



## Full wwPDB EM Validation Report ⓘ

Nov 4, 2024 – 02:12 AM JST

PDB ID : 7CKX  
EMDB ID : EMD-30393  
Title : Cryo-EM structure of A77636 bound dopamine receptor DRD1-Gs signaling complex  
Authors : Yan, W.; Shao, Z.  
Deposited on : 2020-07-20  
Resolution : 3.54 Å(reported)  
Based on initial model : 3SN6

This is a Full wwPDB EM 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/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>.

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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 : 1.8.5 (274361), 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

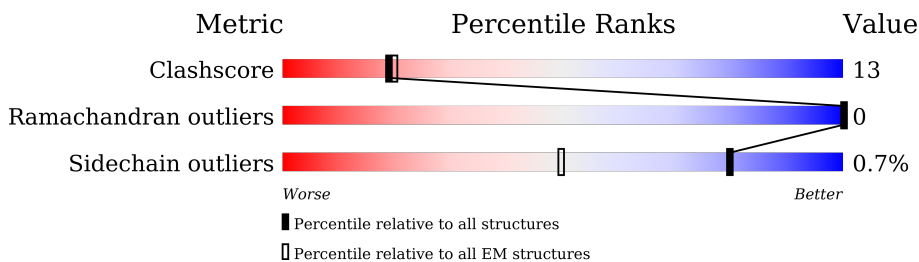
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.54 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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 EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	394	<div> <div>19%</div> <div>47%</div> <div>12%</div> <div>•</div> <div>40%</div> </div>
2	B	356	<div> <div>20%</div> <div>63%</div> <div>33%</div> <div>•</div> </div>
3	G	71	<div> <div>48%</div> <div>65%</div> <div>17%</div> <div>18%</div> </div>
4	N	156	<div> <div>20%</div> <div>56%</div> <div>25%</div> <div>•</div> <div>18%</div> </div>
5	R	453	<div> <div>20%</div> <div>42%</div> <div>18%</div> <div>40%</div> </div>

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 8112 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Guanine nucleotide-binding protein G(s) subunit alpha isoforms short.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	236	Total	C	N	O	S	0	0
			1906	1204	347	348	7		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	205	THR	SER	engineered mutation	UNP P63092
A	226	ALA	GLY	engineered mutation	UNP P63092
A	366	SER	ALA	engineered mutation	UNP P63092

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	340	Total	C	N	O	S	0	0
			2587	1597	462	507	21		

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	MET	-	expression tag	UNP P62873
B	-14	HIS	-	expression tag	UNP P62873
B	-13	HIS	-	expression tag	UNP P62873
B	-12	HIS	-	expression tag	UNP P62873
B	-11	HIS	-	expression tag	UNP P62873
B	-10	LEU	-	expression tag	UNP P62873
B	-9	GLU	-	expression tag	UNP P62873
B	-8	VAL	-	expression tag	UNP P62873
B	-7	LEU	-	expression tag	UNP P62873
B	-6	PHE	-	expression tag	UNP P62873
B	-5	GLN	-	expression tag	UNP P62873
B	-4	GLY	-	expression tag	UNP P62873

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	PRO	-	expression tag	UNP P62873
B	-2	GLY	-	expression tag	UNP P62873
B	-1	SER	-	expression tag	UNP P62873
B	0	SER	-	expression tag	UNP P62873
B	1	GLY	-	expression tag	UNP P62873

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	58	Total	C	N	O	S	0	0
			438	274	76	85	3		

- Molecule 4 is a protein called Nanobody 35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	128	Total	C	N	O	S	0	0
			970	604	170	190	6		

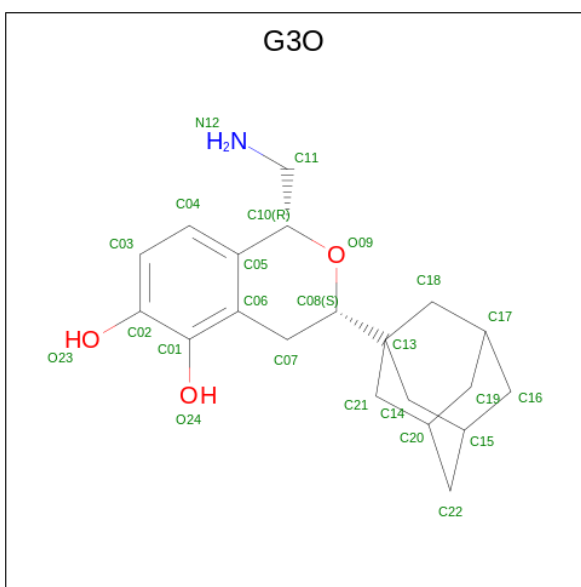
- Molecule 5 is a protein called D(1A) dopamine receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	R	273	Total	C	N	O	S	0	0
			2159	1439	350	354	16		

There are 7 discrepancies between the modelled and reference sequences:

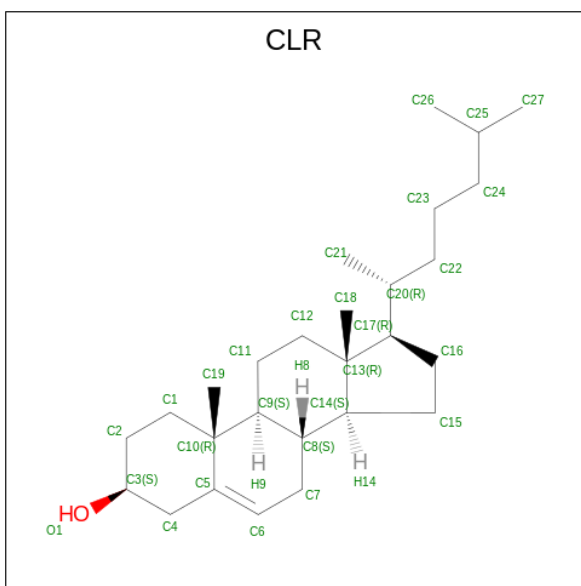
Chain	Residue	Modelled	Actual	Comment	Reference
R	-6	ASP	-	expression tag	UNP P21728
R	-5	TYR	-	expression tag	UNP P21728
R	-4	LYS	-	expression tag	UNP P21728
R	-3	ASP	-	expression tag	UNP P21728
R	-2	ASP	-	expression tag	UNP P21728
R	-1	ASP	-	expression tag	UNP P21728
R	0	ALA	-	expression tag	UNP P21728

- Molecule 6 is (1R,3S)-3-(1-adamantyl)-1-(aminomethyl)-3,4-dihydro-1H-isochromene-5,6-diol (three-letter code: G3O) (formula: C<sub>20</sub>H<sub>27</sub>NO<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
6	R	1	Total	C	N	O	0
			24	20	1	3	

- Molecule 7 is CHOLESTEROL (three-letter code: CLR) (formula:  $C_{27}H_{46}O$ ).

