS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O	175	Total	C	N	O	S	0	0
			1448	919	272	248	9		

- Molecule 13 is a protein called MITORIBOSOMAL PROTEIN BS16M, MRPS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	P	117	Total	C	N	O	S	0	0
			932	588	184	155	5		

- Molecule 14 is a protein called MITORIBOSOMAL PROTEIN US17M, MRPS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	109	Total	C	N	O	S	0	0
			853	555	150	145	3		

- Molecule 15 is a protein called MITORIBOSOMAL PROTEIN BS18M, MRPS18C.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	97	Total	C	N	O	S	0	0
			784	507	132	138	7		

- Molecule 16 is a protein called MITORIBOSOMAL PROTEIN BL19M, MRPL19.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	T	14	Total	C	N	O	0	0
			84	56	14	14		

- Molecule 17 is a protein called MITORIBOSOMAL PROTEIN BS21M, MRPS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	U	86	Total	C	N	O	S	0	0
			734	453	148	125	8		

- Molecule 18 is a RNA chain called P-SITE AND A-SITE TRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	64	Total	C	N	O	P	0	0
			1158	579	134	382	63		
18	Y	64	Total	C	N	O	P	0	0
			1158	579	134	382	63		

- Molecule 19 is a RNA chain called MRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	X	13	Total	C	N	O	P	0	0
			231	117	26	76	12		

- Molecule 20 is a protein called MITORIBOSOMAL PROTEIN MS22, MRPS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	a	292	Total	C	N	O	S	0	0
			2296	1476	394	417	9		

- Molecule 21 is a protein called MITORIBOSOMAL PROTEIN MS23, MRPS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	b	135	Total	C	N	O	S	0	0
			1101	709	199	192	1		

- Molecule 22 is a protein called MITORIBOSOMAL PROTEIN MS25, MRPS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	c	169	Total	C	N	O	S	0	0
			1367	876	236	245	10		

- Molecule 23 is a protein called MITORIBOSOMAL PROTEIN MS26, MRPS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	d	177	Total	C	N	O	S	0	0
			1467	904	288	273	2		

- Molecule 24 is a protein called MITORIBOSOMAL PROTEIN MS27, MRPS27.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	e	336	Total	C	N	O	0	0
			2016	1344	336	336		

- Molecule 25 is a protein called MITORIBOSOMAL PROTEIN MS28, MRPS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	f	99	Total	C	N	O	S	0	0
			778	494	134	146	4		

- Molecule 26 is a protein called MITORIBOSOMAL PROTEIN MS29, MRPS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	g	346	Total	C	N	O	S	0	0
			2774	1786	489	489	10		

- Molecule 27 is a protein called MITORIBOSOMAL PROTEIN MS31, MRPS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	h	103	Total	C	N	O	S	0	0
			876	569	145	159	3		

- Molecule 28 is a protein called MITORIBOSOMAL PROTEIN MS33, MRPS33.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	i	99	Total	C	N	O	S	0	0
			824	522	156	143	3		

- Molecule 29 is a protein called MITORIBOSOMAL PROTEIN MS34, MRPS34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	j	213	Total	C	N	O	S	0	0
			1777	1123	339	308	7		

- Molecule 30 is a protein called MITORIBOSOMAL PROTEIN MS35, MRPS35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	k	275	Total	C	N	O	S	0	0
			2222	1414	380	419	9		

- Molecule 31 is a protein called MITORIBOSOMAL PROTEIN MS37, MRPS37.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	m	116	Total	C	N	O	S	0	0
			930	577	185	160	8		

- Molecule 32 is a protein called MITORIBOSOMAL PROTEIN MS38, MRPS38.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	n	72	Total	C	N	O	S	0	0
			639	407	139	92	1		

- Molecule 33 is a protein called MITORIBOSOMAL PROTEIN MS39, MRPS39.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	o	476	Total	C	N	O	S	0	0
			3028	2007	500	519	2		

There are 525 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
o	153	UNK	SER	conflict	UNP K7GKS8
o	154	UNK	GLU	conflict	UNP K7GKS8
o	155	UNK	ALA	conflict	UNP K7GKS8
o	156	UNK	ALA	conflict	UNP K7GKS8
o	157	UNK	LEU	conflict	UNP K7GKS8
o	158	UNK	GLN	conflict	UNP K7GKS8

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Chain	Residue	Modelled	Actual	Comment	Reference
o	159	UNK	GLU	conflict	UNP K7GKS8
o	160	UNK	ARG	conflict	UNP K7GKS8
o	161	UNK	ILE	conflict	UNP K7GKS8
o	162	UNK	LYS	conflict	UNP K7GKS8
o	163	UNK	LEU	conflict	UNP K7GKS8
o	164	UNK	ARG	conflict	UNP K7GKS8
o	165	UNK	LYS	conflict	UNP K7GKS8
o	166	UNK	VAL	conflict	UNP K7GKS8
o	167	UNK	LYS	conflict	UNP K7GKS8
o	168	UNK	ALA	conflict	UNP K7GKS8
o	169	UNK	SER	conflict	UNP K7GKS8
o	170	UNK	VAL	conflict	UNP K7GKS8
o	171	UNK	ASP	conflict	UNP K7GKS8
o	172	UNK	MET	conflict	UNP K7GKS8
o	173	UNK	PHE	conflict	UNP K7GKS8
o	174	UNK	ASP	conflict	UNP K7GKS8
o	175	UNK	GLN	conflict	UNP K7GKS8
o	176	UNK	LEU	conflict	UNP K7GKS8
o	177	UNK	LEU	conflict	UNP K7GKS8
o	178	UNK	GLN	conflict	UNP K7GKS8
o	179	UNK	ALA	conflict	UNP K7GKS8
o	180	UNK	GLY	conflict	UNP K7GKS8
o	181	UNK	THR	conflict	UNP K7GKS8
o	182	UNK	THR	conflict	UNP K7GKS8
o	183	UNK	VAL	conflict	UNP K7GKS8
o	184	UNK	SER	conflict	UNP K7GKS8
o	185	UNK	LEU	conflict	UNP K7GKS8
o	186	UNK	GLU	conflict	UNP K7GKS8
o	187	UNK	THR	conflict	UNP K7GKS8
o	188	UNK	THR	conflict	UNP K7GKS8
o	189	UNK	ASN	conflict	UNP K7GKS8
o	190	UNK	SER	conflict	UNP K7GKS8
o	191	UNK	LEU	conflict	UNP K7GKS8
o	192	UNK	LEU	conflict	UNP K7GKS8
o	193	UNK	ASP	conflict	UNP K7GKS8
o	194	UNK	LEU	conflict	UNP K7GKS8
o	195	UNK	LEU	conflict	UNP K7GKS8
o	196	UNK	CYS	conflict	UNP K7GKS8
o	197	UNK	TYR	conflict	UNP K7GKS8
o	198	UNK	TYR	conflict	UNP K7GKS8
o	199	UNK	GLY	conflict	UNP K7GKS8
o	200	UNK	ASN	conflict	UNP K7GKS8

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Chain	Residue	Modelled	Actual	Comment	Reference
o	201	UNK	GLN	conflict	UNP K7GKS8
o	202	UNK	GLU	conflict	UNP K7GKS8
o	203	UNK	PRO	conflict	UNP K7GKS8
o	204	UNK	SER	conflict	UNP K7GKS8
o	205	UNK	ALA	conflict	UNP K7GKS8
o	206	UNK	ASN	conflict	UNP K7GKS8
o	207	UNK	TYR	conflict	UNP K7GKS8
o	208	UNK	ASN	conflict	UNP K7GKS8
o	209	UNK	PHE	conflict	UNP K7GKS8
o	210	UNK	GLN	conflict	UNP K7GKS8
o	211	UNK	GLN	conflict	UNP K7GKS8
o	212	UNK	ARG	conflict	UNP K7GKS8
o	213	UNK	GLU	conflict	UNP K7GKS8
o	214	UNK	GLN	conflict	UNP K7GKS8
o	215	UNK	SER	conflict	UNP K7GKS8
o	216	UNK	GLU	conflict	UNP K7GKS8
o	217	UNK	GLU	conflict	UNP K7GKS8
o	218	UNK	LEU	conflict	UNP K7GKS8
o	219	UNK	GLU	conflict	UNP K7GKS8
o	220	UNK	GLU	conflict	UNP K7GKS8
o	221	UNK	ALA	conflict	UNP K7GKS8
o	222	UNK	THR	conflict	UNP K7GKS8
o	223	UNK	GLU	conflict	UNP K7GKS8
o	224	UNK	ALA	conflict	UNP K7GKS8
o	225	UNK	ASP	conflict	UNP K7GKS8
o	226	UNK	ASN	conflict	UNP K7GKS8
o	227	UNK	GLU	conflict	UNP K7GKS8
o	228	UNK	LYS	conflict	UNP K7GKS8
o	229	UNK	SER	conflict	UNP K7GKS8
o	230	UNK	LYS	conflict	UNP K7GKS8
o	231	UNK	THR	conflict	UNP K7GKS8
o	232	UNK	LYS	conflict	UNP K7GKS8
o	233	UNK	ALA	conflict	UNP K7GKS8
o	234	UNK	GLY	conflict	UNP K7GKS8
o	235	UNK	HIS	conflict	UNP K7GKS8
o	236	UNK	HIS	conflict	UNP K7GKS8
o	237	UNK	LEU	conflict	UNP K7GKS8
o	238	UNK	GLY	conflict	UNP K7GKS8
o	239	UNK	VAL	conflict	UNP K7GKS8
o	240	UNK	THR	conflict	UNP K7GKS8
o	241	UNK	TRP	conflict	UNP K7GKS8
o	242	UNK	ARG	conflict	UNP K7GKS8

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Chain	Residue	Modelled	Actual	Comment	Reference
o	243	UNK	THR	conflict	UNP K7GKS8
o	244	UNK	LYS	conflict	UNP K7GKS8
o	245	UNK	ASN	conflict	UNP K7GKS8
o	246	UNK	ASN	conflict	UNP K7GKS8
o	247	UNK	ALA	conflict	UNP K7GKS8
o	248	UNK	GLU	conflict	UNP K7GKS8
o	249	UNK	ARG	conflict	UNP K7GKS8
o	250	UNK	ILE	conflict	UNP K7GKS8
o	251	UNK	PHE	conflict	UNP K7GKS8
o	252	UNK	ALA	conflict	UNP K7GKS8
o	253	UNK	LEU	conflict	UNP K7GKS8
o	254	UNK	MET	conflict	UNP K7GKS8
o	255	UNK	PRO	conflict	UNP K7GKS8
o	256	UNK	GLU	conflict	UNP K7GKS8
o	257	UNK	LYS	conflict	UNP K7GKS8
o	258	UNK	ASN	conflict	UNP K7GKS8
o	259	UNK	ALA	conflict	UNP K7GKS8
o	260	UNK	HIS	conflict	UNP K7GKS8
o	261	UNK	SER	conflict	UNP K7GKS8
o	262	UNK	TYR	conflict	UNP K7GKS8
o	263	UNK	CYS	conflict	UNP K7GKS8
o	264	UNK	THR	conflict	UNP K7GKS8
o	265	UNK	MET	conflict	UNP K7GKS8
o	266	UNK	ILE	conflict	UNP K7GKS8
o	267	UNK	ARG	conflict	UNP K7GKS8
o	268	UNK	GLY	conflict	UNP K7GKS8
o	269	UNK	MET	conflict	UNP K7GKS8
o	270	UNK	VAL	conflict	UNP K7GKS8
o	271	UNK	LYS	conflict	UNP K7GKS8
o	272	UNK	HIS	conflict	UNP K7GKS8
o	273	UNK	GLN	conflict	UNP K7GKS8
o	274	UNK	ALA	conflict	UNP K7GKS8
o	275	UNK	PRO	conflict	UNP K7GKS8
o	276	UNK	THR	conflict	UNP K7GKS8
o	277	UNK	GLN	conflict	UNP K7GKS8
o	278	UNK	ALA	conflict	UNP K7GKS8
o	279	UNK	LEU	conflict	UNP K7GKS8
o	280	UNK	ASN	conflict	UNP K7GKS8
o	281	UNK	LEU	conflict	UNP K7GKS8
o	282	UNK	TYR	conflict	UNP K7GKS8
o	283	UNK	THR	conflict	UNP K7GKS8
o	284	UNK	VAL	conflict	UNP K7GKS8

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Chain	Residue	Modelled	Actual	Comment	Reference
o	285	UNK	LEU	conflict	UNP K7GKS8
o	286	UNK	LEU	conflict	UNP K7GKS8
o	287	UNK	ASN	conflict	UNP K7GKS8
o	288	UNK	ASN	conflict	UNP K7GKS8
o	289	UNK	ARG	conflict	UNP K7GKS8
o	290	UNK	LEU	conflict	UNP K7GKS8
o	291	UNK	ARG	conflict	UNP K7GKS8
o	292	UNK	ALA	conflict	UNP K7GKS8
o	293	UNK	ASP	conflict	UNP K7GKS8
o	294	UNK	VAL	conflict	UNP K7GKS8
o	295	UNK	TYR	conflict	UNP K7GKS8
o	296	UNK	THR	conflict	UNP K7GKS8
o	297	UNK	PHE	conflict	UNP K7GKS8
o	298	UNK	ASN	conflict	UNP K7GKS8
o	299	UNK	SER	conflict	UNP K7GKS8
o	300	UNK	LEU	conflict	UNP K7GKS8
o	301	UNK	ILE	conflict	UNP K7GKS8
o	302	UNK	GLU	conflict	UNP K7GKS8
o	303	UNK	ALA	conflict	UNP K7GKS8
o	304	UNK	THR	conflict	UNP K7GKS8
o	305	UNK	ALA	conflict	UNP K7GKS8
o	306	UNK	LEU	conflict	UNP K7GKS8
o	307	UNK	VAL	conflict	UNP K7GKS8
o	308	UNK	VAL	conflict	UNP K7GKS8
o	309	UNK	ASN	conflict	UNP K7GKS8
o	310	UNK	GLU	conflict	UNP K7GKS8
o	311	UNK	LYS	conflict	UNP K7GKS8
o	312	UNK	PHE	conflict	UNP K7GKS8
o	313	UNK	GLU	conflict	UNP K7GKS8
o	314	UNK	GLU	conflict	UNP K7GKS8
o	315	UNK	LYS	conflict	UNP K7GKS8
o	316	UNK	TRP	conflict	UNP K7GKS8
o	317	UNK	ASN	conflict	UNP K7GKS8
o	318	UNK	ASN	conflict	UNP K7GKS8
o	319	UNK	ILE	conflict	UNP K7GKS8
o	320	UNK	LEU	conflict	UNP K7GKS8
o	321	UNK	ASP	conflict	UNP K7GKS8
o	322	UNK	LEU	conflict	UNP K7GKS8
o	323	UNK	LEU	conflict	UNP K7GKS8
o	324	UNK	LYS	conflict	UNP K7GKS8
o	325	UNK	GLN	conflict	UNP K7GKS8
o	326	UNK	MET	conflict	UNP K7GKS8

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Chain	Residue	Modelled	Actual	Comment	Reference
o	327	UNK	VAL	conflict	UNP K7GKS8
o	328	UNK	THR	conflict	UNP K7GKS8
o	329	UNK	GLN	conflict	UNP K7GKS8
o	330	UNK	ASN	conflict	UNP K7GKS8
o	331	UNK	VAL	conflict	UNP K7GKS8
o	332	UNK	LYS	conflict	UNP K7GKS8
o	333	UNK	PRO	conflict	UNP K7GKS8
o	334	UNK	ASN	conflict	UNP K7GKS8
o	335	UNK	LEU	conflict	UNP K7GKS8
o	336	UNK	GLN	conflict	UNP K7GKS8
o	337	UNK	THR	conflict	UNP K7GKS8
o	338	UNK	PHE	conflict	UNP K7GKS8
o	339	UNK	ASN	conflict	UNP K7GKS8
o	340	UNK	THR	conflict	UNP K7GKS8
o	341	UNK	ILE	conflict	UNP K7GKS8
o	342	UNK	LEU	conflict	UNP K7GKS8
o	343	UNK	LYS	conflict	UNP K7GKS8
o	344	UNK	CYS	conflict	UNP K7GKS8
o	345	UNK	LEU	conflict	UNP K7GKS8
o	346	UNK	ARG	conflict	UNP K7GKS8
o	347	UNK	ARG	conflict	UNP K7GKS8
o	348	UNK	PHE	conflict	UNP K7GKS8
o	349	UNK	TYR	conflict	UNP K7GKS8
o	350	UNK	ALA	conflict	UNP K7GKS8
o	351	UNK	PHE	conflict	UNP K7GKS8
o	352	UNK	GLY	conflict	UNP K7GKS8
o	353	UNK	LYS	conflict	UNP K7GKS8
o	354	UNK	LEU	conflict	UNP K7GKS8
o	355	UNK	PRO	conflict	UNP K7GKS8
o	356	UNK	ALA	conflict	UNP K7GKS8
o	357	UNK	LEU	conflict	UNP K7GKS8
o	358	UNK	GLN	conflict	UNP K7GKS8
o	359	UNK	THR	conflict	UNP K7GKS8
o	360	UNK	LEU	conflict	UNP K7GKS8
o	361	UNK	ARG	conflict	UNP K7GKS8
o	362	UNK	GLU	conflict	UNP K7GKS8
o	363	UNK	MET	conflict	UNP K7GKS8
o	364	UNK	LYS	conflict	UNP K7GKS8
o	365	UNK	ALA	conflict	UNP K7GKS8
o	366	UNK	ILE	conflict	UNP K7GKS8
o	367	UNK	GLY	conflict	UNP K7GKS8
o	368	UNK	ILE	conflict	UNP K7GKS8