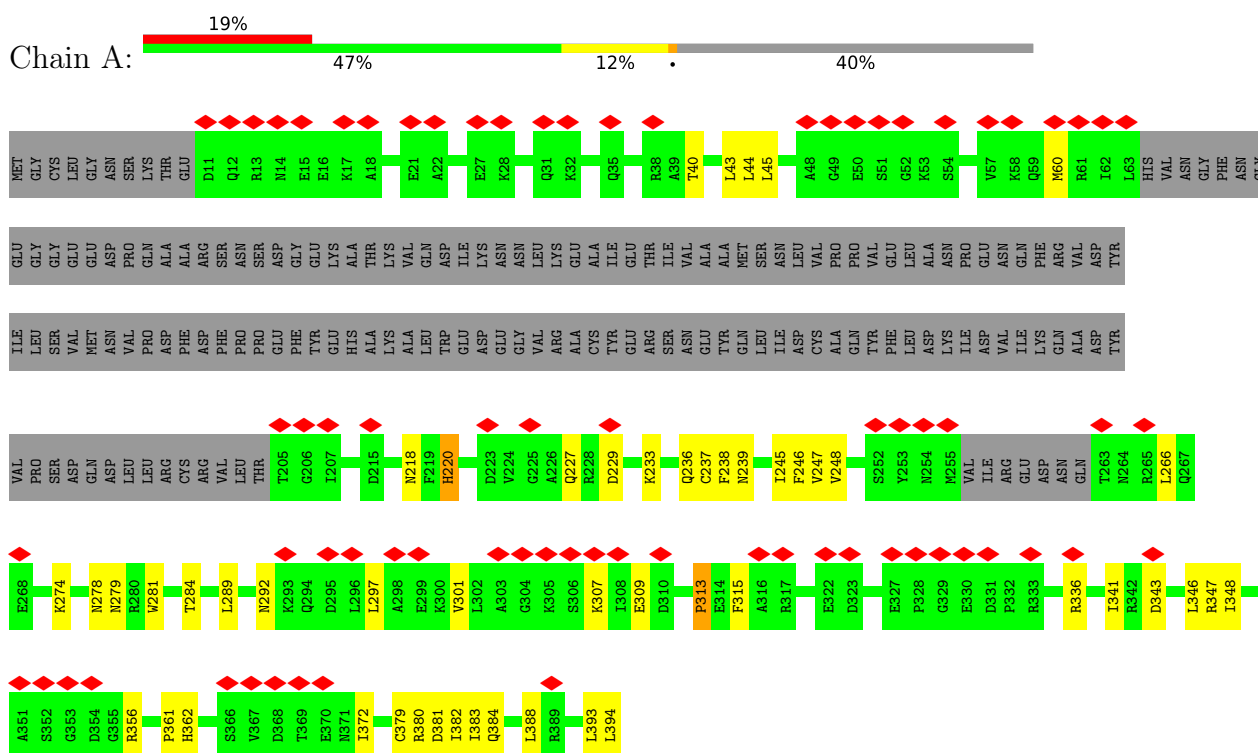


Mol	Chain	Residues	Atoms				AltConf
7	R	1	Total	C	O		0
			28	27	1		

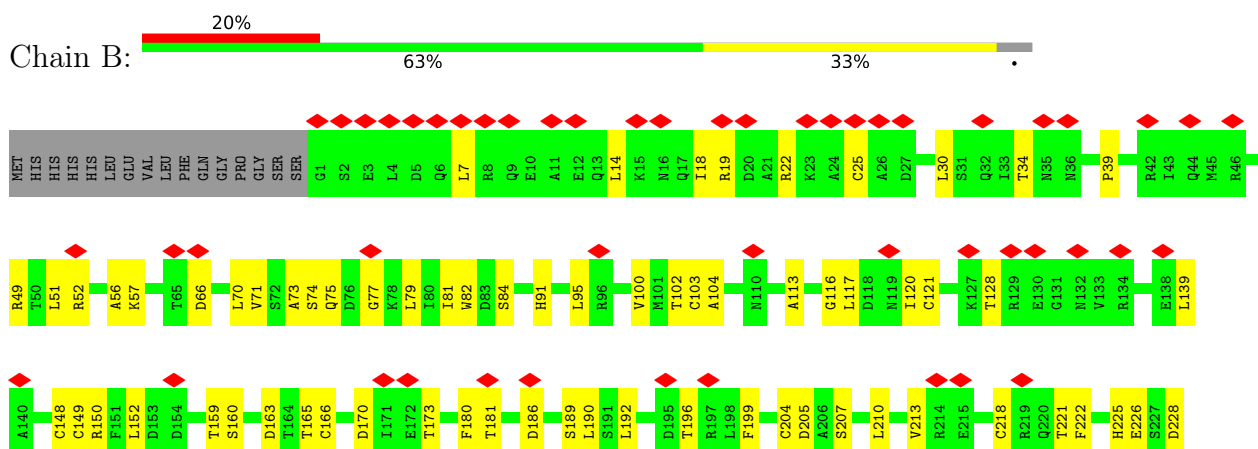
### 3 Residue-property plots

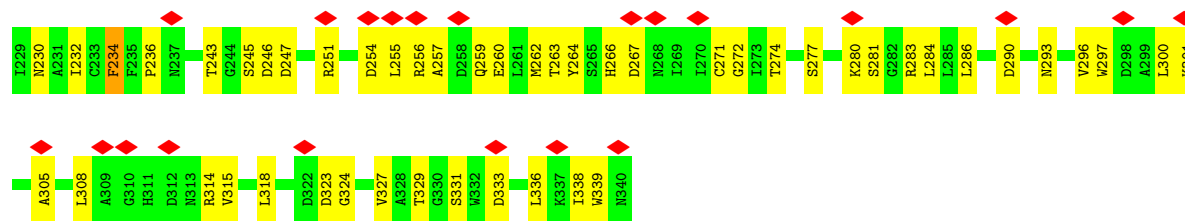
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Guanine nucleotide-binding protein G(s) subunit alpha isoforms short



- Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1





Protein	Position	Residue	Score	Label
SER	1	ALA	L291	
	2	ILE	N292	
	3	GLU	C293	
	4	THR	I294	
	5	VAL		
	6	SER	F297	
	7	ILE	C298	
	8	ASN	GLY	
	9	ASN	SER	
	10	ASP	GLY	
TYR	11	GLY	GLU	
	12	ASP	THR	
	13	THR	GLN	
	14	ALA	PRO	
	15	ASP	ALA	
	16	VAL	HEI	
	17	SER	PHE	
	18	SER	SER	
	19	LEU	SER	
	20	GLU	SER	
ILE	21	HIS	C307	
	22	ILE	I308	
	23	GLN	D309	
	24	PRO	S310	
	25	THR	N311	
	26	GLN	T312	
	27	ASN	F313	
	28	GLY	D314	
	29	GLN		
	30	HIS	F319	
PRO	31	CYS	G320	
	32	ASN	W321	
	33	LEU	A322	
	34	VAL	N323	
	35	THR	S324	
	36	LEU	S325	
	37	ILE	I326	
	38	PRO	N327	
	39	HIS		
	40	ALA	I330	
GLY	41	VAL		
	42	GLY	F333	
	43	SER	N334	
	44	GLU	A335	
	45	ASP	D336	
	46	LEU	F337	
	47	LYS	R339	
	48	LYS	K339	
	49	GLU	A340	
	50	ALA	F341	
ALA	51	GLY	S342	
	52	ILE	T343	
	53	ALA	L344	
	54	ARG	LEU	
	55	PRO	GLY	
	56	LEU	CYS	
	57	GLU	TYR	
	58	LYS	ARG	
	59	LEU	LEU	
	60	LEU	LEU	



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	391771	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	64	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.151	Depositor
Minimum map value	-0.083	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.026	Depositor
Map size (Å)	216.0, 216.0, 216.0	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	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: CLR, G3O

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	0.24	0/1942	0.39	0/2616
2	B	0.24	0/2634	0.44	0/3573
3	G	0.24	0/444	0.38	0/601
4	N	0.25	0/990	0.48	0/1341
5	R	0.24	0/2216	0.37	0/3019
All	All	0.24	0/8226	0.41	0/11150

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1906	0	1842	39	0
2	B	2587	0	2480	85	0
3	G	438	0	443	10	0
4	N	970	0	930	28	0
5	R	2159	0	2204	63	0
6	R	24	0	0	0	0
7	R	28	0	46	4	0
All	All	8112	0	7945	203	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 13.

All (203) 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)
5:R:68:VAL:HG21	7:R:502:CLR:H152	1.14	1.10
5:R:68:VAL:HG21	7:R:502:CLR:C15	1.88	1.02
5:R:68:VAL:CG2	7:R:502:CLR:H152	1.94	0.96
2:B:284:LEU:HD22	2:B:296:VAL:CG1	2.07	0.84
5:R:198:SER:O	5:R:202:SER:HB3	1.77	0.84
5:R:200:VAL:HA	5:R:204:TYR:HB2	1.62	0.81
2:B:207:SER:HA	2:B:222:PHE:O	1.82	0.80
1:A:45:LEU:HD11	1:A:247:VAL:CG2	2.16	0.76
2:B:210:LEU:HD22	2:B:255:LEU:HD22	1.72	0.72
4:N:19:ARG:HE	4:N:80:TYR:HB3	1.54	0.72
4:N:37:VAL:HG12	4:N:47:TRP:HA	1.72	0.71
5:R:76:LEU:HD13	5:R:80:TRP:HE1	1.55	0.69
2:B:73:ALA:HB2	2:B:79:LEU:HD12	1.73	0.69
1:A:45:LEU:HD11	1:A:247:VAL:HG23	1.77	0.67
1:A:45:LEU:CD1	1:A:247:VAL:HG23	2.26	0.65
5:R:92:PHE:HB3	5:R:95:PHE:HB2	1.79	0.65
1:A:388:LEU:HB3	1:A:394:LEU:HB2	1.79	0.64
2:B:225:HIS:NE2	2:B:243:THR:OG1	2.24	0.64
1:A:284:THR:HG22	1:A:356:ARG:HD2	1.79	0.64
5:R:336:ASP:OD1	5:R:337:PHE:N	2.31	0.64
1:A:393:LEU:HA	5:R:273:THR:HG21	1.79	0.63
2:B:286:LEU:HG	2:B:327:VAL:HG21	1.79	0.63
2:B:245:SER:OG	2:B:247:ASP:OD1	2.16	0.63
2:B:228:ASP:OD1	4:N:117:TYR:OH	2.18	0.62
2:B:56:ALA:HB3	2:B:74:SER:HB2	1.82	0.61
4:N:33:LYS:HE2	4:N:52:SER:HA	1.81	0.61
4:N:94:TYR:O	4:N:121:GLY:HA2	2.00	0.61
2:B:271:CYS:HB2	2:B:290:ASP:HB2	1.83	0.61
2:B:284:LEU:HD22	2:B:296:VAL:HG12	1.83	0.61
1:A:45:LEU:HD11	1:A:247:VAL:HG21	1.83	0.60
2:B:121:CYS:HB3	2:B:139:LEU:HD12	1.83	0.59
1:A:236:GLN:O	1:A:239:ASN:ND2	2.35	0.59
5:R:48:VAL:HG11	5:R:64:ILE:HG12	1.84	0.59
2:B:186:ASP:N	2:B:186:ASP:OD1	2.37	0.57
4:N:39:GLN:HB2	4:N:45:LEU:HG	1.85	0.57
2:B:232:ILE:HG13	2:B:243:THR:HG22	1.85	0.56
2:B:149:CYS:O	2:B:150:ARG:NH1	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:218:CYS:SG	3:G:18:GLN:NE2	2.79	0.56
2:B:274:THR:OG1	2:B:290:ASP:OD1	2.23	0.56
2:B:327:VAL:HG13	2:B:339:TRP:HB2	1.87	0.56
5:R:48:VAL:HG13	5:R:55:ARG:HB3	1.88	0.56
5:R:279:GLY:HA2	5:R:282:VAL:HG22	1.86	0.56
2:B:152:LEU:HD21	2:B:213:VAL:HG11	1.88	0.56
2:B:104:ALA:HB3	2:B:113:ALA:HB3	1.87	0.56
3:G:48:ASP:HB3	3:G:51:LEU:HB2	1.87	0.55
2:B:102:THR:HG1	2:B:149:CYS:HG	1.54	0.55
5:R:57:LYS:HB3	5:R:60:ASN:HD22	1.73	0.54
5:R:75:VAL:HG23	5:R:76:LEU:HD23	1.89	0.54
1:A:384:GLN:OE1	5:R:224:GLN:NE2	2.41	0.54
5:R:277:ILE:HG22	5:R:330:ILE:HG23	1.89	0.54
5:R:291:LEU:HB3	5:R:308:ILE:HD13	1.90	0.53
2:B:39:PRO:HB3	2:B:301:LYS:HG3	1.90	0.53
5:R:116:VAL:HA	5:R:119:VAL:HG12	1.89	0.53
5:R:273:THR:HA	5:R:276:VAL:HG12	1.89	0.53
2:B:77:GLY:O	2:B:95:LEU:N	2.38	0.53
2:B:315:VAL:HA	2:B:331:SER:HA	1.90	0.53
1:A:227:GLN:NE2	2:B:117:LEU:O	2.42	0.53
2:B:290:ASP:OD1	2:B:314:ARG:NE	2.38	0.53
3:G:20:LYS:O	3:G:24:ASN:ND2	2.42	0.53
4:N:45:LEU:HD13	4:N:112:SER:HA	1.90	0.52
1:A:307:LYS:HG2	1:A:309:GLU:H	1.73	0.52
1:A:229:ASP:N	1:A:229:ASP:OD1	2.42	0.52
2:B:277:SER:HB2	2:B:318:LEU:HD22	1.91	0.52
5:R:58:VAL:HG23	5:R:140:ALA:HB2	1.92	0.52
2:B:163:ASP:OD1	2:B:165:THR:OG1	2.21	0.52
2:B:100:VAL:HA	2:B:116:GLY:HA3	1.92	0.51
2:B:254:ASP:HB3	2:B:257:ALA:HB3	1.93	0.51
2:B:280:LYS:HD3	2:B:323:ASP:HA	1.92	0.51
1:A:279:ASN:HA	4:N:106:ASP:OD2	2.11	0.51
2:B:264:TYR:HB3	2:B:297:TRP:CE3	2.46	0.51
4:N:61:THR:HG22	4:N:64:VAL:HG22	1.93	0.51
1:A:44:LEU:O	1:A:245:ILE:N	2.43	0.51
2:B:284:LEU:HD22	2:B:296:VAL:HG13	1.91	0.50
2:B:165:THR:HG22	2:B:181:THR:HG22	1.93	0.50
2:B:14:LEU:HD23	3:G:19:LEU:HB3	1.93	0.50
2:B:30:LEU:HD21	2:B:300:LEU:HA	1.93	0.50
1:A:266:LEU:HD21	1:A:341:ILE:HD12	1.94	0.50
2:B:226:GLU:OE1	2:B:251:ARG:NH2	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:64:ILE:HD12	5:R:67:ALA:HB3	1.94	0.50
1:A:361:PRO:O	1:A:362:HIS:ND1	2.45	0.50
2:B:260:GLU:OE1	2:B:263:THR:OG1	2.22	0.50
2:B:293:ASN:ND2	2:B:308:LEU:O	2.43	0.50
2:B:22:ARG:NH2	2:B:221:THR:O	2.45	0.50
2:B:318:LEU:HG	2:B:329:THR:HG22	1.93	0.50
4:N:52:SER:OG	4:N:53:GLN:N	2.45	0.50
4:N:53:GLN:NE2	4:N:104:THR:O	2.41	0.49
1:A:40:THR:OG1	1:A:218:ASN:ND2	2.45	0.49
2:B:52:ARG:HD3	5:R:52:ARG:HG3	1.94	0.49
2:B:160:SER:HB3	2:B:190:LEU:HD22	1.93	0.49
5:R:103:ASP:CG	5:R:321:TRP:HZ2	2.15	0.49
4:N:36:TRP:CG	4:N:81:LEU:HD22	2.48	0.49
1:A:309:GLU:HG3	1:A:315:PHE:HD2	1.78	0.49
1:A:248:VAL:O	1:A:292:ASN:N	2.46	0.49
2:B:71:VAL:HG23	2:B:81:ILE:HG12	1.96	0.48
5:R:66:LEU:HD11	5:R:114:LEU:HG	1.95	0.48
5:R:33:LEU:HD11	5:R:322:ALA:HB2	1.95	0.48
1:A:237:CYS:O	2:B:57:LYS:NZ	2.30	0.48
2:B:246:ASP:HA	2:B:272:GLY:HA3	1.96	0.47
4:N:91:THR:OG1	4:N:125:THR:HA	2.15	0.47
5:R:291:LEU:HA	5:R:294:ILE:HG12	1.96	0.47
2:B:148:CYS:SG	2:B:149:CYS:N	2.88	0.47
2:B:280:LYS:HB2	2:B:324:GLY:HA3	1.96	0.47
5:R:70:ASP:HA	5:R:73:VAL:HG12	1.97	0.47
1:A:388:LEU:HD13	1:A:394:LEU:HD13	1.97	0.47
5:R:149:THR:O	5:R:153:LEU:HG	2.13	0.47
4:N:35:ASN:ND2	4:N:109:ASP:OD2	2.47	0.47
1:A:343:ASP:HA	1:A:346:LEU:HB2	1.97	0.47
2:B:19:ARG:HH21	4:N:1:GLN:HB3	1.79	0.47