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Chain	Residue	Modelled	Actual	Comment	Reference
o	369	UNK	GLU	conflict	UNP K7GKS8
o	370	UNK	PRO	conflict	UNP K7GKS8
o	371	UNK	SER	conflict	UNP K7GKS8
o	372	UNK	LEU	conflict	UNP K7GKS8
o	373	UNK	ALA	conflict	UNP K7GKS8
o	374	UNK	THR	conflict	UNP K7GKS8
o	375	UNK	TYR	conflict	UNP K7GKS8
o	376	UNK	HIS	conflict	UNP K7GKS8
o	377	UNK	TYR	conflict	UNP K7GKS8
o	378	UNK	VAL	conflict	UNP K7GKS8
o	379	UNK	ILE	conflict	UNP K7GKS8
o	380	UNK	GLN	conflict	UNP K7GKS8
o	381	UNK	LEU	conflict	UNP K7GKS8
o	382	UNK	PHE	conflict	UNP K7GKS8
o	383	UNK	TYR	conflict	UNP K7GKS8
o	384	UNK	GLN	conflict	UNP K7GKS8
o	385	UNK	HIS	conflict	UNP K7GKS8
o	386	UNK	GLU	conflict	UNP K7GKS8
o	387	UNK	SER	conflict	UNP K7GKS8
o	388	UNK	PRO	conflict	UNP K7GKS8
o	389	UNK	SER	conflict	UNP K7GKS8
o	390	UNK	LYS	conflict	UNP K7GKS8
o	391	UNK	GLY	conflict	UNP K7GKS8
o	392	UNK	SER	conflict	UNP K7GKS8
o	393	UNK	SER	conflict	UNP K7GKS8
o	394	UNK	LEU	conflict	UNP K7GKS8
o	395	UNK	ILE	conflict	UNP K7GKS8
o	396	UNK	ILE	conflict	UNP K7GKS8
o	397	UNK	TYR	conflict	UNP K7GKS8
o	398	UNK	ASP	conflict	UNP K7GKS8
o	399	UNK	ILE	conflict	UNP K7GKS8
o	400	UNK	MET	conflict	UNP K7GKS8
o	401	UNK	ASN	conflict	UNP K7GKS8
o	402	UNK	GLU	conflict	UNP K7GKS8
o	403	UNK	VAL	conflict	UNP K7GKS8
o	404	UNK	MET	conflict	UNP K7GKS8
o	405	UNK	GLY	conflict	UNP K7GKS8
o	406	UNK	LYS	conflict	UNP K7GKS8
o	407	UNK	ARG	conflict	UNP K7GKS8
o	408	UNK	PHE	conflict	UNP K7GKS8
o	409	UNK	SER	conflict	UNP K7GKS8
o	410	UNK	PRO	conflict	UNP K7GKS8

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Chain	Residue	Modelled	Actual	Comment	Reference
o	411	UNK	ARG	conflict	UNP K7GKS8
o	412	UNK	ASP	conflict	UNP K7GKS8
o	413	UNK	PRO	conflict	UNP K7GKS8
o	414	UNK	ASP	conflict	UNP K7GKS8
o	415	UNK	ASP	conflict	UNP K7GKS8
o	416	UNK	ASP	conflict	UNP K7GKS8
o	417	UNK	MET	conflict	UNP K7GKS8
o	418	UNK	PHE	conflict	UNP K7GKS8
o	419	UNK	PHE	conflict	UNP K7GKS8
o	420	UNK	GLN	conflict	UNP K7GKS8
o	421	UNK	SER	conflict	UNP K7GKS8
o	422	UNK	ALA	conflict	UNP K7GKS8
o	423	UNK	MET	conflict	UNP K7GKS8
o	424	UNK	ARG	conflict	UNP K7GKS8
o	425	UNK	VAL	conflict	UNP K7GKS8
o	426	UNK	CYS	conflict	UNP K7GKS8
o	427	UNK	SER	conflict	UNP K7GKS8
o	428	UNK	SER	conflict	UNP K7GKS8
o	429	UNK	LEU	conflict	UNP K7GKS8
o	430	UNK	ARG	conflict	UNP K7GKS8
o	431	UNK	ASP	conflict	UNP K7GKS8
o	432	UNK	LEU	conflict	UNP K7GKS8
o	433	UNK	GLU	conflict	UNP K7GKS8
o	434	UNK	LEU	conflict	UNP K7GKS8
o	435	UNK	ALA	conflict	UNP K7GKS8
o	436	UNK	TYR	conflict	UNP K7GKS8
o	437	UNK	GLN	conflict	UNP K7GKS8
o	438	UNK	VAL	conflict	UNP K7GKS8
o	439	UNK	HIS	conflict	UNP K7GKS8
o	440	UNK	GLY	conflict	UNP K7GKS8
o	441	UNK	LEU	conflict	UNP K7GKS8
o	442	UNK	LEU	conflict	UNP K7GKS8
o	443	UNK	ASN	conflict	UNP K7GKS8
o	444	UNK	THR	conflict	UNP K7GKS8
o	445	UNK	GLY	conflict	UNP K7GKS8
o	446	UNK	ASP	conflict	UNP K7GKS8
o	447	UNK	ASN	conflict	UNP K7GKS8
o	448	UNK	TRP	conflict	UNP K7GKS8
o	449	UNK	LYS	conflict	UNP K7GKS8
o	450	UNK	LEU	conflict	UNP K7GKS8
o	451	UNK	ILE	conflict	UNP K7GKS8
o	452	UNK	GLY	conflict	UNP K7GKS8

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Chain	Residue	Modelled	Actual	Comment	Reference
o	453	UNK	SER	conflict	UNP K7GKS8
o	454	UNK	ASP	conflict	UNP K7GKS8
o	455	UNK	HIS	conflict	UNP K7GKS8
o	456	UNK	ARG	conflict	UNP K7GKS8
o	457	UNK	ARG	conflict	UNP K7GKS8
o	458	UNK	ASN	conflict	UNP K7GKS8
o	459	UNK	PHE	conflict	UNP K7GKS8
o	460	UNK	TYR	conflict	UNP K7GKS8
o	461	UNK	TYR	conflict	UNP K7GKS8
o	462	UNK	SER	conflict	UNP K7GKS8
o	463	UNK	LYS	conflict	UNP K7GKS8
o	464	UNK	PHE	conflict	UNP K7GKS8
o	465	UNK	PHE	conflict	UNP K7GKS8
o	466	UNK	ASN	conflict	UNP K7GKS8
o	467	UNK	LEU	conflict	UNP K7GKS8
o	468	UNK	LEU	conflict	UNP K7GKS8
o	469	UNK	CYS	conflict	UNP K7GKS8
o	470	UNK	PHE	conflict	UNP K7GKS8
o	471	UNK	MET	conflict	UNP K7GKS8
o	472	UNK	GLU	conflict	UNP K7GKS8
o	473	UNK	GLN	conflict	UNP K7GKS8
o	474	UNK	ILE	conflict	UNP K7GKS8
o	475	UNK	ASP	conflict	UNP K7GKS8
o	476	UNK	VAL	conflict	UNP K7GKS8
o	477	UNK	THR	conflict	UNP K7GKS8
o	478	UNK	LEU	conflict	UNP K7GKS8
o	479	UNK	LYS	conflict	UNP K7GKS8
o	480	UNK	TRP	conflict	UNP K7GKS8
o	481	UNK	TYR	conflict	UNP K7GKS8
o	482	UNK	LYS	conflict	UNP K7GKS8
o	483	UNK	ASP	conflict	UNP K7GKS8
o	484	UNK	LEU	conflict	UNP K7GKS8
o	485	UNK	ILE	conflict	UNP K7GKS8
o	486	UNK	PRO	conflict	UNP K7GKS8
o	487	UNK	SER	conflict	UNP K7GKS8
o	488	UNK	VAL	conflict	UNP K7GKS8
o	489	UNK	PHE	conflict	UNP K7GKS8
o	490	UNK	PHE	conflict	UNP K7GKS8
o	491	UNK	PRO	conflict	UNP K7GKS8
o	492	UNK	HIS	conflict	UNP K7GKS8
o	493	UNK	SER	conflict	UNP K7GKS8
o	494	UNK	GLN	conflict	UNP K7GKS8

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Chain	Residue	Modelled	Actual	Comment	Reference
o	495	UNK	THR	conflict	UNP K7GKS8
o	496	UNK	MET	conflict	UNP K7GKS8
o	497	UNK	ILE	conflict	UNP K7GKS8
o	498	UNK	ASP	conflict	UNP K7GKS8
o	499	UNK	LEU	conflict	UNP K7GKS8
o	500	UNK	LEU	conflict	UNP K7GKS8
o	501	UNK	GLN	conflict	UNP K7GKS8
o	502	UNK	ALA	conflict	UNP K7GKS8
o	503	UNK	LEU	conflict	UNP K7GKS8
o	504	UNK	ASP	conflict	UNP K7GKS8
o	505	UNK	VAL	conflict	UNP K7GKS8
o	506	UNK	ALA	conflict	UNP K7GKS8
o	507	UNK	ASN	conflict	UNP K7GKS8
o	508	UNK	ARG	conflict	UNP K7GKS8
o	509	UNK	LEU	conflict	UNP K7GKS8
o	510	UNK	ASP	conflict	UNP K7GKS8
o	511	UNK	MET	conflict	UNP K7GKS8
o	512	UNK	VAL	conflict	UNP K7GKS8
o	513	UNK	PRO	conflict	UNP K7GKS8
o	514	UNK	GLN	conflict	UNP K7GKS8
o	515	UNK	ILE	conflict	UNP K7GKS8
o	516	UNK	TRP	conflict	UNP K7GKS8
o	517	UNK	LYS	conflict	UNP K7GKS8
o	518	UNK	ASP	conflict	UNP K7GKS8
o	519	UNK	SER	conflict	UNP K7GKS8
o	520	UNK	LYS	conflict	UNP K7GKS8
o	521	UNK	GLU	conflict	UNP K7GKS8
o	522	UNK	TYR	conflict	UNP K7GKS8
o	523	UNK	GLY	conflict	UNP K7GKS8
o	524	UNK	HIS	conflict	UNP K7GKS8
o	525	UNK	THR	conflict	UNP K7GKS8
o	526	UNK	PHE	conflict	UNP K7GKS8
o	527	UNK	ARG	conflict	UNP K7GKS8
o	528	UNK	ASN	conflict	UNP K7GKS8
o	529	UNK	GLU	conflict	UNP K7GKS8
o	530	UNK	LEU	conflict	UNP K7GKS8
o	531	UNK	LYS	conflict	UNP K7GKS8
o	532	UNK	GLU	conflict	UNP K7GKS8
o	533	UNK	GLU	conflict	UNP K7GKS8
o	534	UNK	ILE	conflict	UNP K7GKS8
o	535	UNK	LEU	conflict	UNP K7GKS8
o	536	UNK	MET	conflict	UNP K7GKS8

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Chain	Residue	Modelled	Actual	Comment	Reference
o	537	UNK	LEU	conflict	UNP K7GKS8
o	538	UNK	MET	conflict	UNP K7GKS8
o	539	UNK	ALA	conflict	UNP K7GKS8
o	540	UNK	ARG	conflict	UNP K7GKS8
o	541	UNK	ASP	conflict	UNP K7GKS8
o	542	UNK	GLN	conflict	UNP K7GKS8
o	543	UNK	HIS	conflict	UNP K7GKS8
o	544	UNK	PRO	conflict	UNP K7GKS8
o	545	UNK	PRO	conflict	UNP K7GKS8
o	546	UNK	GLU	conflict	UNP K7GKS8
o	547	UNK	LEU	conflict	UNP K7GKS8
o	548	UNK	GLN	conflict	UNP K7GKS8
o	549	UNK	VAL	conflict	UNP K7GKS8
o	550	UNK	ALA	conflict	UNP K7GKS8
o	551	UNK	PHE	conflict	UNP K7GKS8
o	552	UNK	ALA	conflict	UNP K7GKS8
o	553	UNK	ASP	conflict	UNP K7GKS8
o	554	UNK	CYS	conflict	UNP K7GKS8
o	555	UNK	ALA	conflict	UNP K7GKS8
o	556	UNK	ALA	conflict	UNP K7GKS8
o	557	UNK	ASP	conflict	UNP K7GKS8
o	558	UNK	ILE	conflict	UNP K7GKS8
o	559	UNK	LYS	conflict	UNP K7GKS8
o	560	UNK	SER	conflict	UNP K7GKS8
o	561	UNK	THR	conflict	UNP K7GKS8
o	562	UNK	TYR	conflict	UNP K7GKS8
o	563	UNK	GLU	conflict	UNP K7GKS8
o	564	UNK	SER	conflict	UNP K7GKS8
o	565	UNK	GLN	conflict	UNP K7GKS8
o	566	UNK	ASP	conflict	UNP K7GKS8
o	567	UNK	ALA	conflict	UNP K7GKS8
o	568	UNK	ARG	conflict	UNP K7GKS8
o	569	UNK	GLN	conflict	UNP K7GKS8
o	570	UNK	THR	conflict	UNP K7GKS8
o	571	UNK	ALA	conflict	UNP K7GKS8
o	572	UNK	PRO	conflict	UNP K7GKS8
o	573	UNK	GLU	conflict	UNP K7GKS8
o	574	UNK	TRP	conflict	UNP K7GKS8
o	575	UNK	PRO	conflict	UNP K7GKS8
o	576	UNK	ALA	conflict	UNP K7GKS8
o	577	UNK	SER	conflict	UNP K7GKS8
o	578	UNK	SER	conflict	UNP K7GKS8

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Chain	Residue	Modelled	Actual	Comment	Reference
o	579	UNK	LEU	conflict	UNP K7GKS8
o	580	UNK	ASN	conflict	UNP K7GKS8
o	581	UNK	TYR	conflict	UNP K7GKS8
o	582	UNK	VAL	conflict	UNP K7GKS8
o	583	UNK	ALA	conflict	UNP K7GKS8
o	584	UNK	VAL	conflict	UNP K7GKS8
o	585	UNK	LEU	conflict	UNP K7GKS8
o	586	UNK	PHE	conflict	UNP K7GKS8
o	587	UNK	LEU	conflict	UNP K7GKS8
o	588	UNK	ARG	conflict	UNP K7GKS8
o	589	UNK	ALA	conflict	UNP K7GKS8
o	590	UNK	GLY	conflict	UNP K7GKS8
o	591	UNK	ARG	conflict	UNP K7GKS8
o	592	UNK	THR	conflict	UNP K7GKS8
o	593	UNK	GLN	conflict	UNP K7GKS8
o	594	UNK	GLU	conflict	UNP K7GKS8
o	595	UNK	ALA	conflict	UNP K7GKS8
o	596	UNK	TRP	conflict	UNP K7GKS8
o	597	UNK	LYS	conflict	UNP K7GKS8
o	598	UNK	MET	conflict	UNP K7GKS8
o	599	UNK	LEU	conflict	UNP K7GKS8
o	600	UNK	GLY	conflict	UNP K7GKS8
o	601	UNK	LEU	conflict	UNP K7GKS8
o	602	UNK	PHE	conflict	UNP K7GKS8
o	603	UNK	ARG	conflict	UNP K7GKS8
o	604	UNK	LYS	conflict	UNP K7GKS8
o	605	UNK	HIS	conflict	UNP K7GKS8
o	606	UNK	ASN	conflict	UNP K7GKS8
o	607	UNK	LYS	conflict	UNP K7GKS8
o	608	UNK	ILE	conflict	UNP K7GKS8
o	609	UNK	PRO	conflict	UNP K7GKS8
o	610	UNK	ARG	conflict	UNP K7GKS8
o	611	UNK	ALA	conflict	UNP K7GKS8
o	612	UNK	GLU	conflict	UNP K7GKS8
o	613	UNK	LEU	conflict	UNP K7GKS8
o	614	UNK	LEU	conflict	UNP K7GKS8
o	615	UNK	ASN	conflict	UNP K7GKS8
o	616	UNK	GLU	conflict	UNP K7GKS8
o	617	UNK	PHE	conflict	UNP K7GKS8
o	618	UNK	LEU	conflict	UNP K7GKS8
o	619	UNK	ASP	conflict	UNP K7GKS8
o	620	UNK	SER	conflict	UNP K7GKS8

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Chain	Residue	Modelled	Actual	Comment	Reference
o	621	UNK	ALA	conflict	UNP K7GKS8
o	622	UNK	LYS	conflict	UNP K7GKS8
o	623	UNK	ALA	conflict	UNP K7GKS8
o	624	UNK	SER	conflict	UNP K7GKS8
o	625	UNK	SER	conflict	UNP K7GKS8
o	626	UNK	SER	conflict	UNP K7GKS8
o	627	UNK	PRO	conflict	UNP K7GKS8
o	628	UNK	ALA	conflict	UNP K7GKS8
o	629	UNK	GLN	conflict	UNP K7GKS8
o	630	UNK	ALA	conflict	UNP K7GKS8
o	631	UNK	ILE	conflict	UNP K7GKS8
o	632	UNK	GLU	conflict	UNP K7GKS8
o	633	UNK	LEU	conflict	UNP K7GKS8
o	634	UNK	VAL	conflict	UNP K7GKS8
o	635	UNK	LYS	conflict	UNP K7GKS8
o	636	UNK	LEU	conflict	UNP K7GKS8
o	637	UNK	ALA	conflict	UNP K7GKS8
o	638	UNK	SER	conflict	UNP K7GKS8
o	639	UNK	ALA	conflict	UNP K7GKS8
o	640	UNK	PHE	conflict	UNP K7GKS8
o	641	UNK	SER	conflict	UNP K7GKS8
o	642	UNK	LEU	conflict	UNP K7GKS8
o	643	UNK	PRO	conflict	UNP K7GKS8
o	644	UNK	VAL	conflict	UNP K7GKS8
o	645	UNK	CYS	conflict	UNP K7GKS8
o	646	UNK	GLU	conflict	UNP K7GKS8
o	647	UNK	GLY	conflict	UNP K7GKS8
o	648	UNK	LEU	conflict	UNP K7GKS8
o	649	UNK	THR	conflict	UNP K7GKS8
o	650	UNK	ARG	conflict	UNP K7GKS8
o	651	UNK	ARG	conflict	UNP K7GKS8
o	652	UNK	VAL	conflict	UNP K7GKS8
o	653	UNK	MET	conflict	UNP K7GKS8
o	654	UNK	ALA	conflict	UNP K7GKS8
o	655	UNK	GLU	conflict	UNP K7GKS8
o	656	UNK	PHE	conflict	UNP K7GKS8
o	657	UNK	THR	conflict	UNP K7GKS8
o	658	UNK	LEU	conflict	UNP K7GKS8
o	659	UNK	THR	conflict	UNP K7GKS8
o	660	UNK	GLN	conflict	UNP K7GKS8
o	661	UNK	GLU	conflict	UNP K7GKS8
o	662	UNK	GLN	conflict	UNP K7GKS8

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Chain	Residue	Modelled	Actual	Comment	Reference
o	663	UNK	ARG	conflict	UNP K7GKS8
o	664	UNK	GLU	conflict	UNP K7GKS8
o	665	UNK	ALA	conflict	UNP K7GKS8
o	666	UNK	LEU	conflict	UNP K7GKS8
o	667	UNK	GLY	conflict	UNP K7GKS8
o	668	UNK	GLU	conflict	UNP K7GKS8
o	669	UNK	LEU	conflict	UNP K7GKS8
o	670	UNK	THR	conflict	UNP K7GKS8
o	671	UNK	ALA	conflict	UNP K7GKS8
o	672	UNK	LEU	conflict	UNP K7GKS8
o	673	UNK	THR	conflict	UNP K7GKS8
o	674	UNK	SER	conflict	UNP K7GKS8
o	675	UNK	ASP	conflict	UNP K7GKS8
o	676	UNK	SER	conflict	UNP K7GKS8
o	677	UNK	SER	conflict	UNP K7GKS8

- Molecule 34 is a protein called MITORIBOSOMAL PROTEIN MS40, MRPS18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	p	188	Total	C	N	O	S	0	0
			1551	983	290	270	8		

- Molecule 35 is a protein called UNASSIGNED HELICES.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	s	16	Total	C	N	O	0	0
			96	64	16	16		

- Molecule 36 is a protein called UNASSIGNED HELICES.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	z	17	Total	C	N	O	0	0
			102	68	17	17		

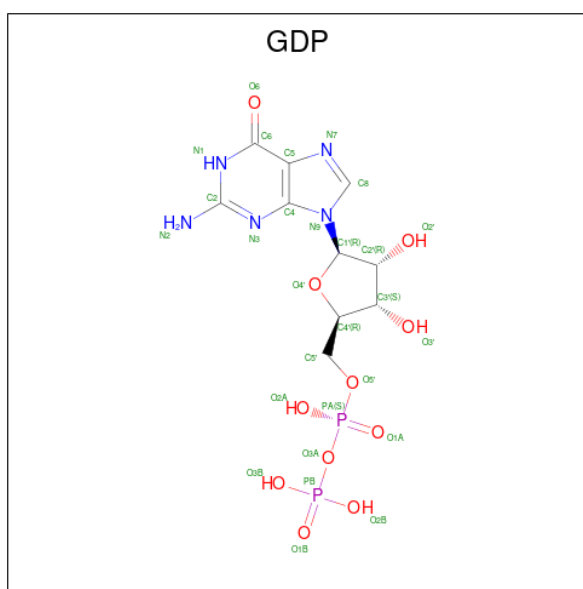
- Molecule 37 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	A	143	Total	Mg	0
			143	143	
37	g	1	Total	Mg	0
			1	1	

- Molecule 38 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
38	R	1	Total	Zn	0
			1	1	
38	c	1	Total	Zn	0
			1	1	
38	p	1	Total	Zn	0
			1	1	

- Molecule 39 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
39	g	1	Total	C	N	O	P	0
			28	10	5	11	2	

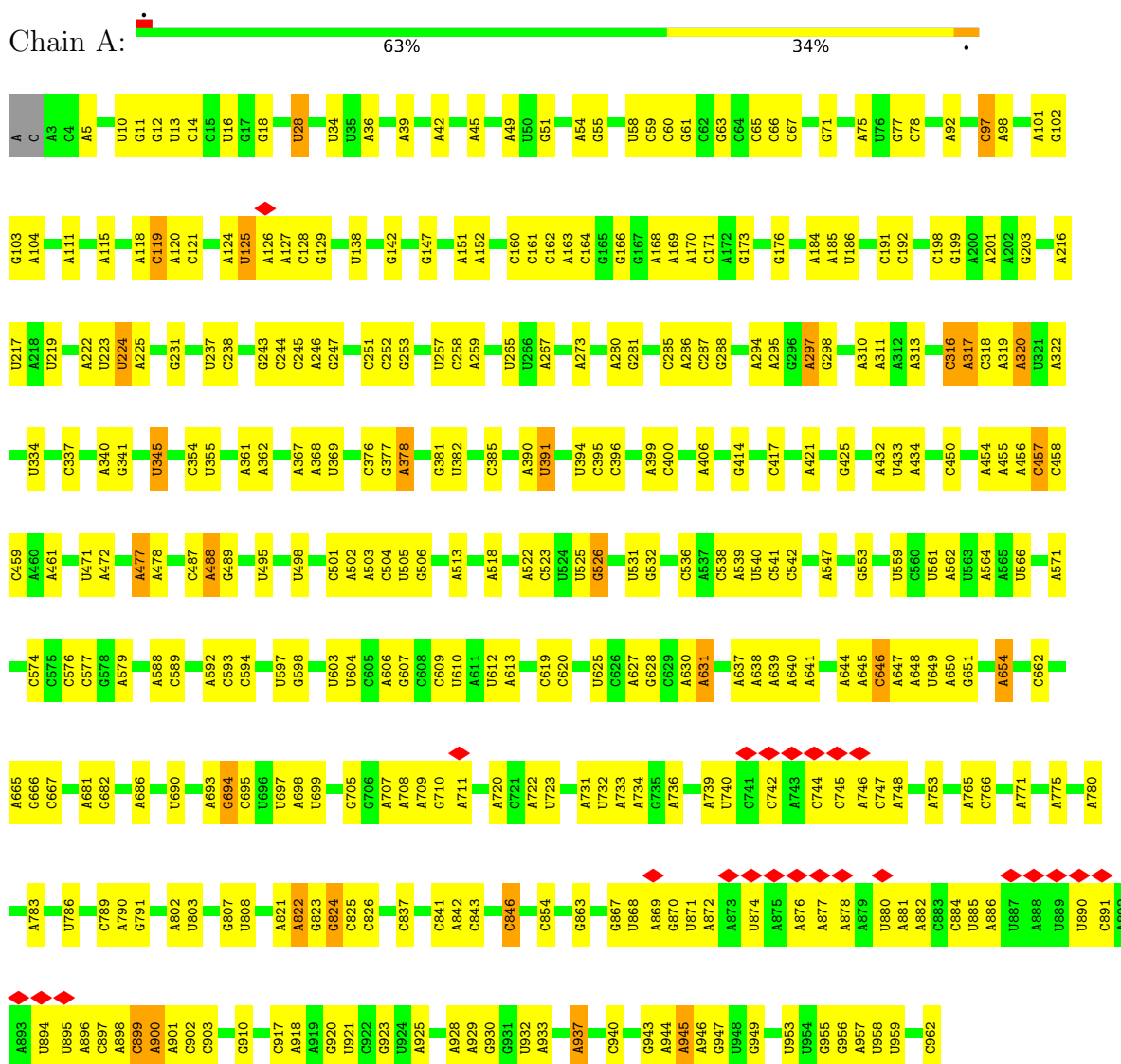
- Molecule 40 is water.

Mol	Chain	Residues	Atoms		AltConf
40	A	114	Total	O	0
			114	114	
40	g	4	Total	O	0
			4	4	

3 Residue-property plots

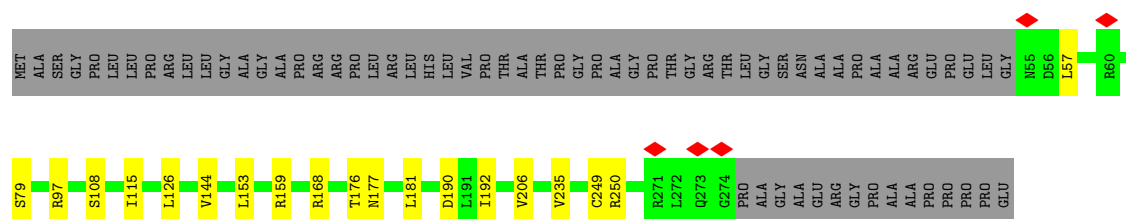
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: MITORIBOSOMAL 12S RRNA

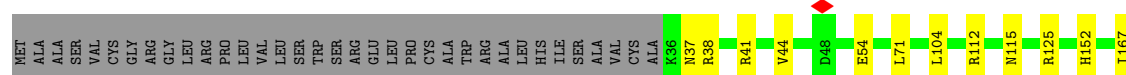


• Molecule 2: MITORIBOSOMAL PROTEIN US2M, MRPS2

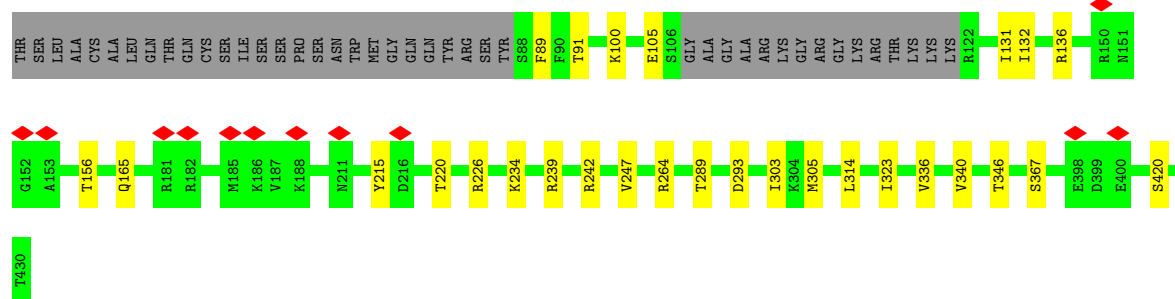
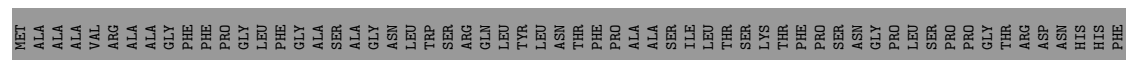




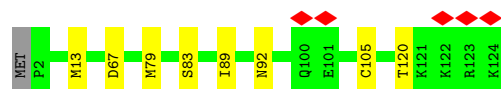
• Molecule 3: MITORIBOSOMAL PROTEIN US3M, MRPS24



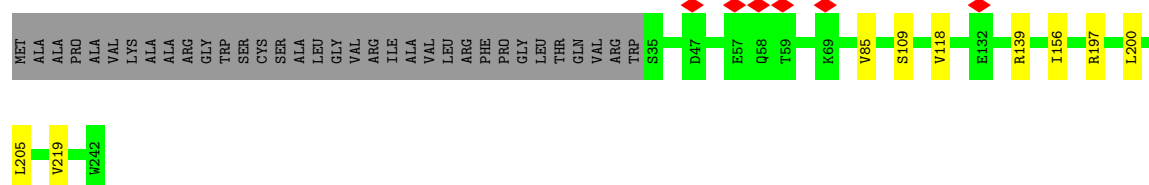
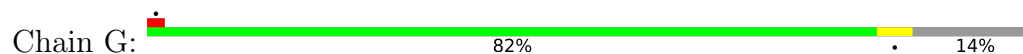
• Molecule 4: MITORIBOSOMAL PROTEIN US5M, MRPS5



• Molecule 5: MITORIBOSOMAL PROTEIN BS6M, MRPS6



• Molecule 6: MITORIBOSOMAL PROTEIN US7M, MRPS7



• Molecule 7: MITORIBOSOMAL PROTEIN US9M, MRPS9

Chain I:  73% 6% 22%

MET ALA ALA PRO CYS VAL PHE GLY CYS ALA ALA VAL SER THR ARG LEU PHE LEU GLY CYS ARG VAL PHE ARG ALA ARG GLY LEU VAL ARG LEU TRP LYS ALA ALA ALA PRO GLU LEU GLN ALA GLY ALA ASP CYS ARG CYS ILE LEU LEU ARG LEU ARG HIS THR VAL THR THR LYS LYS ASN

VAL ALA ALA ARG THR ARG ARG THR TYR T70 N90 T98 F99 T153 Q156 L161 D171 N177 GLN LEU ARG VAL ARG LEU LYS ASP LEU LEU ALA ALA GLU LEU THR LYS LYS ILE ALA GLY ALA ASP P195 I196 I202 L206 M209 S215 C234 G235 A236 T237 P250 K251
K252 K264 R293 Y301 L302 L303 C331 R338 L353 V357 R366 L371 T372 V377 R397

- Molecule 8: MITORIBOSOMAL PROTEIN US10M, MRPS10

Chain J:  57% 7% 36%

MET ALA ALA ARG THR PHE GLY ALA ALA ARG LEU TRP GLN TRP GLY SER ARG ASN ARG PHE VAL SER SER ARG SER THR ALA LYS ASN GLY LEU PHE LEU LEU SER THR MET LYS TRP VAL GLN PHE SER SER ASN LEU HIS VAL ASP PRO LYS ASP MET THR LYS

P61 L72 D84 E92 E116 I126 M136 L143 E144 L145 L148 T149 I160 E166 Q179 R185 K186 V189 GLU THR MET PRO GLU GLU GLU LYS LYS SER