2:B:81:ILE:HB	2:B:91:HIS:HB2	1.97	0.47
5:R:103:ASP:OD2	5:R:321:TRP:HZ2	1.98	0.47
4:N:127:SER:OG	4:N:128:SER:N	2.47	0.47
5:R:48:VAL:HG21	5:R:64:ILE:HD13	1.96	0.47
5:R:164:HIS:HB2	5:R:190:LEU:HA	1.96	0.46
2:B:230:ASN:ND2	2:B:246:ASP:OD1	2.47	0.46
4:N:94:TYR:O	4:N:121:GLY:CA	2.62	0.46
2:B:49:ARG:HD3	3:G:61:PHE:HD2	1.81	0.46
5:R:84:ALA:HB2	5:R:90:TRP:HE3	1.80	0.46
2:B:51:LEU:HD12	2:B:336:LEU:HD13	1.96	0.46
2:B:120:ILE:HA	2:B:139:LEU:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:114:LEU:HD21	5:R:327:ASN:HD21	1.80	0.46
5:R:44:VAL:HG22	5:R:341:PHE:HZ	1.79	0.46
1:A:381:ASP:OD2	5:R:227:ARG:NH2	2.48	0.46
4:N:52:SER:O	4:N:72:ARG:NE	2.49	0.46
2:B:30:LEU:HD22	2:B:262:MET:HG3	1.98	0.46
4:N:51:ILE:HG13	4:N:58:ILE:HG12	1.97	0.46
5:R:234:ALA:HA	5:R:237:HIS:CD2	2.50	0.46
5:R:41:ASN:ND2	5:R:70:ASP:OD2	2.40	0.46
5:R:292:ASN:HD22	5:R:313:PHE:HZ	1.62	0.45
1:A:274:LYS:HB2	1:A:348:ILE:HD13	1.98	0.45
2:B:283:ARG:HB3	3:G:51:LEU:HD11	1.99	0.45
4:N:83:MET:SD	4:N:83:MET:N	2.88	0.45
1:A:346:LEU:HD21	5:R:231:LEU:HD22	1.99	0.45
5:R:153:LEU:HA	5:R:157:ILE:HG12	1.98	0.45
2:B:152:LEU:HD23	2:B:196:THR:HG22	1.98	0.45
5:R:41:ASN:HB2	5:R:71:LEU:HD13	1.99	0.45
5:R:90:TRP:HE1	5:R:96:CYS:HB3	1.81	0.45
1:A:281:TRP:HH2	2:B:290:ASP:HB3	1.82	0.45
2:B:51:LEU:HD13	2:B:82:TRP:CG	2.52	0.45
2:B:204:CYS:HA	2:B:228:ASP:HA	1.99	0.45
5:R:192:ARG:HH21	5:R:297:PHE:HE1	1.64	0.45
5:R:52:ARG:O	5:R:56:SER:OG	2.30	0.45
5:R:40:GLY:O	5:R:44:VAL:HG23	2.17	0.44
5:R:107:SER:O	5:R:111:ILE:HG12	2.17	0.44
4:N:29:PHE:CE1	4:N:34:MET:HG3	2.53	0.44
1:A:278:ASN:ND2	4:N:105:ARG:HE	2.16	0.44
2:B:7:LEU:HD12	2:B:7:LEU:HA	1.88	0.44
4:N:95:TYR:HB3	4:N:118:ARG:HG3	1.99	0.44
1:A:43:LEU:N	1:A:220:HIS:O	2.44	0.44
5:R:73:VAL:O	5:R:77:VAL:HB	2.18	0.44
5:R:113:ASN:HA	5:R:116:VAL:HG12	1.99	0.44
5:R:207:VAL:O	5:R:211:ILE:HG12	2.18	0.44
2:B:166:CYS:HB2	2:B:180:PHE:HB2	2.00	0.44
2:B:256:ARG:NH2	3:G:36:ASP:OD2	2.51	0.44
1:A:315:PHE:O	1:A:336:ARG:NH2	2.51	0.43
2:B:149:CYS:HB2	2:B:159:THR:HG22	1.99	0.43
2:B:192:LEU:HD22	2:B:199:PHE:HB2	2.00	0.43
2:B:170:ASP:HB2	2:B:173:THR:HG22	2.00	0.43
5:R:309:ASP:N	5:R:309:ASP:OD1	2.51	0.43
1:A:297:LEU:O	1:A:301:VAL:HG22	2.18	0.43
1:A:343:ASP:O	1:A:347:ARG:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:CYS:HA	1:A:382:ILE:HD12	2.00	0.43
2:B:57:LYS:HZ3	2:B:75:GLN:HG3	1.83	0.43
1:A:289:LEU:HD23	1:A:361:PRO:HB3	1.99	0.43
2:B:84:SER:HB2	2:B:338:ILE:HD13	2.01	0.43
5:R:52:ARG:HD2	5:R:55:ARG:HD3	2.00	0.43
5:R:80:TRP:HA	5:R:83:VAL:HG12	2.01	0.43
1:A:233:LYS:HD3	1:A:233:LYS:HA	1.81	0.43
4:N:68:PHE:HA	4:N:82:GLN:O	2.19	0.43
1:A:380:ARG:NH2	5:R:126:SER:O	2.52	0.43
4:N:33:LYS:HG3	4:N:51:ILE:O	2.19	0.43
1:A:60:MET:HA	1:A:372:ILE:HD11	2.00	0.42
2:B:25:CYS:SG	2:B:259:GLN:NE2	2.92	0.42
5:R:273:THR:O	5:R:277:ILE:HG12	2.19	0.42
2:B:70:LEU:HD23	2:B:84:SER:HB3	2.00	0.42
1:A:44:LEU:HD22	1:A:238:PHE:CG	2.54	0.42
2:B:267:ASP:OD1	2:B:267:ASP:N	2.53	0.42
3:G:10:ALA:O	3:G:14:LYS:HG2	2.20	0.42
5:R:57:LYS:HG3	5:R:59:THR:HG22	2.02	0.42
2:B:148:CYS:HB3	2:B:189:SER:HA	2.01	0.41
5:R:72:LEU:HG	5:R:106:CYS:SG	2.60	0.41
2:B:51:LEU:HB3	2:B:82:TRP:CE3	2.55	0.41
5:R:335:ALA:O	5:R:339:LYS:HG2	2.21	0.41
5:R:207:VAL:HG23	5:R:281:PHE:HE2	1.85	0.41
2:B:103:CYS:O	2:B:150:ARG:NH1	2.53	0.41
5:R:44:VAL:HG22	5:R:341:PHE:CZ	2.56	0.41
1:A:379:CYS:O	1:A:383:ILE:HG12	2.20	0.41
2:B:51:LEU:HB2	2:B:336:LEU:HB2	2.03	0.41
2:B:66:ASP:OD1	2:B:66:ASP:N	2.54	0.41
2:B:331:SER:OG	2:B:333:ASP:OD1	2.28	0.41
5:R:105:MET:HE2	7:R:502:CLR:H271	2.03	0.41
5:R:274:LEU:HD23	5:R:274:LEU:HA	1.98	0.41
1:A:313:PRO:HG2	4:N:65:LYS:HB3	2.01	0.41
2:B:210:LEU:HD13	2:B:234:PHE:HZ	1.86	0.40
2:B:281:SER:HB2	3:G:44:HIS:O	2.21	0.40
2:B:296:VAL:O	2:B:305:ALA:N	2.54	0.40
2:B:236:PRO:HB2	3:G:40:TYR:CE2	2.56	0.40
2:B:266:HIS:HB2	2:B:297:TRP:HH2	1.86	0.40
4:N:47:TRP:HB2	4:N:110:VAL:HG23	2.03	0.40
2:B:34:THR:O	2:B:301:LYS:NZ	2.55	0.40
5:R:103:ASP:OD2	5:R:321:TRP:CZ2	2.74	0.40
2:B:14:LEU:O	2:B:18:ILE:HG12	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:70:ASP:OD1	5:R:324:SER:HB3	2.22	0.40
2:B:205:ASP:HA	4:N:116:ALA:HB1	2.04	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	230/394 (58%)	224 (97%)	6 (3%)	0	100	100
2	B	338/356 (95%)	325 (96%)	13 (4%)	0	100	100
3	G	56/71 (79%)	56 (100%)	0	0	100	100
4	N	126/156 (81%)	117 (93%)	9 (7%)	0	100	100
5	R	265/453 (58%)	261 (98%)	4 (2%)	0	100	100
All	All	1015/1430 (71%)	983 (97%)	32 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	197/351 (56%)	194 (98%)	3 (2%)	60	78
2	B	277/296 (94%)	275 (99%)	2 (1%)	81	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	G	46/58 (79%)	46 (100%)	0	100	100
4	N	104/126 (82%)	103 (99%)	1 (1%)	73	85
5	R	237/395 (60%)	237 (100%)	0	100	100
All	All	861/1226 (70%)	855 (99%)	6 (1%)	80	90