- Molecule 9: MITORIBOSOMAL PROTEIN US11M, MRPS11

Chain K:  65% 5% 31%

MET GLN VAL VAL ASN ALA GLY SER LEU LEU GLN SER TRP ALA TRP PRO PRO LYS THR ARG ILE VAL ALA GLY LEU PRO ALA THR TLE HIS ARG SER ALA PRO HIS LEU GLN ASP ALA ALA LYS LEU ASP ILE GLU ASP LYS GLU ALA ARG THR PRO SER HIS SER

S61 T64 Y65 E72 L75 Q98 I128 V151 V152 V153 S176 I177 T178 R194 R195 L196

- Molecule 10: MITORIBOSOMAL PROTEIN US12M, MRPS12

Chain L:  71% 8% 22%

MET SER TRP TRP GLY LEU ARG GLY ARG GLY THR SER LEU CYS ASN TRP VAL LEU LEU ALA VAL PRO ARG TRP ALA THR ARG MET A31 L39 T52 R55 V61 S75 A76 N77 T95 V110 R114 L118 R127 K138 K139

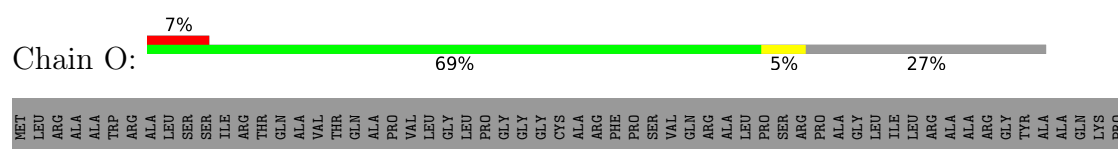
- Molecule 11: MITORIBOSOMAL PROTEIN US14M, MRPS14

Chain N:  62% 16% 21%

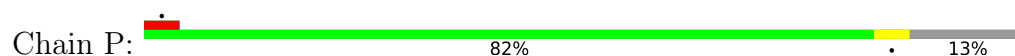
MET ALA ALA SER MET MET GLY PHE LEU LEU ARG THR VAL ARG GLN MET MET VAL PRO SER SER ALA VAL SER GLY GLN TRP VAL ARG Y28 M34 D37 S66 L57 R58 I75 R80 D81 S82 C83 V92 M93 T94 S95 R98 S107 R108 I109 L120 V123 Q124 R125

W128

- Molecule 12: MITORIBOSOMAL PROTEIN US15M, MRPS15



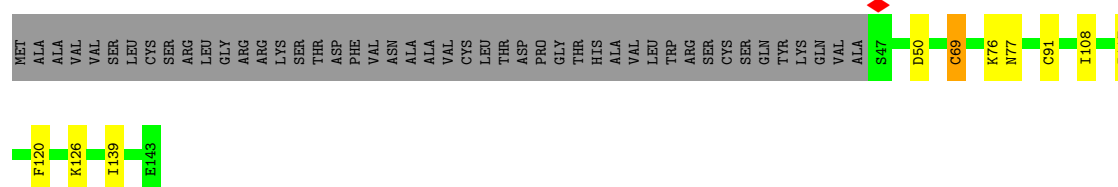
- Molecule 13: MITORIBOSOMAL PROTEIN BS16M, MRPS16



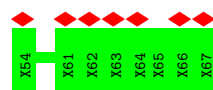
- Molecule 14: MITORIBOSOMAL PROTEIN US17M, MRPS17



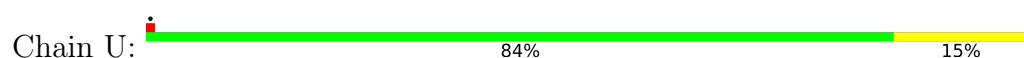
- Molecule 15: MITORIBOSOMAL PROTEIN BS18M, MRPS18C



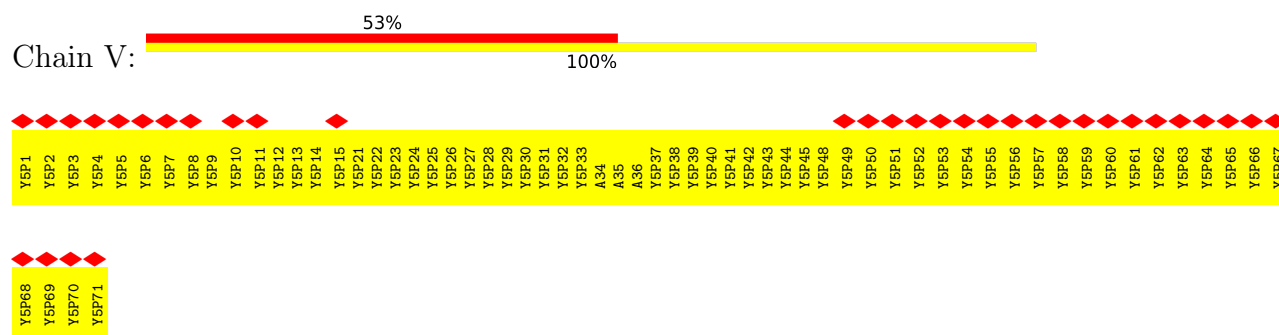
- Molecule 16: MITORIBOSOMAL PROTEIN BL19M, MRPL19



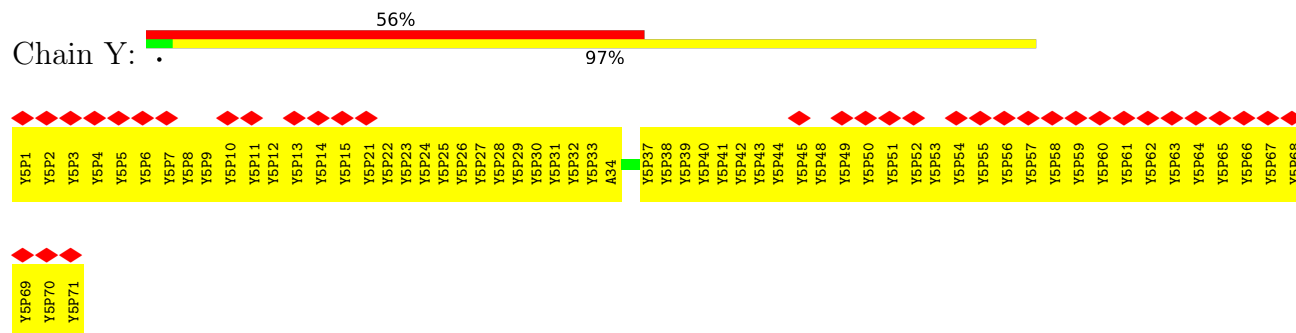
- Molecule 17: MITORIBOSOMAL PROTEIN BS21M, MRPS21



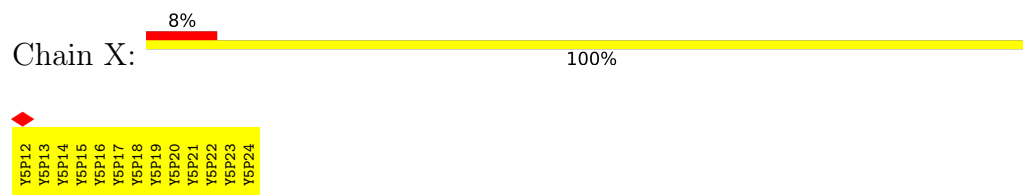
- Molecule 18: P-SITE AND A-SITE TRNA



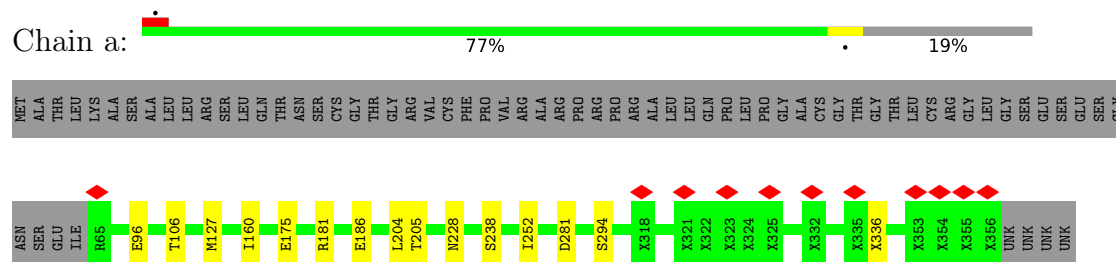
- Molecule 18: P-SITE AND A-SITE TRNA



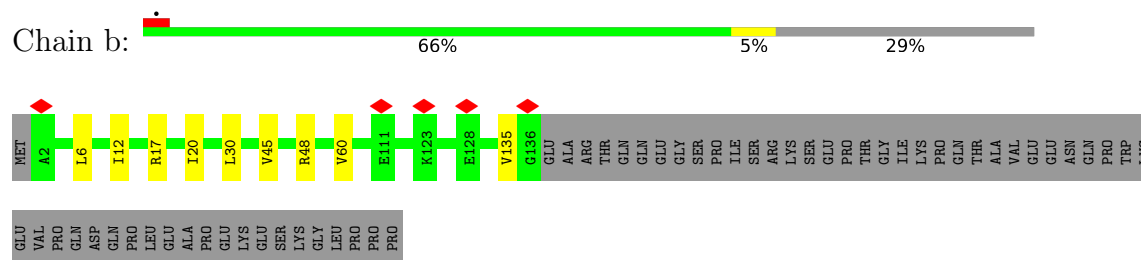
- Molecule 19: MRNA



- Molecule 20: MITORIBOSOMAL PROTEIN MS22, MRPS22



- Molecule 21: MITORIBOSOMAL PROTEIN MS23, MRPS23

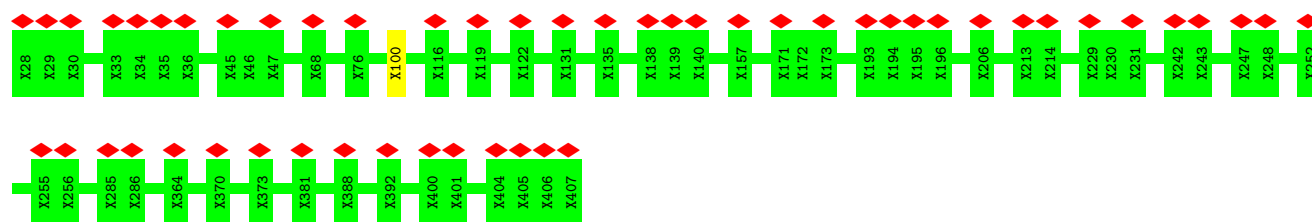


- Molecule 22: MITORIBOSOMAL PROTEIN MS25, MRPS25

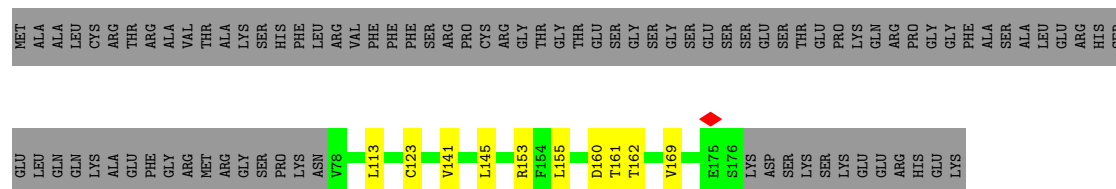
MET	P2	M3	K4	I9	T12	F23	K24	D25	S26	V27	N33	N59	M70	S82	N95	L106	R137	C141	L152	T170	ALA	GLN	ASP
-----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	-----	-----	-----

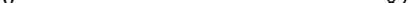
- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|-----|
| Met | Leu | Arg | Val | Leu | Gly | Gly | Leu | Gly | Ala | Arg | Pro | K28 | Gly | Arg | Leu | Pro | Ala | Ala | Pro | Leu | Leu | Leu | Pro | Thr | Arg | Gly | R27 | K28 | T29 | R30 | R41 | E92 | R115 | R144 | T166 | S186 | I191 | L196 | V197 | V198 | Q201 | Q202 | K203 | Gly |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|-----|

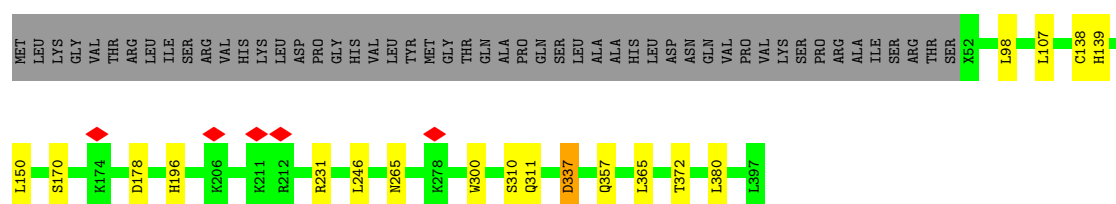
- Chain e:  15% 100%



- Chain f:

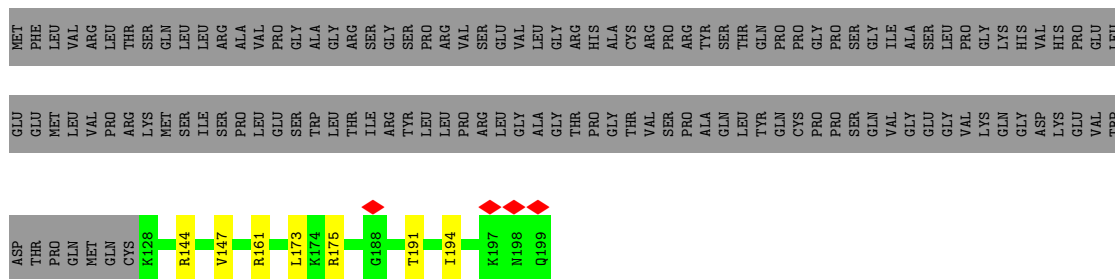


- Chain g:  82% 5% 13%

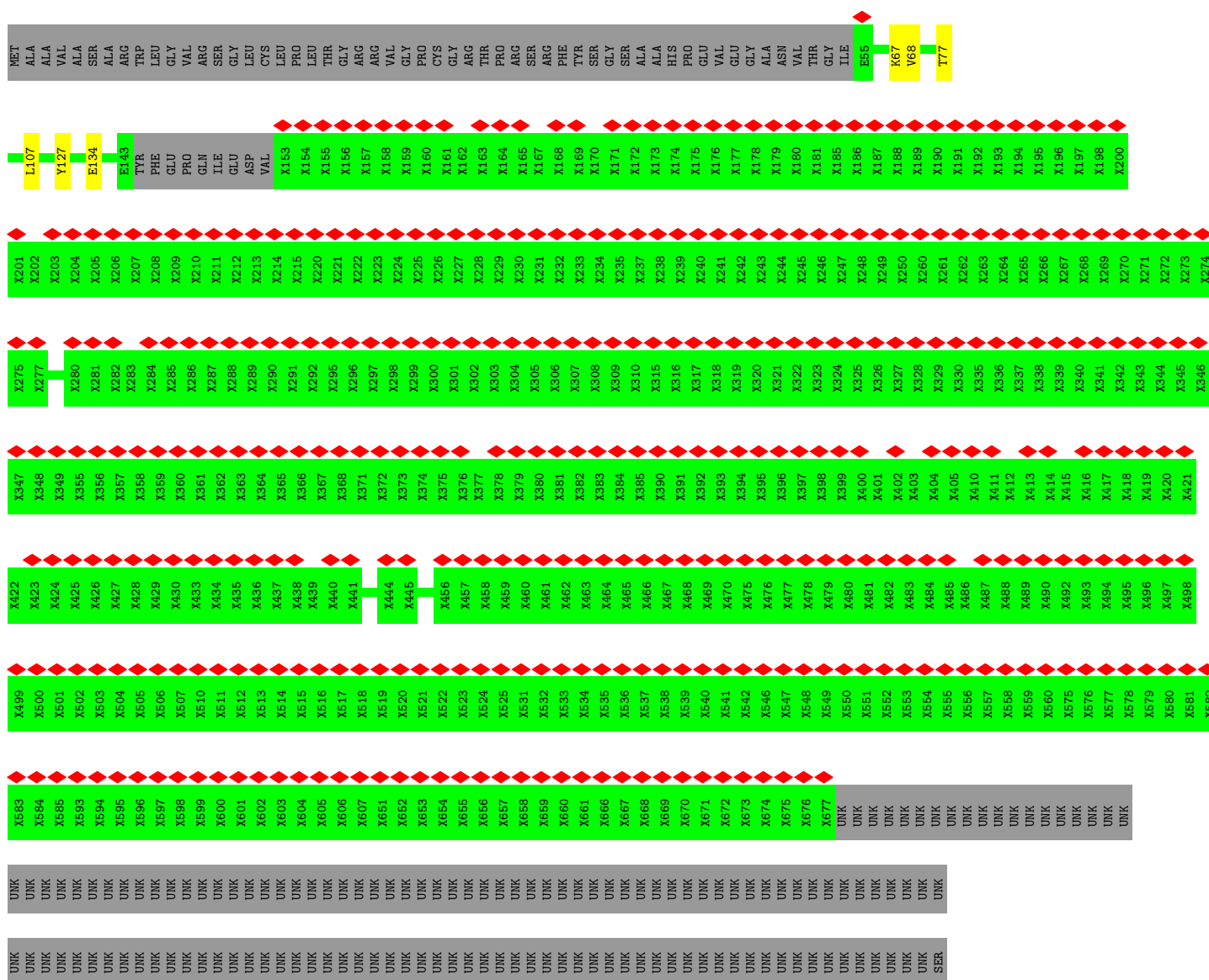


- Chain h:

Chain n:  33% 64%



Chain o:  53% 68% 31%



X692
X693
X694
X695

X708

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	78783	Depositor
Resolution determination method	Not provided	
CTF correction method	PER DETECTOR FRAME	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	100000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.529	Depositor
Minimum map value	-0.250	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.06	Depositor
Map size (\AA)	300.24, 300.24, 300.24	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.39, 1.39, 1.39	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: ZN, GDP, Y5P, P5P, 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	0.67	4/22852 (0.0%)	1.16	72/35580 (0.2%)
2	B	0.48	0/1804	0.61	0/2445
3	C	0.41	0/1105	0.65	0/1496
4	E	0.46	0/2673	0.59	0/3591
5	F	0.42	0/1008	0.63	1/1358 (0.1%)
6	G	0.39	0/1763	0.54	0/2368
7	I	0.39	0/2455	0.52	0/3291
8	J	0.45	0/1091	0.63	0/1474
9	K	0.44	0/1021	0.65	0/1381
10	L	0.42	0/858	0.60	0/1152
11	N	0.45	0/874	0.60	0/1171
12	O	0.42	0/1473	0.58	0/1970
13	P	0.45	0/954	0.62	0/1284
14	Q	0.43	0/871	0.64	0/1181
15	R	0.55	1/802 (0.1%)	0.69	0/1079
17	U	0.46	0/745	0.59	0/993
20	a	0.35	0/2052	0.52	0/2774
21	b	0.39	0/1126	0.54	0/1514
22	c	0.45	0/1399	0.64	1/1881 (0.1%)
23	d	0.40	0/1490	0.51	0/2005
25	f	0.42	0/790	0.60	0/1064
26	g	0.34	0/2731	0.52	0/3696
27	h	0.35	0/903	0.52	0/1215
28	i	0.38	0/841	0.53	0/1121
29	j	0.34	0/1779	0.59	0/2404
30	k	0.35	0/2268	0.54	0/3069
31	m	0.42	0/947	0.56	0/1268
32	n	0.51	0/650	0.60	0/858
33	o	0.36	0/726	0.53	0/988
34	p	0.44	1/1602 (0.1%)	0.60	0/2175
All	All	0.52	6/61653 (0.0%)	0.86	74/87846 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
8	J	0	2
9	K	0	1
20	a	0	1
24	e	0	1
All	All	0	5

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	R	69	CYS	CB-SG	6.80	1.93	1.82
1	A	843	C	N1-C6	-6.07	1.33	1.37
1	A	822	A	N9-C4	5.59	1.41	1.37
1	A	406	A	N9-C4	-5.18	1.34	1.37
34	p	105	CYS	CB-SG	-5.15	1.73	1.81

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	297	A	C8-N9-C4	7.75	108.90	105.80
1	A	488	A	N1-C2-N3	7.73	133.17	129.30
1	A	28	U	C5-C6-N1	-7.65	118.87	122.70
1	A	119	C	N1-C2-O2	7.53	123.42	118.90
22	c	141	CYS	CA-CB-SG	7.37	127.27	114.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	J	185	ARG	Peptide
8	J	186	LYS	Peptide
9	K	194	ARG	Peptide
20	a	336	UNK	Peptide
24	e	100	UNK	Peptide

5.2 Too-close contacts

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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 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	
2	B	218/289 (75%)	209 (96%)	9 (4%)	0	100	100
3	C	130/167 (78%)	123 (95%)	7 (5%)	0	100	100
4	E	324/430 (75%)	308 (95%)	16 (5%)	0	100	100
5	F	121/124 (98%)	118 (98%)	3 (2%)	0	100	100
6	G	206/242 (85%)	204 (99%)	2 (1%)	0	100	100
7	I	291/397 (73%)	280 (96%)	11 (4%)	0	100	100
8	J	127/201 (63%)	117 (92%)	7 (6%)	3 (2%)	5	30
9	K	134/196 (68%)	128 (96%)	6 (4%)	0	100	100
10	L	107/139 (77%)	101 (94%)	6 (6%)	0	100	100
11	N	99/128 (77%)	97 (98%)	2 (2%)	0	100	100
12	O	173/239 (72%)	165 (95%)	8 (5%)	0	100	100
13	P	115/135 (85%)	112 (97%)	3 (3%)	0	100	100
14	Q	107/130 (82%)	102 (95%)	4 (4%)	1 (1%)	14	48
15	R	95/143 (66%)	93 (98%)	2 (2%)	0	100	100
17	U	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
20	a	243/360 (68%)	236 (97%)	7 (3%)	0	100	100
21	b	133/190 (70%)	128 (96%)	5 (4%)	0	100	100
22	c	167/173 (96%)	158 (95%)	9 (5%)	0	100	100
23	d	175/205 (85%)	173 (99%)	2 (1%)	0	100	100
25	f	97/188 (52%)	90 (93%)	7 (7%)	0	100	100
26	g	327/397 (82%)	319 (98%)	7 (2%)	1 (0%)	37	67
27	h	101/387 (26%)	97 (96%)	4 (4%)	0	100	100
28	i	97/106 (92%)	90 (93%)	7 (7%)	0	100	100
29	j	204/218 (94%)	191 (94%)	13 (6%)	0	100	100
30	k	273/325 (84%)	266 (97%)	7 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	m	114/118 (97%)	110 (96%)	4 (4%)	0	100	100
32	n	70/199 (35%)	66 (94%)	4 (6%)	0	100	100
33	o	87/692 (13%)	83 (95%)	4 (5%)	0	100	100
34	p	186/258 (72%)	175 (94%)	11 (6%)	0	100	100
All	All	4605/6863 (67%)	4422 (96%)	178 (4%)	5 (0%)	50	79

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	J	179	GLN
8	J	185	ARG
14	Q	95	VAL
8	J	160	ILE
26	g	337	ASP

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	
2	B	187/233 (80%)	168 (90%)	19 (10%)	6	27
3	C	115/142 (81%)	103 (90%)	12 (10%)	5	26
4	E	273/351 (78%)	245 (90%)	28 (10%)	6	27
5	F	108/109 (99%)	101 (94%)	7 (6%)	14	42
6	G	181/205 (88%)	172 (95%)	9 (5%)	20	49
7	I	250/317 (79%)	227 (91%)	23 (9%)	7	31
8	J	119/181 (66%)	108 (91%)	11 (9%)	7	31
9	K	102/151 (68%)	94 (92%)	8 (8%)	10	36
10	L	92/116 (79%)	81 (88%)	11 (12%)	4	21
11	N	92/114 (81%)	71 (77%)	21 (23%)	0	4
12	O	159/205 (78%)	148 (93%)	11 (7%)	13	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	P	97/113 (86%)	91 (94%)	6 (6%)	15	44
14	Q	94/114 (82%)	81 (86%)	13 (14%)	3	17
15	R	89/127 (70%)	79 (89%)	10 (11%)	5	24
17	U	77/78 (99%)	64 (83%)	13 (17%)	1	11
20	a	222/272 (82%)	208 (94%)	14 (6%)	15	44
21	b	113/162 (70%)	104 (92%)	9 (8%)	10	35
22	c	152/155 (98%)	137 (90%)	15 (10%)	6	28
23	d	149/168 (89%)	137 (92%)	12 (8%)	9	35
25	f	86/160 (54%)	76 (88%)	10 (12%)	4	23
26	g	290/334 (87%)	271 (93%)	19 (7%)	14	42
27	h	95/345 (28%)	90 (95%)	5 (5%)	19	48
28	i	86/93 (92%)	80 (93%)	6 (7%)	12	40
29	j	182/184 (99%)	172 (94%)	10 (6%)	18	47
30	k	249/289 (86%)	229 (92%)	20 (8%)	10	35
31	m	100/102 (98%)	91 (91%)	9 (9%)	8	32
32	n	66/174 (38%)	59 (89%)	7 (11%)	5	26
33	o	79/141 (56%)	73 (92%)	6 (8%)	11	37
34	p	168/225 (75%)	151 (90%)	17 (10%)	6	27
All	All	4072/5360 (76%)	3711 (91%)	361 (9%)	10	32

5 of 361 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	c	27	VAL
28	i	11	MET
22	c	137	ARG
25	f	162	THR
29	j	186	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 98 such sidechains are listed below:

Mol	Chain	Res	Type
20	a	213	ASN
22	c	125	HIS
20	a	223	HIS

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Mol	Chain	Res	Type
22	c	51	ASN
23	d	126	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	959/962 (99%)	329 (34%)	10 (1%)
18	V	0/64	-	-
18	Y	0/64	-	-
19	X	0/13	-	-
All	All	959/1103 (86%)	329 (34%)	10 (1%)

5 of 329 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	5	A
1	A	10	U
1	A	11	G
1	A	14	C
1	A	18	G

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	899	C
1	A	900	A
1	A	901	A
1	A	317	A
1	A	390	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

141 non-standard protein/DNA/RNA residues are modelled in this entry.