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	220	HIS
1	A	246	PHE
1	A	313	PRO
2	B	128	THR
2	B	234	PHE
4	N	117	TYR

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

Mol	Chain	Res	Type
1	A	31	GLN
1	A	278	ASN
2	B	17	GLN
2	B	119	ASN
2	B	125	ASN
2	B	259	GLN
3	G	18	GLN
3	G	24	ASN
3	G	44	HIS
4	N	31	ASN
4	N	39	GLN
5	R	60	ASN
5	R	292	ASN
5	R	323	ASN
5	R	327	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

2 ligands 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
7	CLR	R	502	-	31,31,31	0.28	0	48,48,48	0.33	0
6	G3O	R	501	-	27,28,28	2.24	8 (29%)	37,44,44	1.09	1 (2%)

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
7	CLR	R	502	-	-	5/10/68/68	0/4/4/4
6	G3O	R	501	-	-	0/7/47/47	0/6/5/5

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	R	501	G3O	C06-C05	-7.07	1.29	1.40
6	R	501	G3O	C05-C10	3.76	1.55	1.51
6	R	501	G3O	C04-C05	3.74	1.44	1.39
6	R	501	G3O	C01-C06	2.92	1.44	1.40
6	R	501	G3O	C07-C08	-2.58	1.48	1.52
6	R	501	G3O	C18-C17	-2.52	1.47	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	R	501	G3O	C07-C06	-2.44	1.47	1.51
6	R	501	G3O	O23-C02	2.25	1.41	1.36

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	R	501	G3O	C18-C13-C14	3.53	112.96	108.02

There are no chirality outliers.

All (5) torsion outliers are listed below:

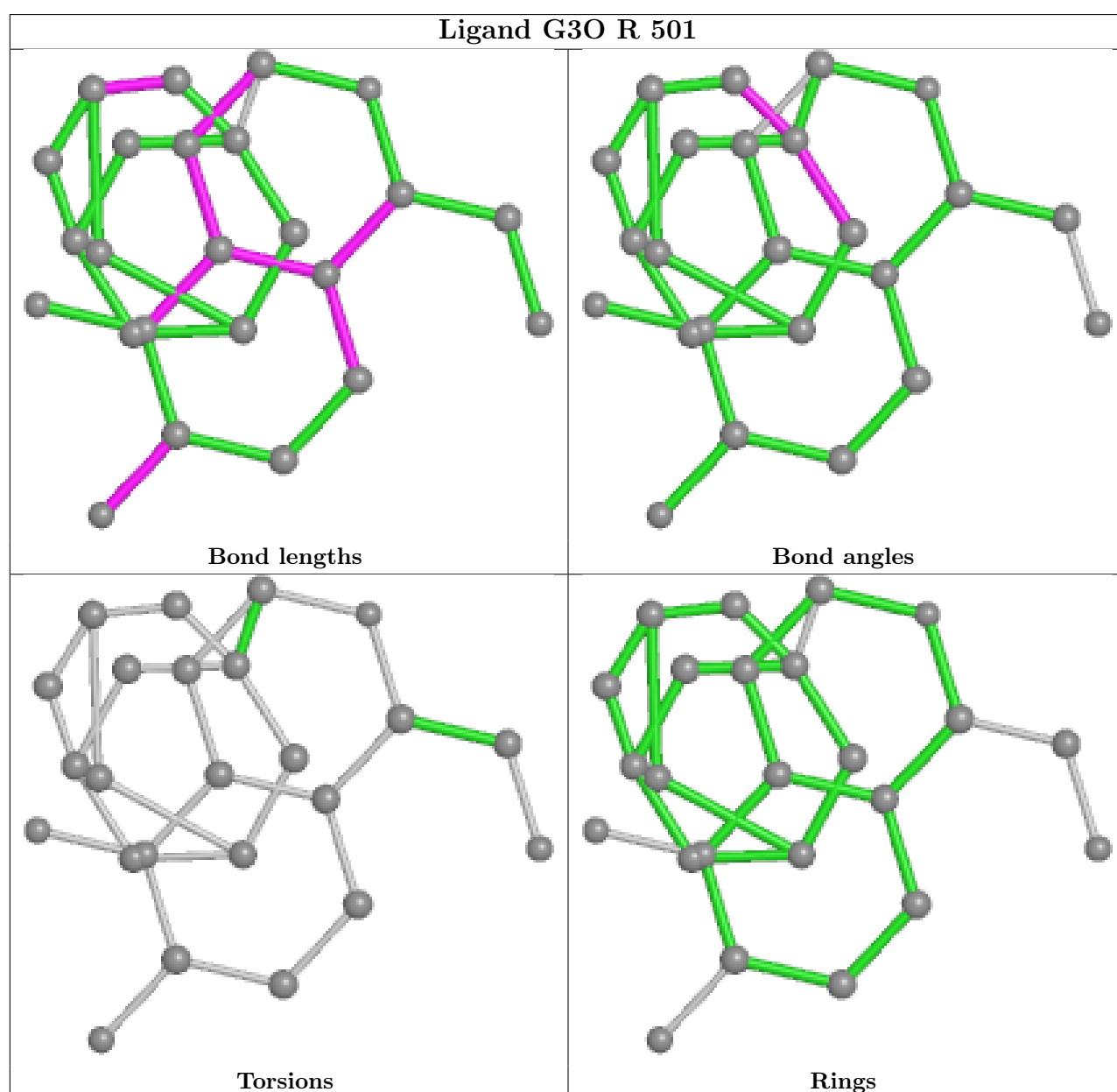
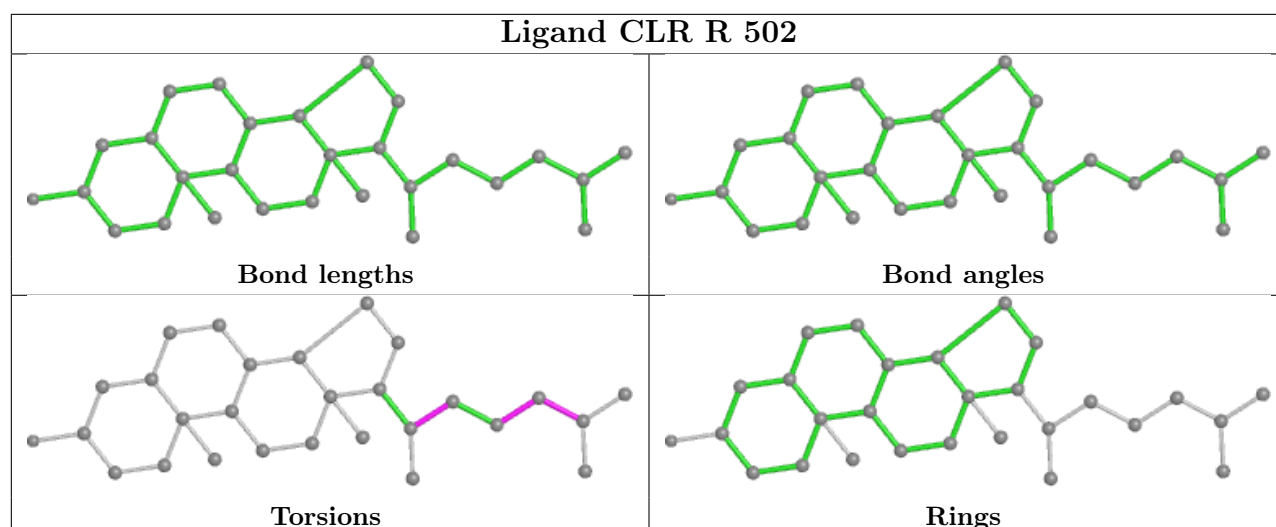
Mol	Chain	Res	Type	Atoms
7	R	502	CLR	C17-C20-C22-C23
7	R	502	CLR	C21-C20-C22-C23
7	R	502	CLR	C23-C24-C25-C27
7	R	502	CLR	C22-C23-C24-C25
7	R	502	CLR	C23-C24-C25-C26

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	R	502	CLR	4	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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

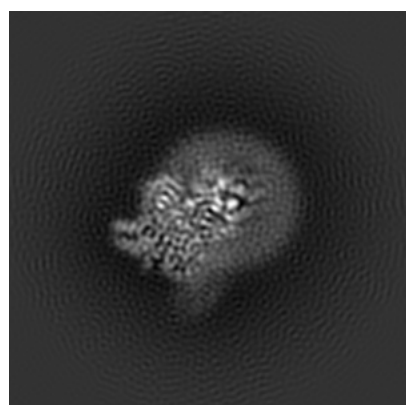
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30393. These allow visual inspection of the internal detail of the map and identification of artifacts.