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
18	Y5P	V	64	18	14,19,20	2.70	2 (14%)	18,26,29	1.05	1 (5%)
18	Y5P	V	25	18	14,19,20	3.57	1 (7%)	18,26,29	0.84	2 (11%)
18	Y5P	V	7	18	14,19,20	2.62	2 (14%)	18,26,29	1.00	1 (5%)
18	Y5P	V	51	18	14,19,20	2.31	1 (7%)	18,26,29	0.94	1 (5%)
18	Y5P	V	8	18	14,19,20	2.31	1 (7%)	18,26,29	0.96	1 (5%)
18	Y5P	Y	69	18	14,19,20	2.72	2 (14%)	18,26,29	1.10	1 (5%)
18	Y5P	Y	50	18	14,19,20	2.14	1 (7%)	18,26,29	1.05	1 (5%)
19	Y5P	X	19	19,37	14,19,20	2.61	1 (7%)	18,26,29	0.99	1 (5%)
18	Y5P	V	26	18	14,19,20	2.73	2 (14%)	18,26,29	1.06	1 (5%)
19	Y5P	X	22	19	14,19,20	2.18	1 (7%)	18,26,29	1.08	1 (5%)
18	Y5P	V	4	18	14,19,20	3.62	1 (7%)	18,26,29	0.77	1 (5%)
18	Y5P	V	38	18	14,19,20	2.68	2 (14%)	18,26,29	1.09	1 (5%)
18	Y5P	V	23	18	14,19,20	2.68	2 (14%)	18,26,29	1.02	1 (5%)
18	P5P	Y	34	18	16,23,24	1.45	2 (12%)	14,33,36	2.11	2 (14%)
18	Y5P	Y	22	18	14,19,20	2.66	2 (14%)	18,26,29	1.03	1 (5%)
18	Y5P	V	12	18	14,19,20	2.19	1 (7%)	18,26,29	1.02	1 (5%)
18	Y5P	V	21	18	14,19,20	2.83	2 (14%)	18,26,29	1.19	2 (11%)
18	Y5P	Y	27	18	14,19,20	2.70	2 (14%)	18,26,29	1.27	2 (11%)
18	Y5P	V	62	18	14,19,20	3.52	2 (14%)	18,26,29	0.85	2 (11%)
18	Y5P	V	49	18	14,19,20	3.50	1 (7%)	18,26,29	0.86	2 (11%)
18	Y5P	V	53	18	14,19,20	2.74	2 (14%)	18,26,29	1.02	1 (5%)
18	Y5P	V	2	18	14,19,20	3.68	1 (7%)	18,26,29	0.82	2 (11%)
19	Y5P	X	12	19	14,16,20	2.08	1 (7%)	18,22,29	1.10	1 (5%)
18	Y5P	V	14	18	14,19,20	2.71	2 (14%)	18,26,29	1.16	2 (11%)
18	Y5P	Y	33	18	14,19,20	2.49	1 (7%)	18,26,29	0.97	1 (5%)
18	Y5P	V	55	18	14,19,20	2.25	1 (7%)	18,26,29	1.05	1 (5%)
18	Y5P	V	10	18	14,19,20	2.68	2 (14%)	18,26,29	1.06	1 (5%)
18	Y5P	V	39	18	14,19,20	2.48	1 (7%)	18,26,29	1.05	1 (5%)
18	Y5P	V	37	18	14,19,20	2.70	2 (14%)	18,26,29	1.09	1 (5%)
18	Y5P	Y	13	18	14,19,20	3.58	1 (7%)	18,26,29	0.81	2 (11%)
18	Y5P	V	57	18	14,19,20	2.68	2 (14%)	18,26,29	1.04	1 (5%)
18	Y5P	Y	30	18	14,19,20	2.65	2 (14%)	18,26,29	1.09	1 (5%)
18	Y5P	Y	49	18	14,19,20	3.52	1 (7%)	18,26,29	0.84	1 (5%)
18	Y5P	V	13	18	14,19,20	3.45	1 (7%)	18,26,29	0.84	2 (11%)
18	Y5P	Y	52	18	14,19,20	2.66	2 (14%)	18,26,29	1.10	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
18	P5P	V	36	18	16,23,24	0.96	2 (12%)	14,33,36	0.82	0
18	Y5P	V	71	18	14,19,20	2.69	2 (14%)	18,26,29	1.01	1 (5%)
18	Y5P	V	52	18	14,19,20	2.69	2 (14%)	18,26,29	1.08	1 (5%)
18	Y5P	Y	64	18	14,19,20	2.67	2 (14%)	18,26,29	1.10	1 (5%)
18	Y5P	V	33	18	14,19,20	2.98	1 (7%)	18,26,29	0.81	1 (5%)
18	Y5P	Y	7	18	14,19,20	2.65	2 (14%)	18,26,29	1.01	1 (5%)
18	Y5P	V	5	18	14,19,20	2.69	2 (14%)	18,26,29	1.03	1 (5%)
18	Y5P	Y	25	18	14,19,20	3.67	1 (7%)	18,26,29	0.79	0
18	Y5P	V	59	18	14,19,20	2.18	1 (7%)	18,26,29	0.94	1 (5%)
18	Y5P	V	60	18	14,19,20	2.22	1 (7%)	18,26,29	1.08	1 (5%)
18	Y5P	V	66	18	14,19,20	2.17	1 (7%)	18,26,29	1.12	1 (5%)
18	Y5P	Y	68	18	14,19,20	3.61	1 (7%)	18,26,29	0.85	1 (5%)
18	P5P	V	35	18	16,23,24	0.89	1 (6%)	14,33,36	0.80	0
18	Y5P	Y	51	18	14,19,20	2.15	1 (7%)	18,26,29	1.08	1 (5%)
18	Y5P	Y	62	18	14,19,20	3.69	2 (14%)	18,26,29	0.83	1 (5%)
18	Y5P	V	41	18	14,19,20	4.10	1 (7%)	18,26,29	0.65	0
18	Y5P	V	31	18	14,19,20	2.65	2 (14%)	18,26,29	0.99	1 (5%)
18	Y5P	Y	48	18	14,19,20	3.73	1 (7%)	18,26,29	0.75	0
19	Y5P	X	17	19	14,19,20	2.61	1 (7%)	18,26,29	0.97	1 (5%)
18	Y5P	V	3	18	14,19,20	3.59	1 (7%)	18,26,29	0.81	1 (5%)
18	Y5P	V	45	18	14,19,20	2.29	1 (7%)	18,26,29	0.96	1 (5%)
18	Y5P	Y	26	18	14,19,20	2.73	2 (14%)	18,26,29	1.04	1 (5%)
18	Y5P	V	63	18	14,19,20	2.68	2 (14%)	18,26,29	1.09	1 (5%)
18	Y5P	V	1	18	14,16,20	2.67	2 (14%)	18,22,29	1.00	1 (5%)
18	Y5P	Y	56	18	14,19,20	3.62	1 (7%)	18,26,29	0.79	1 (5%)
18	Y5P	Y	38	18	14,19,20	2.77	2 (14%)	18,26,29	1.12	1 (5%)
18	Y5P	Y	23	18	14,19,20	2.71	2 (14%)	18,26,29	1.00	1 (5%)
18	Y5P	Y	4	18	14,19,20	3.59	1 (7%)	18,26,29	0.79	1 (5%)
18	Y5P	Y	6	18	14,19,20	2.74	2 (14%)	18,26,29	1.02	1 (5%)
18	Y5P	V	70	18	14,19,20	2.69	2 (14%)	18,26,29	1.02	1 (5%)
18	Y5P	V	54	18	14,19,20	2.18	1 (7%)	18,26,29	1.02	1 (5%)
18	Y5P	Y	32	18	14,19,20	2.33	1 (7%)	18,26,29	0.96	1 (5%)
18	Y5P	V	65	18	14,19,20	2.70	2 (14%)	18,26,29	1.09	1 (5%)
18	Y5P	Y	57	18	14,19,20	2.68	2 (14%)	18,26,29	0.99	1 (5%)
18	Y5P	Y	12	18	14,19,20	2.27	1 (7%)	18,26,29	0.99	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
18	Y5P	Y	21	18	14,19,20	2.75	2 (14%)	18,26,29	1.04	1 (5%)
18	Y5P	V	48	18	14,19,20	3.67	2 (14%)	18,26,29	0.87	1 (5%)
18	Y5P	V	58	18	14,19,20	2.66	2 (14%)	18,26,29	1.07	1 (5%)
18	Y5P	V	32	18	14,19,20	2.25	1 (7%)	18,26,29	0.95	1 (5%)
18	Y5P	V	30	18	14,19,20	2.67	2 (14%)	18,26,29	1.11	1 (5%)
18	Y5P	V	27	18	14,19,20	2.67	2 (14%)	18,26,29	1.06	1 (5%)
18	Y5P	V	61	18	14,19,20	3.63	1 (7%)	18,26,29	0.80	1 (5%)
18	Y5P	V	9	18	14,19,20	2.66	2 (14%)	18,26,29	1.04	1 (5%)
19	Y5P	X	20	19	14,19,20	2.42	1 (7%)	18,26,29	0.98	1 (5%)
19	Y5P	X	14	19	14,19,20	2.20	1 (7%)	18,26,29	0.96	1 (5%)
18	Y5P	V	56	18	14,19,20	3.59	1 (7%)	18,26,29	0.79	1 (5%)
19	Y5P	X	23	19	14,19,20	2.19	1 (7%)	18,26,29	1.00	1 (5%)
18	Y5P	V	40	18	14,19,20	3.86	1 (7%)	18,26,29	0.80	0
18	Y5P	Y	44	18	14,19,20	2.68	2 (14%)	18,26,29	1.04	1 (5%)
18	Y5P	Y	14	18	14,19,20	2.72	2 (14%)	18,26,29	0.99	1 (5%)
18	Y5P	Y	53	18	14,19,20	2.71	2 (14%)	18,26,29	1.08	1 (5%)
18	Y5P	Y	2	18	14,19,20	3.59	1 (7%)	18,26,29	0.79	1 (5%)
18	Y5P	V	42	18	14,19,20	4.00	1 (7%)	18,26,29	0.69	0
18	Y5P	Y	55	18	14,19,20	2.42	1 (7%)	18,26,29	1.03	1 (5%)
18	Y5P	Y	10	18	14,19,20	2.68	2 (14%)	18,26,29	1.05	1 (5%)
18	Y5P	Y	31	18	14,19,20	2.71	2 (14%)	18,26,29	1.05	1 (5%)
18	Y5P	Y	39	18	14,19,20	2.32	1 (7%)	18,26,29	1.05	1 (5%)
18	Y5P	Y	43	18	14,19,20	3.64	1 (7%)	18,26,29	0.78	0
18	Y5P	Y	24	18	14,19,20	2.63	2 (14%)	18,26,29	1.03	1 (5%)
18	Y5P	V	68	18	14,19,20	3.65	1 (7%)	18,26,29	0.88	0
19	Y5P	X	24	19	14,19,20	2.20	1 (7%)	18,26,29	0.97	1 (5%)
18	Y5P	V	29	18	14,19,20	2.58	2 (14%)	18,26,29	1.16	1 (5%)
18	Y5P	V	28	18	14,19,20	2.69	2 (14%)	18,26,29	1.05	1 (5%)
18	Y5P	Y	1	18	14,16,20	2.68	2 (14%)	18,22,29	1.02	1 (5%)
18	Y5P	Y	28	18	14,19,20	2.73	2 (14%)	18,26,29	1.07	1 (5%)
18	Y5P	V	22	18	14,19,20	2.74	2 (14%)	18,26,29	1.05	1 (5%)
18	Y5P	Y	67	18	14,19,20	3.67	1 (7%)	18,26,29	0.81	0
18	Y5P	Y	60	18	14,19,20	2.24	1 (7%)	18,26,29	0.99	1 (5%)
18	Y5P	Y	5	18	14,19,20	2.71	2 (14%)	18,26,29	1.02	1 (5%)
18	Y5P	Y	65	18	14,19,20	2.69	2 (14%)	18,26,29	1.04	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
18	Y5P	Y	59	18	14,19,20	2.32	1 (7%)	18,26,29	0.94	1 (5%)
18	Y5P	Y	8	18	14,19,20	2.34	1 (7%)	18,26,29	1.00	1 (5%)
18	Y5P	V	67	18	14,19,20	3.52	1 (7%)	18,26,29	0.87	2 (11%)
18	P5P	Y	35	18	16,23,24	0.84	0	14,33,36	0.94	0
18	Y5P	Y	41	18	14,19,20	3.66	1 (7%)	18,26,29	0.82	1 (5%)
19	Y5P	X	16	19	14,19,20	2.61	1 (7%)	18,26,29	1.12	1 (5%)
19	Y5P	X	18	19	14,19,20	3.72	2 (14%)	18,26,29	0.79	0
18	Y5P	V	6	18	14,19,20	2.66	2 (14%)	18,26,29	1.05	1 (5%)
18	Y5P	Y	71	18	14,19,20	2.70	2 (14%)	18,26,29	1.12	2 (11%)
18	Y5P	Y	15	18	14,19,20	2.66	2 (14%)	18,26,29	1.10	2 (11%)
18	Y5P	Y	3	18	14,19,20	3.61	1 (7%)	18,26,29	0.76	0
18	Y5P	V	50	18	14,19,20	2.11	1 (7%)	18,26,29	1.00	1 (5%)
18	Y5P	Y	45	18	14,19,20	2.46	1 (7%)	18,26,29	1.04	1 (5%)
18	Y5P	Y	11	18	14,19,20	3.64	1 (7%)	18,26,29	0.85	0
18	P5P	V	34	18	16,23,24	1.54	2 (12%)	14,33,36	2.08	2 (14%)
18	Y5P	Y	63	18	14,19,20	2.68	2 (14%)	18,26,29	1.07	1 (5%)
18	Y5P	V	11	18	14,19,20	3.55	1 (7%)	18,26,29	0.88	1 (5%)
18	Y5P	V	69	18	14,19,20	2.69	2 (14%)	18,26,29	1.00	1 (5%)
18	Y5P	Y	54	18	14,19,20	2.21	1 (7%)	18,26,29	1.01	1 (5%)
19	Y5P	X	15	19	14,19,20	2.19	1 (7%)	18,26,29	1.05	1 (5%)
19	Y5P	X	21	19	14,19,20	3.86	1 (7%)	18,26,29	0.80	0
18	Y5P	Y	58	18	14,19,20	2.67	2 (14%)	18,26,29	1.07	1 (5%)
18	Y5P	Y	61	18	14,19,20	3.58	1 (7%)	18,26,29	0.77	1 (5%)
18	Y5P	Y	9	18	14,19,20	2.71	2 (14%)	18,26,29	1.06	1 (5%)
18	Y5P	Y	70	18	14,19,20	2.67	2 (14%)	18,26,29	1.01	1 (5%)
18	Y5P	Y	37	18	14,19,20	2.85	2 (14%)	18,26,29	1.12	1 (5%)
18	Y5P	Y	40	37,18	14,19,20	3.79	1 (7%)	18,26,29	0.77	1 (5%)
18	Y5P	V	15	18	14,19,20	2.65	2 (14%)	18,26,29	1.01	1 (5%)
18	Y5P	V	24	18	14,19,20	2.67	2 (14%)	18,26,29	1.03	1 (5%)
18	Y5P	Y	42	18	14,19,20	3.66	1 (7%)	18,26,29	0.82	1 (5%)
18	P5P	Y	36	18	16,23,24	0.82	0	14,33,36	0.85	0
18	Y5P	V	44	18	14,19,20	2.74	2 (14%)	18,26,29	1.07	1 (5%)
18	Y5P	V	43	18	14,19,20	3.66	2 (14%)	18,26,29	0.77	0
19	Y5P	X	13	19	14,19,20	2.24	1 (7%)	18,26,29	0.97	1 (5%)
18	Y5P	Y	29	18	14,19,20	2.73	2 (14%)	18,26,29	1.05	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
18	Y5P	Y	66	18	14,19,20	2.25	1 (7%)	18,26,29	1.01	1 (5%)

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
18	Y5P	V	64	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	25	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	7	18	-	3/7/33/34	0/2/2/2
18	Y5P	V	51	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	8	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	69	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	50	18	-	1/7/33/34	0/2/2/2
19	Y5P	X	19	19,37	-	2/7/33/34	0/2/2/2
18	Y5P	V	26	18	-	1/7/33/34	0/2/2/2
19	Y5P	X	22	19	-	3/7/33/34	0/2/2/2
18	Y5P	V	4	18	-	3/7/33/34	0/2/2/2
18	Y5P	V	38	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	23	18	-	3/7/33/34	0/2/2/2
18	P5P	Y	34	18	-	2/3/25/26	0/3/3/3
18	Y5P	Y	22	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	12	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	21	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	27	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	62	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	49	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	53	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	2	18	-	3/7/33/34	0/2/2/2
19	Y5P	X	12	19	-	3/6/30/34	0/2/2/2
18	Y5P	V	14	18	-	6/7/33/34	0/2/2/2
18	Y5P	Y	33	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	55	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	10	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	39	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	37	18	-	3/7/33/34	0/2/2/2
18	Y5P	Y	13	18	-	3/7/33/34	0/2/2/2
18	Y5P	V	57	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	30	18	-	4/7/33/34	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
18	Y5P	Y	49	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	13	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	52	18	-	3/7/33/34	0/2/2/2
18	P5P	V	36	18	-	0/3/25/26	0/3/3/3
18	Y5P	V	71	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	52	18	-	2/7/33/34	0/2/2/2
18	Y5P	Y	64	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	33	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	7	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	5	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	25	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	59	18	-	3/7/33/34	0/2/2/2
18	Y5P	V	60	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	66	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	68	18	-	3/7/33/34	0/2/2/2
18	P5P	V	35	18	-	0/3/25/26	0/3/3/3
18	Y5P	Y	51	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	62	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	41	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	31	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	48	18	-	1/7/33/34	0/2/2/2
19	Y5P	X	17	19	-	1/7/33/34	0/2/2/2
18	Y5P	V	3	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	45	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	26	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	63	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	1	18	-	1/6/30/34	0/2/2/2
18	Y5P	Y	56	18	-	3/7/33/34	0/2/2/2
18	Y5P	Y	38	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	23	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	4	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	6	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	70	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	54	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	32	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	65	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	57	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	12	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	21	18	-	2/7/33/34	0/2/2/2
18	Y5P	V	48	18	-	3/7/33/34	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
18	Y5P	V	58	18	-	4/7/33/34	0/2/2/2
18	Y5P	V	32	18	-	3/7/33/34	0/2/2/2
18	Y5P	V	30	18	-	2/7/33/34	0/2/2/2
18	Y5P	V	27	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	61	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	9	18	-	5/7/33/34	0/2/2/2
19	Y5P	X	20	19	-	1/7/33/34	0/2/2/2
19	Y5P	X	14	19	-	1/7/33/34	0/2/2/2
18	Y5P	V	56	18	-	1/7/33/34	0/2/2/2
19	Y5P	X	23	19	-	3/7/33/34	0/2/2/2
18	Y5P	V	40	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	44	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	14	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	53	18	-	3/7/33/34	0/2/2/2
18	Y5P	Y	2	18	-	2/7/33/34	0/2/2/2
18	Y5P	V	42	18	-	3/7/33/34	0/2/2/2
18	Y5P	Y	55	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	10	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	31	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	39	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	43	18	-	4/7/33/34	0/2/2/2
18	Y5P	Y	24	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	68	18	-	1/7/33/34	0/2/2/2
19	Y5P	X	24	19	-	1/7/33/34	0/2/2/2
18	Y5P	V	29	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	28	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	1	18	-	1/6/30/34	0/2/2/2
18	Y5P	Y	28	18	-	2/7/33/34	0/2/2/2
18	Y5P	V	22	18	-	3/7/33/34	0/2/2/2
18	Y5P	Y	67	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	60	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	5	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	65	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	59	18	-	3/7/33/34	0/2/2/2
18	Y5P	Y	8	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	67	18	-	1/7/33/34	0/2/2/2
18	P5P	Y	35	18	-	0/3/25/26	0/3/3/3
18	Y5P	Y	41	18	-	3/7/33/34	0/2/2/2
19	Y5P	X	16	19	-	1/7/33/34	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
19	Y5P	X	18	19	-	1/7/33/34	0/2/2/2
18	Y5P	V	6	18	-	4/7/33/34	0/2/2/2
18	Y5P	Y	71	18	-	4/7/33/34	0/2/2/2
18	Y5P	Y	15	18	-	3/7/33/34	0/2/2/2
18	Y5P	Y	3	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	50	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	45	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	11	18	-	1/7/33/34	0/2/2/2
18	P5P	V	34	18	-	0/3/25/26	0/3/3/3
18	Y5P	Y	63	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	11	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	69	18	-	3/7/33/34	0/2/2/2
18	Y5P	Y	54	18	-	1/7/33/34	0/2/2/2
19	Y5P	X	15	19	-	4/7/33/34	0/2/2/2
19	Y5P	X	21	19	-	1/7/33/34	0/2/2/2
18	Y5P	Y	58	18	-	4/7/33/34	0/2/2/2
18	Y5P	Y	61	18	-	3/7/33/34	0/2/2/2
18	Y5P	Y	9	18	-	3/7/33/34	0/2/2/2
18	Y5P	Y	70	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	37	18	-	3/7/33/34	0/2/2/2
18	Y5P	Y	40	37,18	-	1/7/33/34	0/2/2/2
18	Y5P	V	15	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	24	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	42	18	-	3/7/33/34	0/2/2/2
18	P5P	Y	36	18	-	0/3/25/26	0/3/3/3
18	Y5P	V	44	18	-	1/7/33/34	0/2/2/2
18	Y5P	V	43	18	-	1/7/33/34	0/2/2/2
19	Y5P	X	13	19	-	3/7/33/34	0/2/2/2
18	Y5P	Y	29	18	-	1/7/33/34	0/2/2/2
18	Y5P	Y	66	18	-	1/7/33/34	0/2/2/2

The worst 5 of 209 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	V	41	Y5P	C4-N3	-15.17	1.32	1.46
18	V	42	Y5P	C4-N3	-14.76	1.32	1.46
19	X	21	Y5P	C4-N3	-14.30	1.33	1.46
18	V	40	Y5P	C4-N3	-14.28	1.33	1.46
18	Y	40	Y5P	C4-N3	-14.04	1.33	1.46

The worst 5 of 138 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	V	34	P5P	C6-N1-C2	7.06	125.96	115.84
18	Y	34	P5P	C6-N1-C2	6.96	125.81	115.84
18	Y	51	Y5P	N1-C2-N3	-3.85	114.03	125.33
19	X	12	Y5P	N1-C2-N3	-3.81	114.17	125.33
18	Y	50	Y5P	N1-C2-N3	-3.73	114.39	125.33

There are no chirality outliers.

5 of 227 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
18	Y	3	Y5P	O4'-C1'-N1-C2
18	V	6	Y5P	O4'-C4'-C5'-O5'
18	V	6	Y5P	C3'-C4'-C5'-O5'
18	Y	6	Y5P	O4'-C1'-N1-C2
18	V	8	Y5P	O4'-C1'-N1-C2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 148 ligands modelled in this entry, 147 are monoatomic - leaving 1 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	$\# Z > 2$
39	GDP	g	500	37	24,30,30	0.95	1 (4%)	30,47,47	1.32	3 (10%)

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
39	GDP	g	500	37	-	0/12/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	g	500	GDP	C6-N1	-2.33	1.34	1.37

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	g	500	GDP	C3'-C2'-C1'	3.34	106.00	100.98
39	g	500	GDP	PA-O3A-PB	-2.29	124.98	132.83
39	g	500	GDP	O3B-PB-O3A	2.17	111.92	104.64

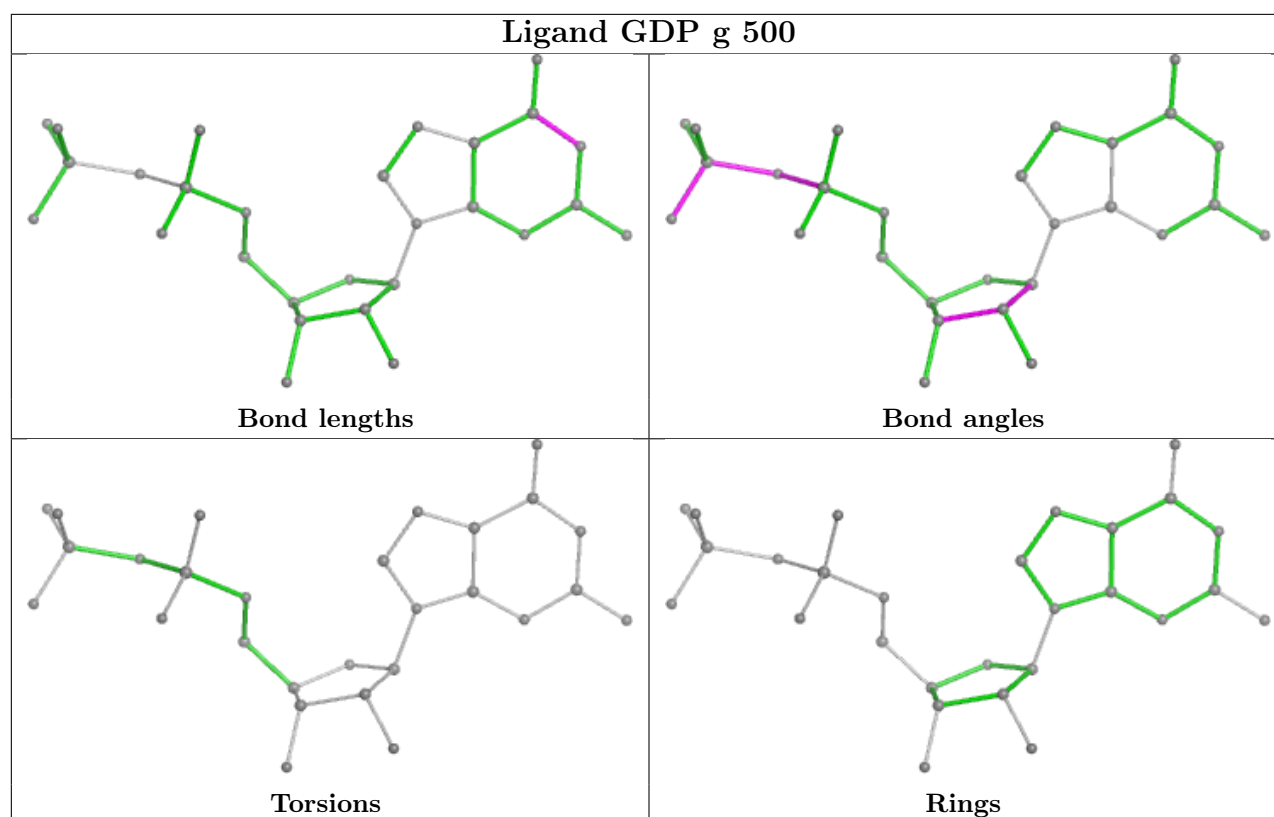
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
33	o	25
24	e	4
18	Y	3
18	V	2

The worst 5 of 34 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	e	262:UNK	C	263:UNK	N	41.49
1	e	309:UNK	C	354:UNK	N	30.03
1	o	405:UNK	C	410:UNK	N	21.38
1	o	368:UNK	C	371:UNK	N	15.76
1	Y	15:Y5P	O3'	21:Y5P	P	15.57

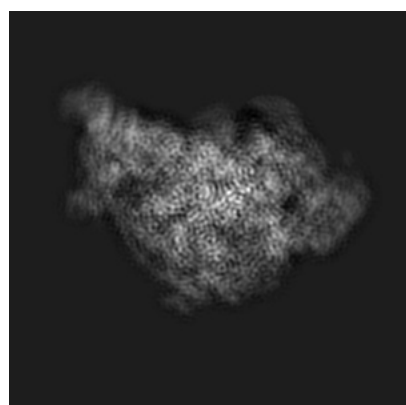
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2913. These allow visual inspection of the internal detail of the map and identification of artifacts.

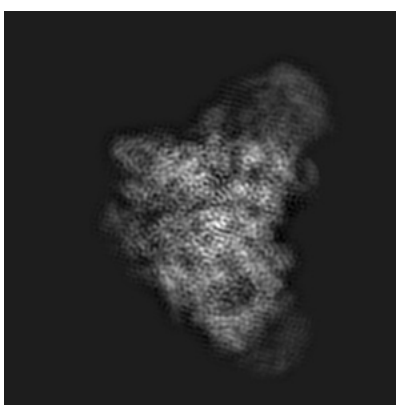
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

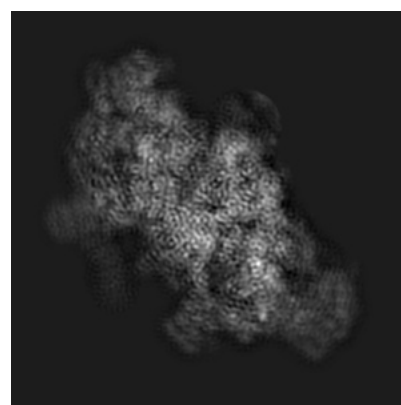
6.1.1 Primary map



X



Y

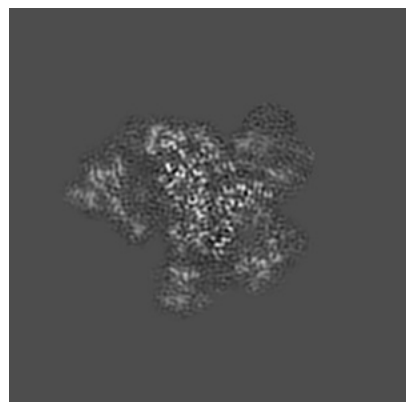


Z

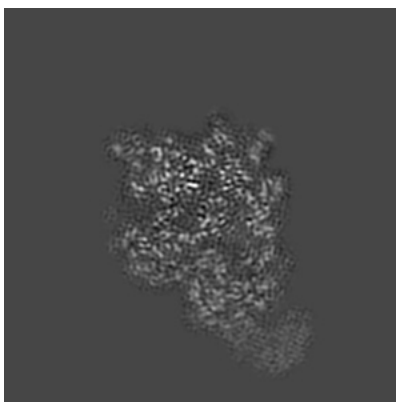
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

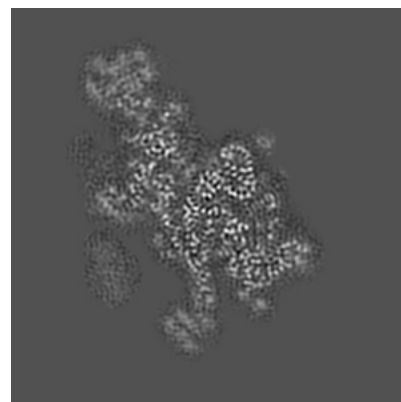
6.2.1 Primary map



X Index: 108



Y Index: 108

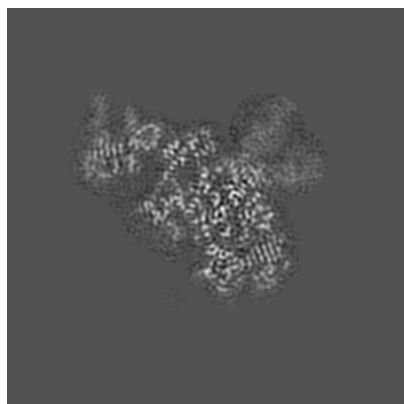


Z Index: 108

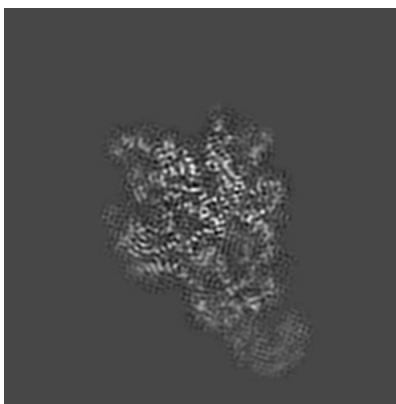
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

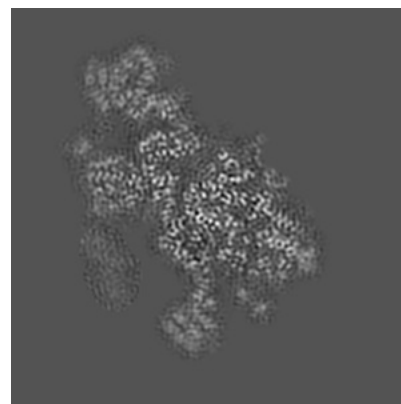
6.3.1 Primary map



X Index: 118



Y Index: 106

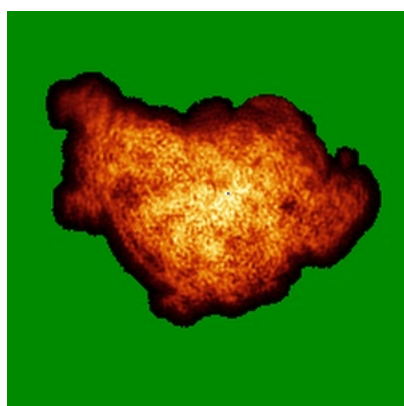


Z Index: 112

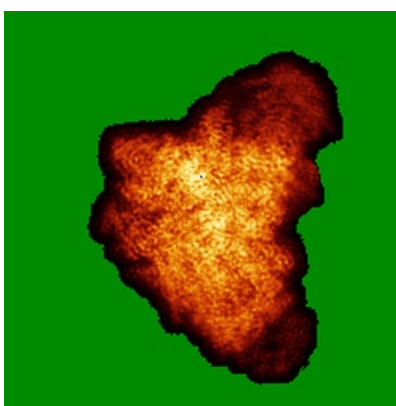
The images above show the largest variance slices of the map in three orthogonal directions.

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

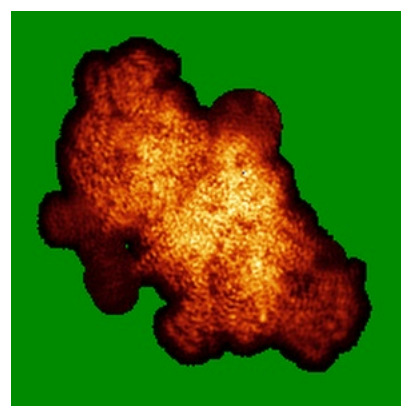
6.4.1 Primary map



X



Y



Z

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 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

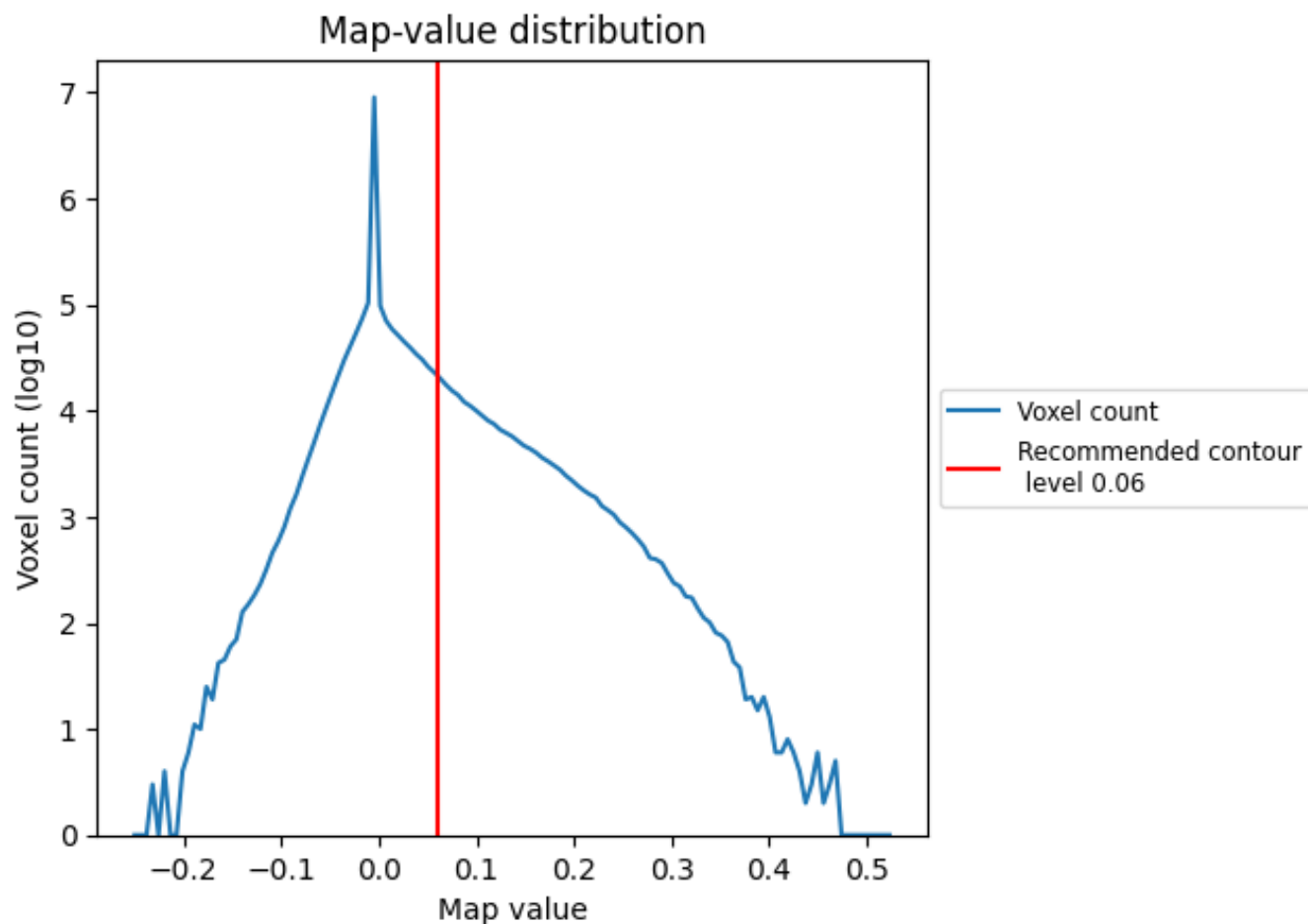
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

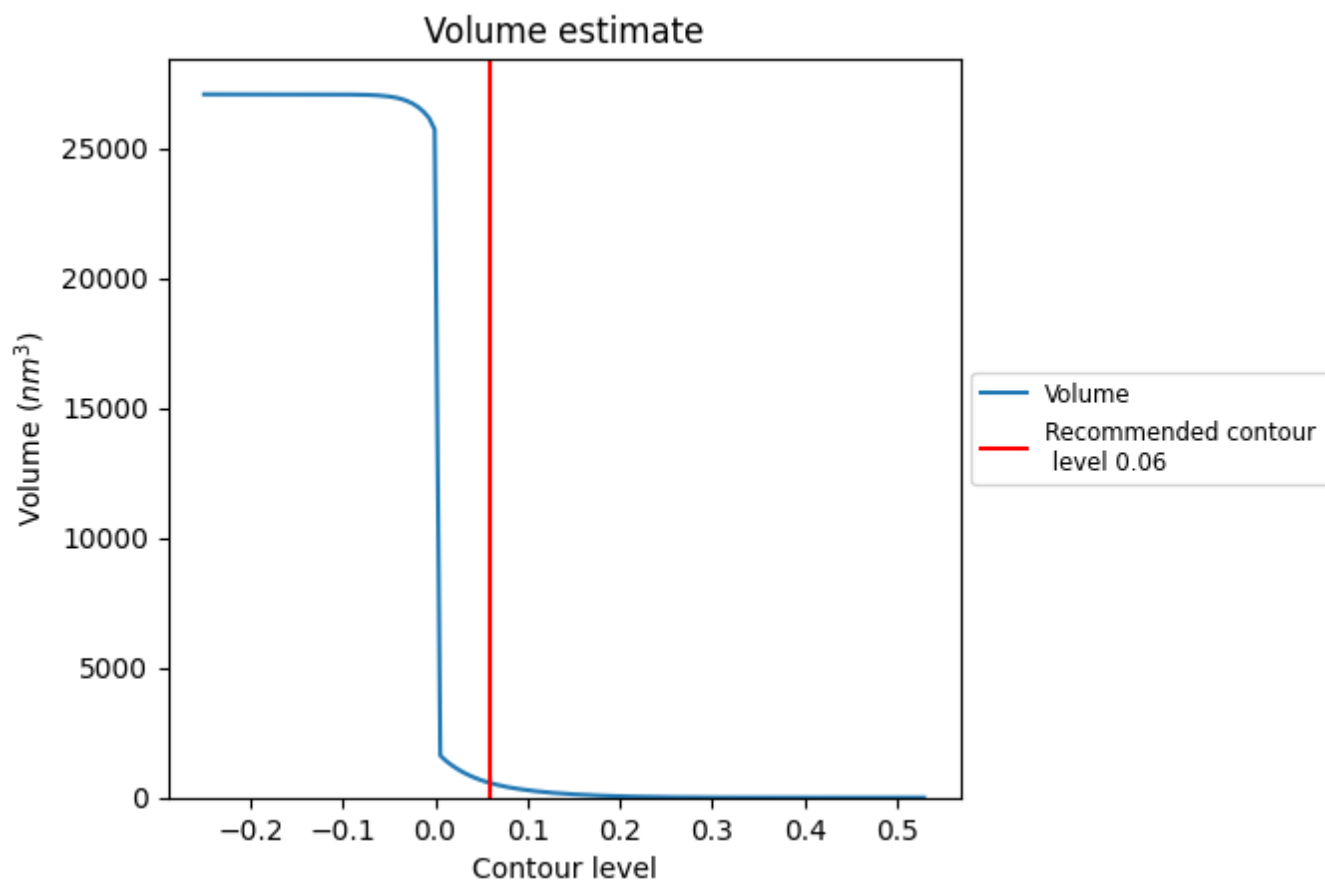
This section contains the results of statistical analysis of the map.