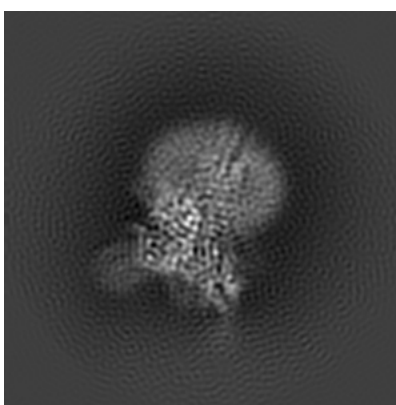
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

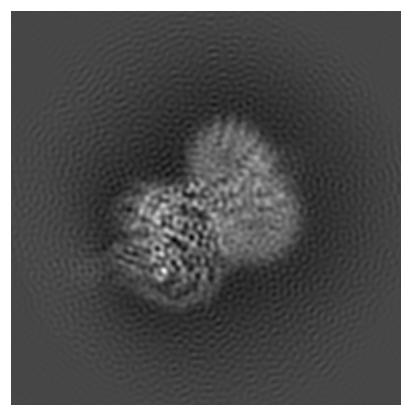
#### 6.1.1 Primary map



X



Y

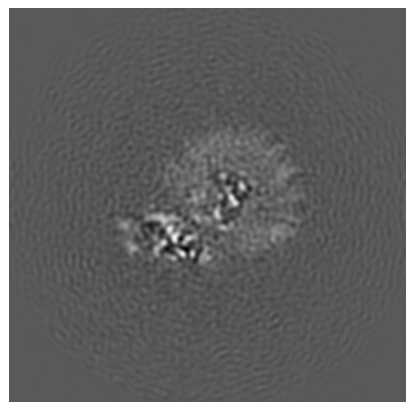


Z

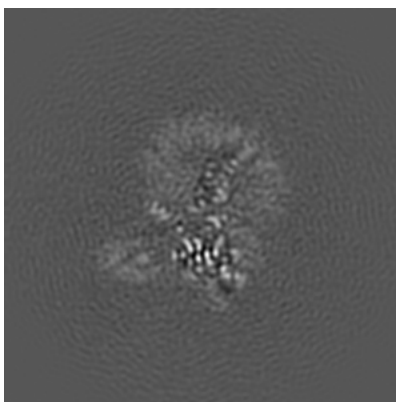
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

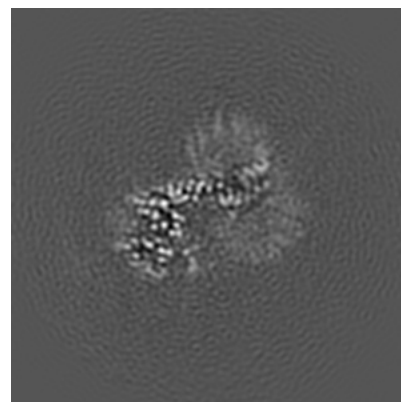
#### 6.2.1 Primary map



X Index: 108



Y Index: 108

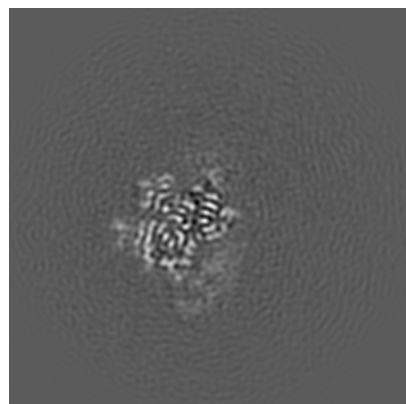


Z Index: 108

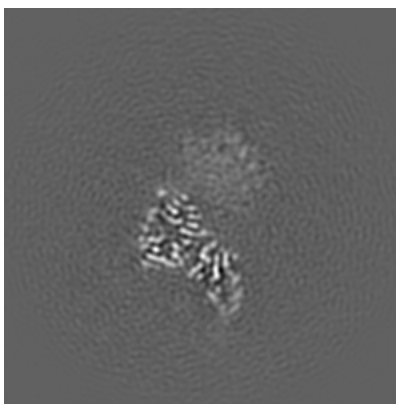
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

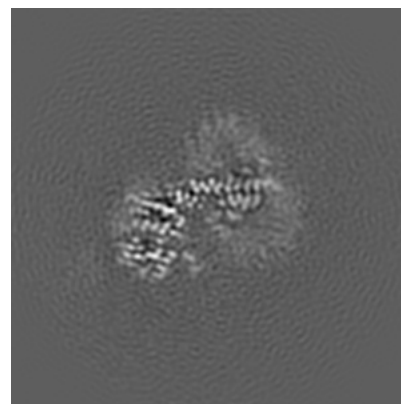
### 6.3.1 Primary map



X Index: 82



Y Index: 84

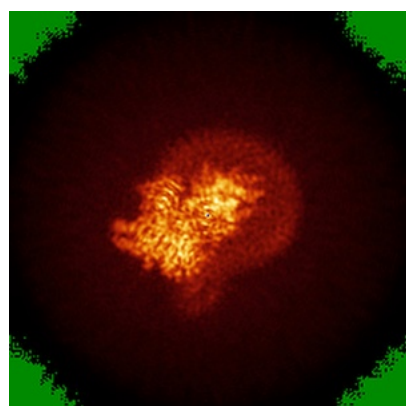


Z Index: 110

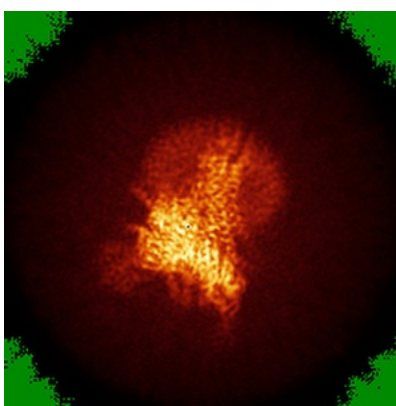
The images above show the largest variance slices of the map in three orthogonal directions.

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

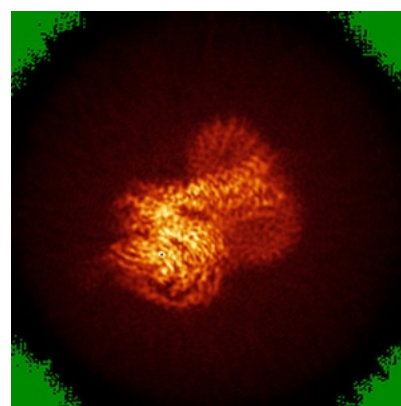
### 6.4.1 Primary map



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 0.026. 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](#)