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.

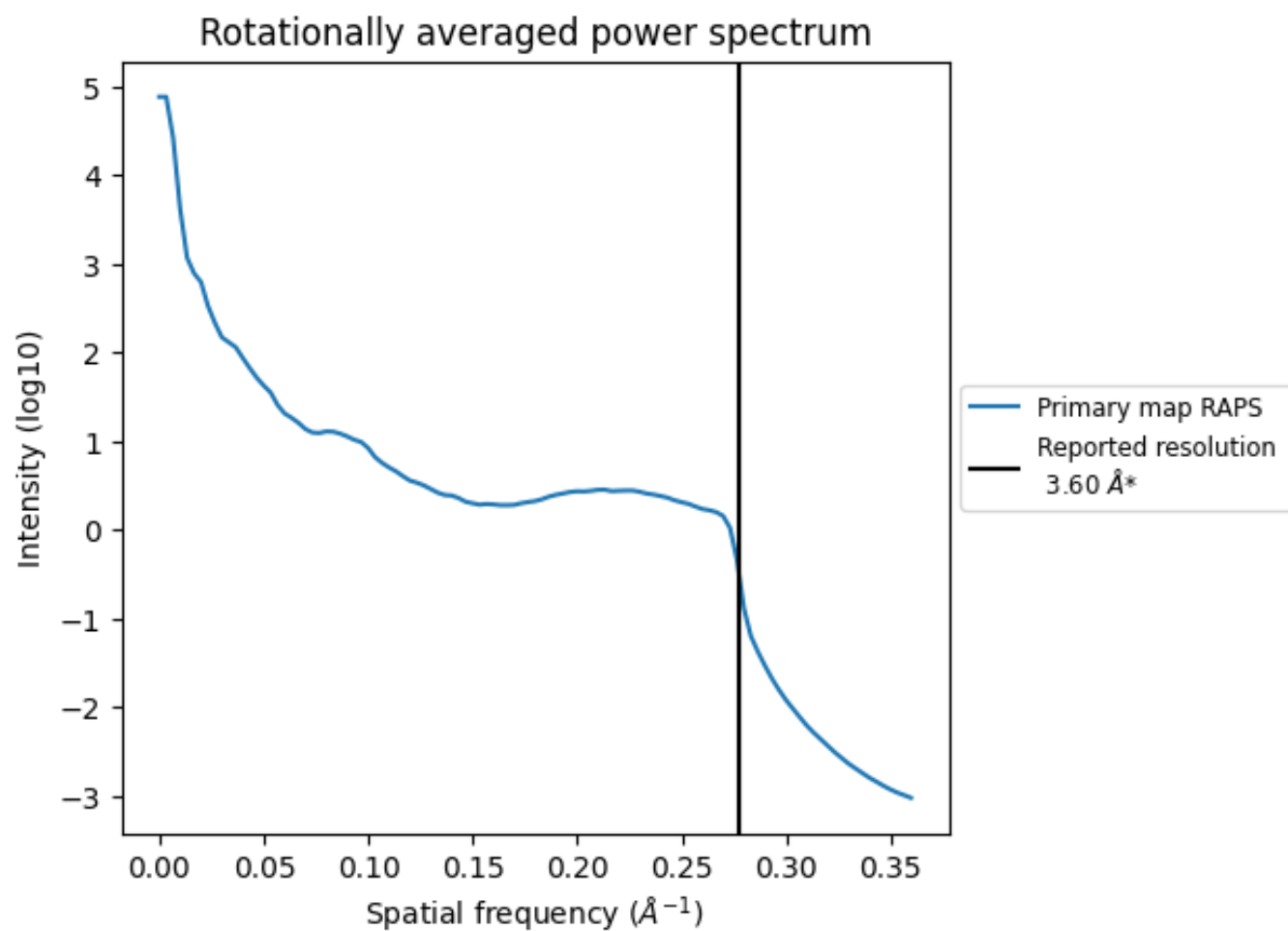
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 556 nm³; this corresponds to an approximate mass of 502 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 0.278 Å⁻¹

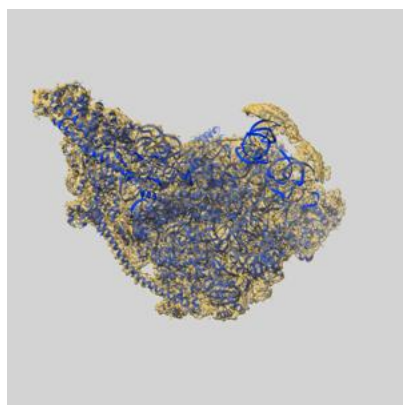
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

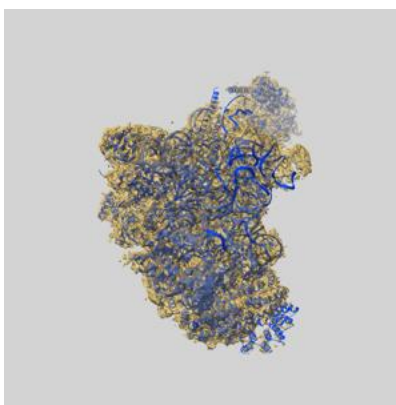
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2913 and PDB model 5AJ3. Per-residue inclusion information can be found in section 3 on page 24.

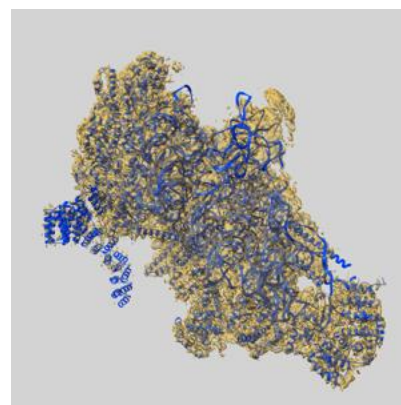
9.1 Map-model overlay [i](#)



X



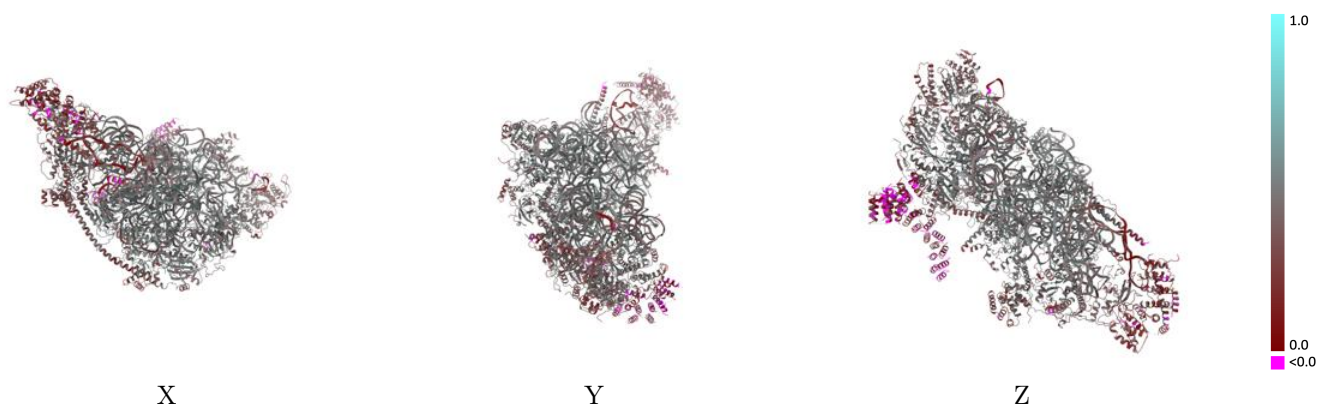
Y



Z

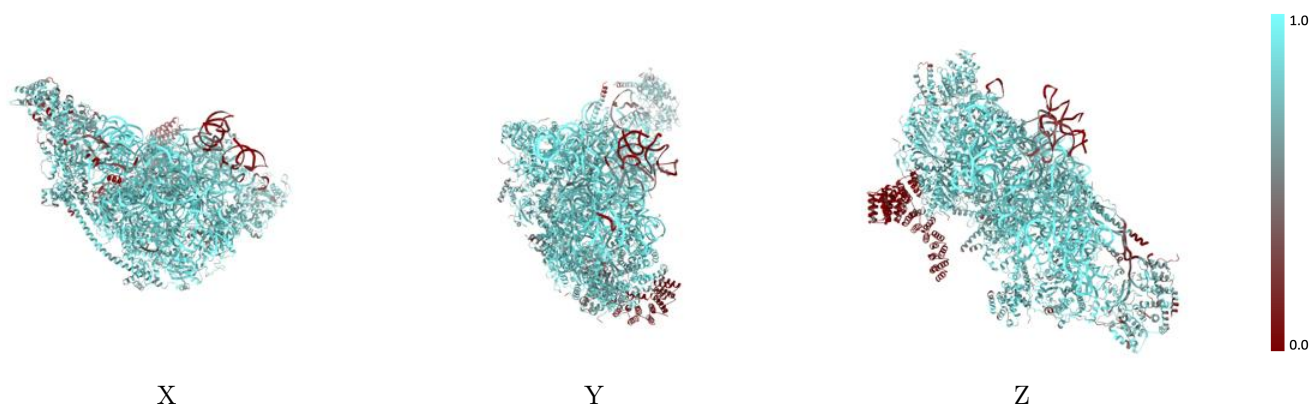
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



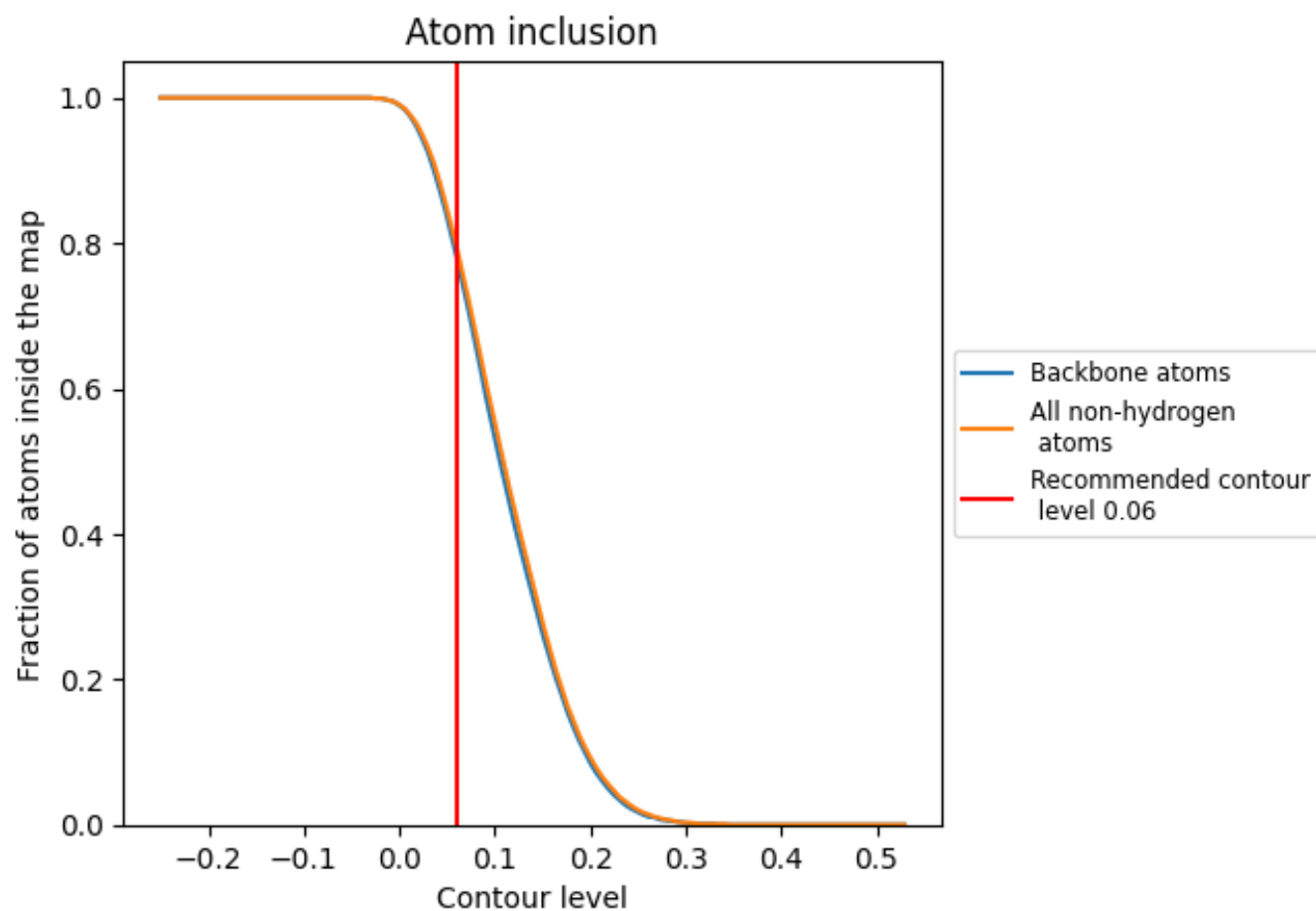
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 78% of all backbone atoms, 80% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7960	 0.4110
A	 0.9300	 0.4520
B	 0.8740	 0.4690
C	 0.8340	 0.4850
E	 0.8210	 0.4570
F	 0.8070	 0.4530
G	 0.7920	 0.4250
I	 0.8150	 0.4340
J	 0.8150	 0.4560
K	 0.8350	 0.4620
L	 0.8410	 0.4810
N	 0.8860	 0.4770
O	 0.7770	 0.4280
P	 0.8450	 0.4440
Q	 0.8380	 0.4570
R	 0.8670	 0.4870
T	 0.3810	 0.2350
U	 0.8610	 0.4760
V	 0.4430	 0.2670
X	 0.8230	 0.4690
Y	 0.4040	 0.1900
a	 0.8010	 0.3820
b	 0.7720	 0.3960
c	 0.8420	 0.4560
d	 0.7870	 0.3670
e	 0.6470	 0.2410
f	 0.8350	 0.4590
g	 0.8060	 0.3770
h	 0.8290	 0.4180
i	 0.8070	 0.4400
j	 0.6660	 0.3510
k	 0.7740	 0.3990
m	 0.7790	 0.4500
n	 0.7750	 0.4560
o	 0.2420	 0.1750



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Chain	Atom inclusion	Q-score
p	 0.8560	 0.4410
s	 0.0420	 0.0500
z	 0.6760	 0.2370