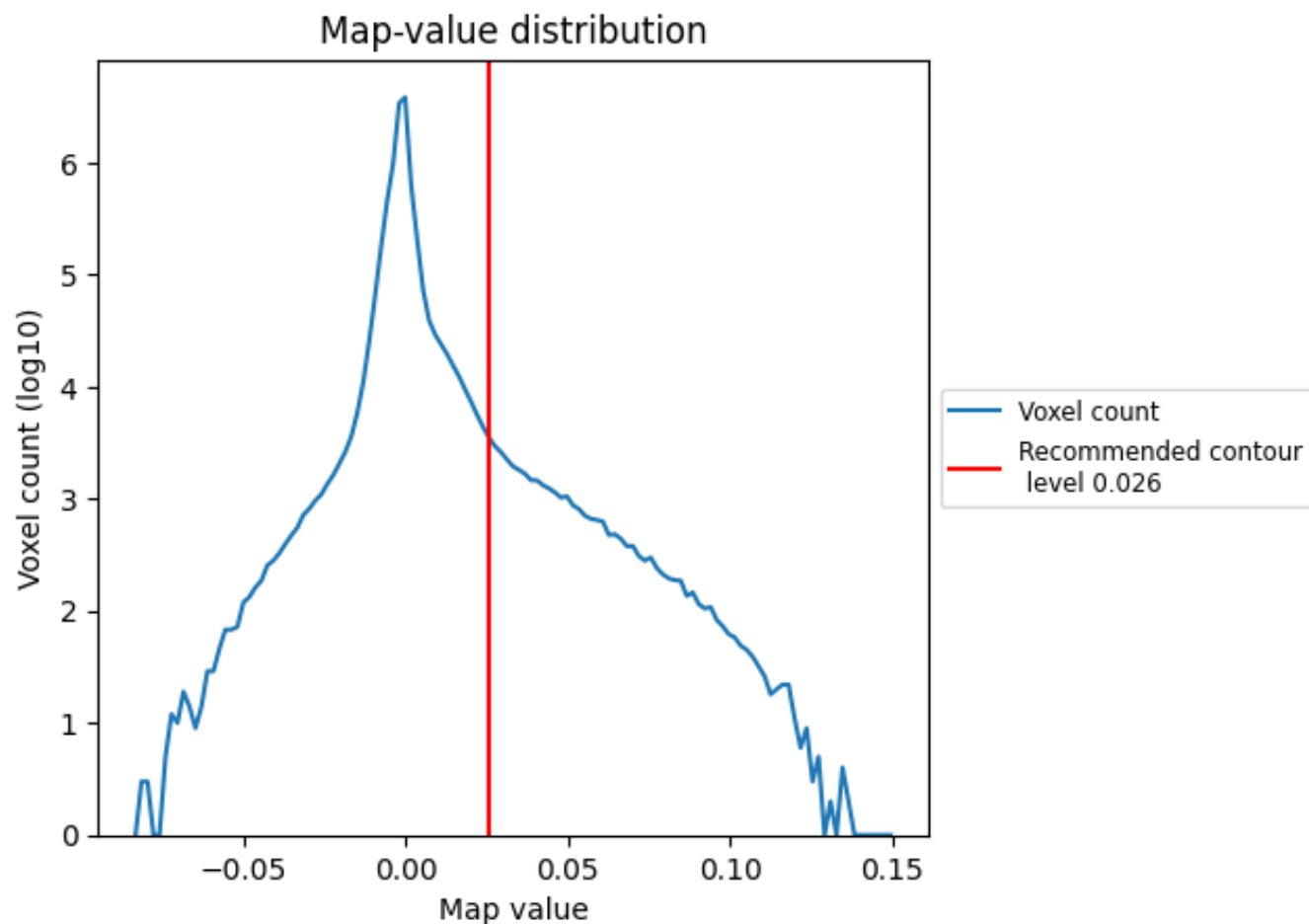
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

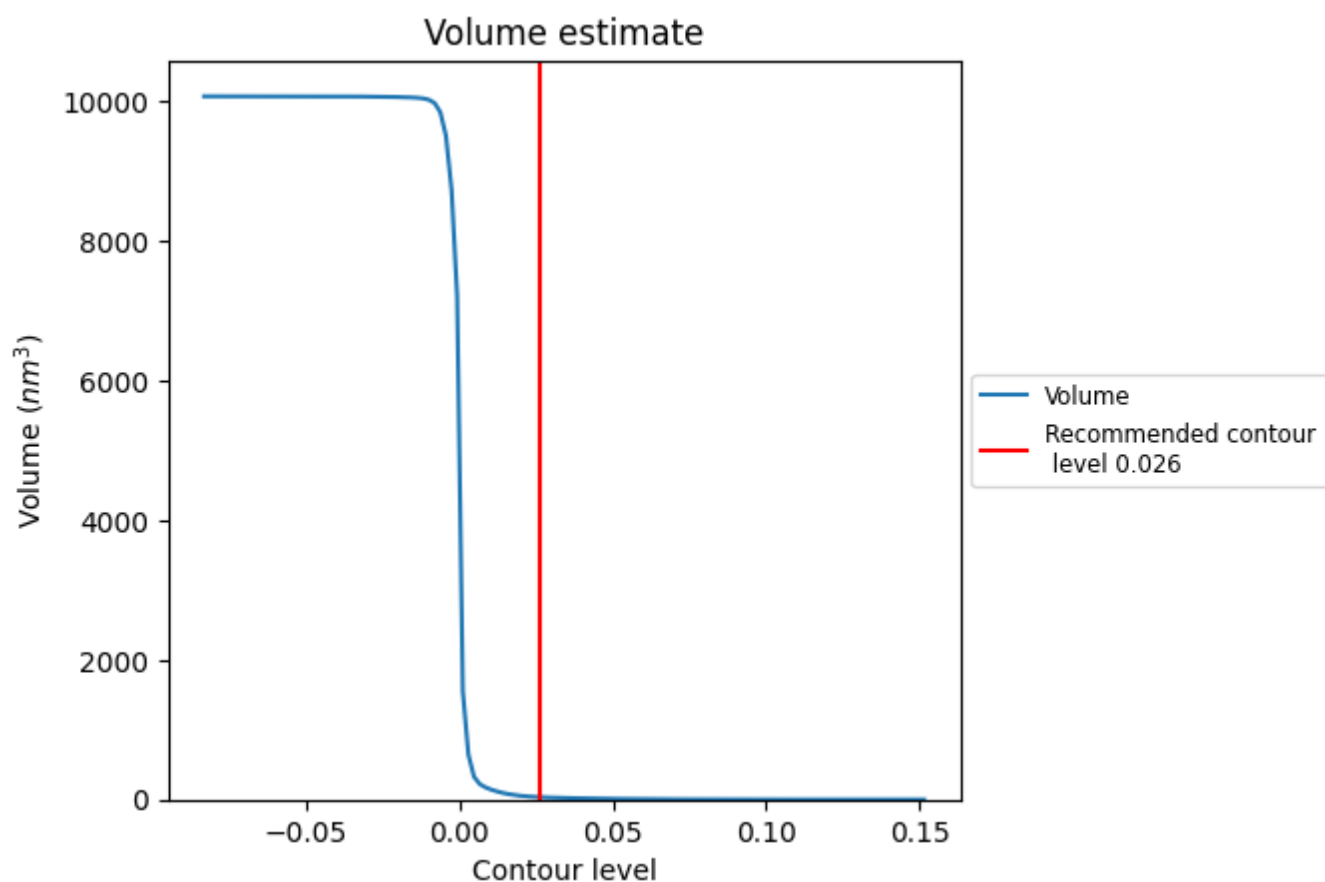
This section contains the results of statistical analysis of the map.

### 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.

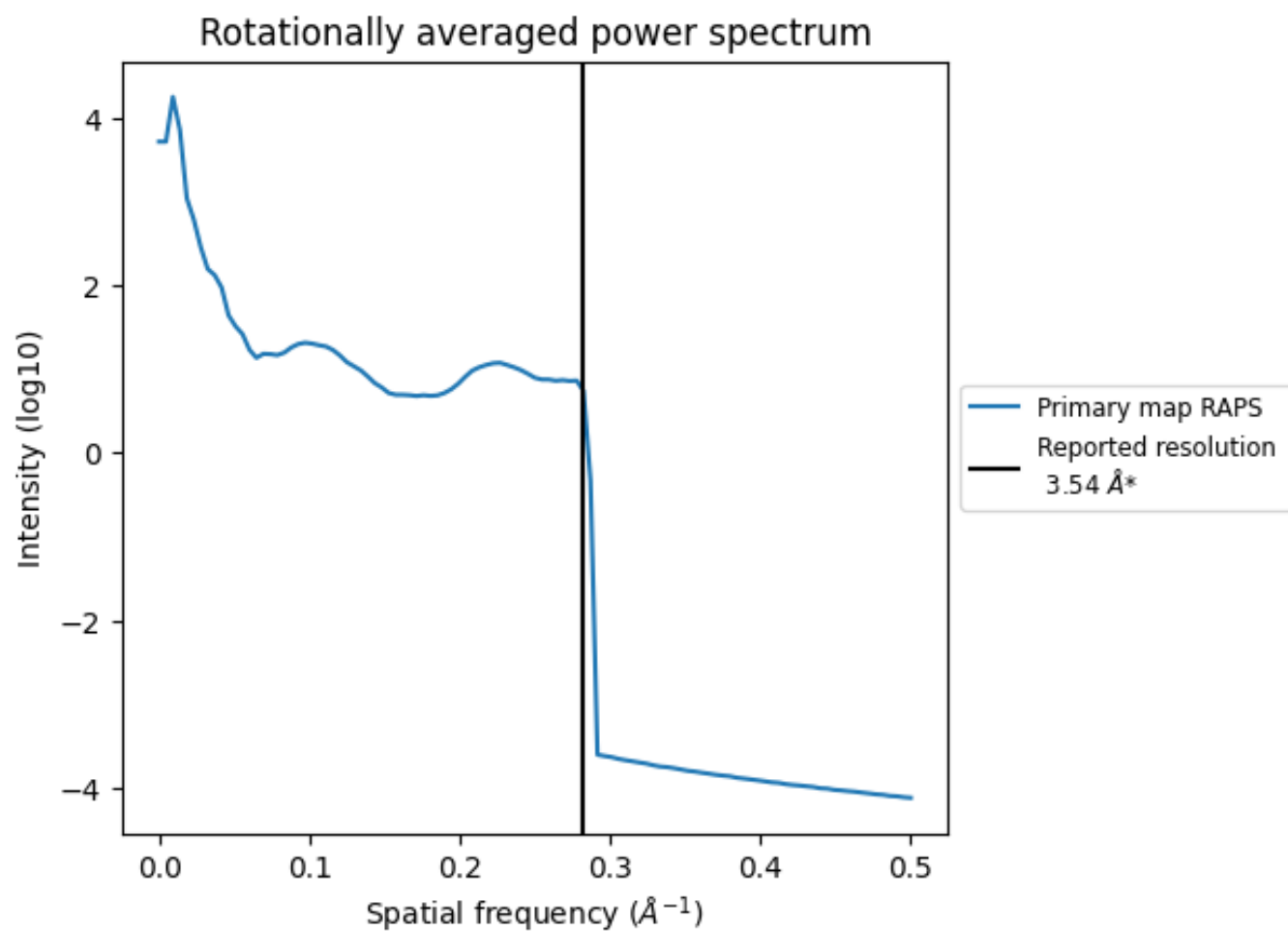
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 35 nm<sup>3</sup>; this corresponds to an approximate mass of 31 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 0.282 Å<sup>-1</sup>

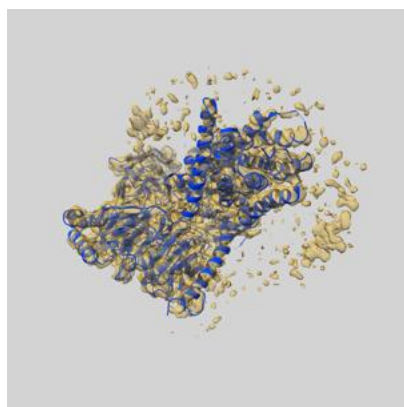
## 8 Fourier-Shell correlation ⓘ

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

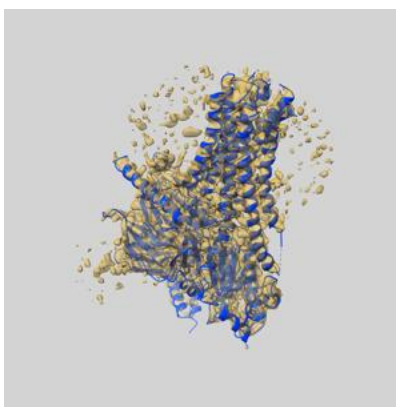
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30393 and PDB model 7CKX. Per-residue inclusion information can be found in section [3](#) on page [6](#).

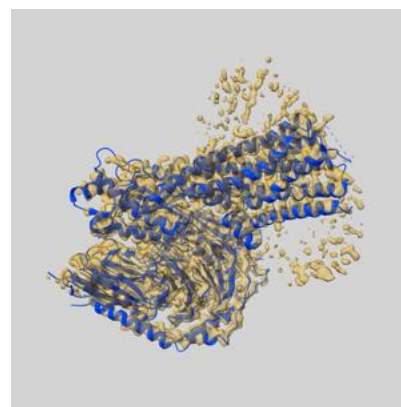
### 9.1 Map-model overlay [i](#)



X



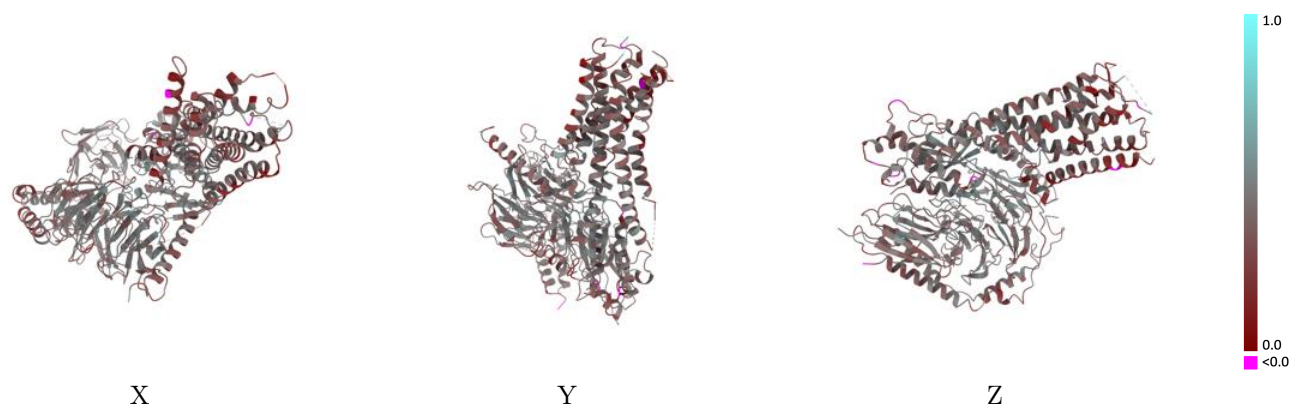
Y



Z

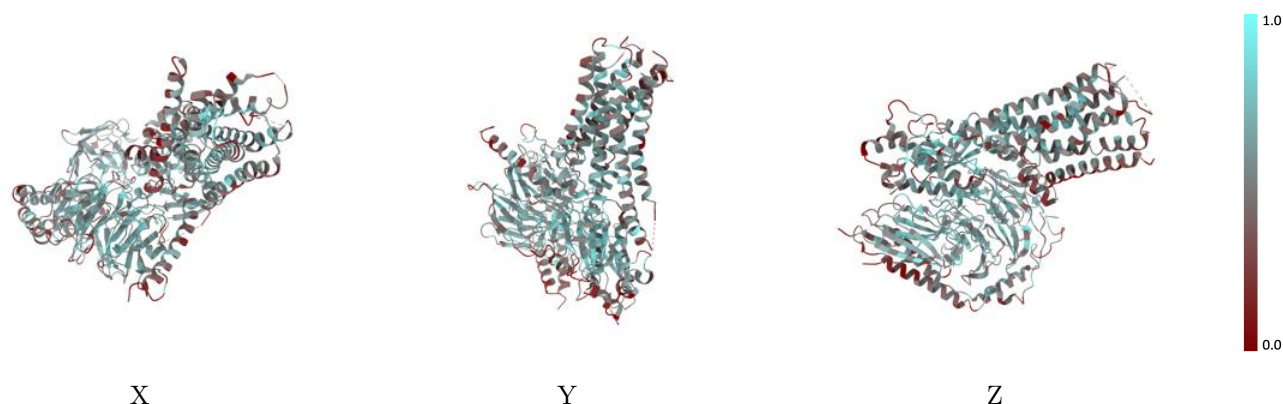
The images above show the 3D surface view of the map at the recommended contour level 0.026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



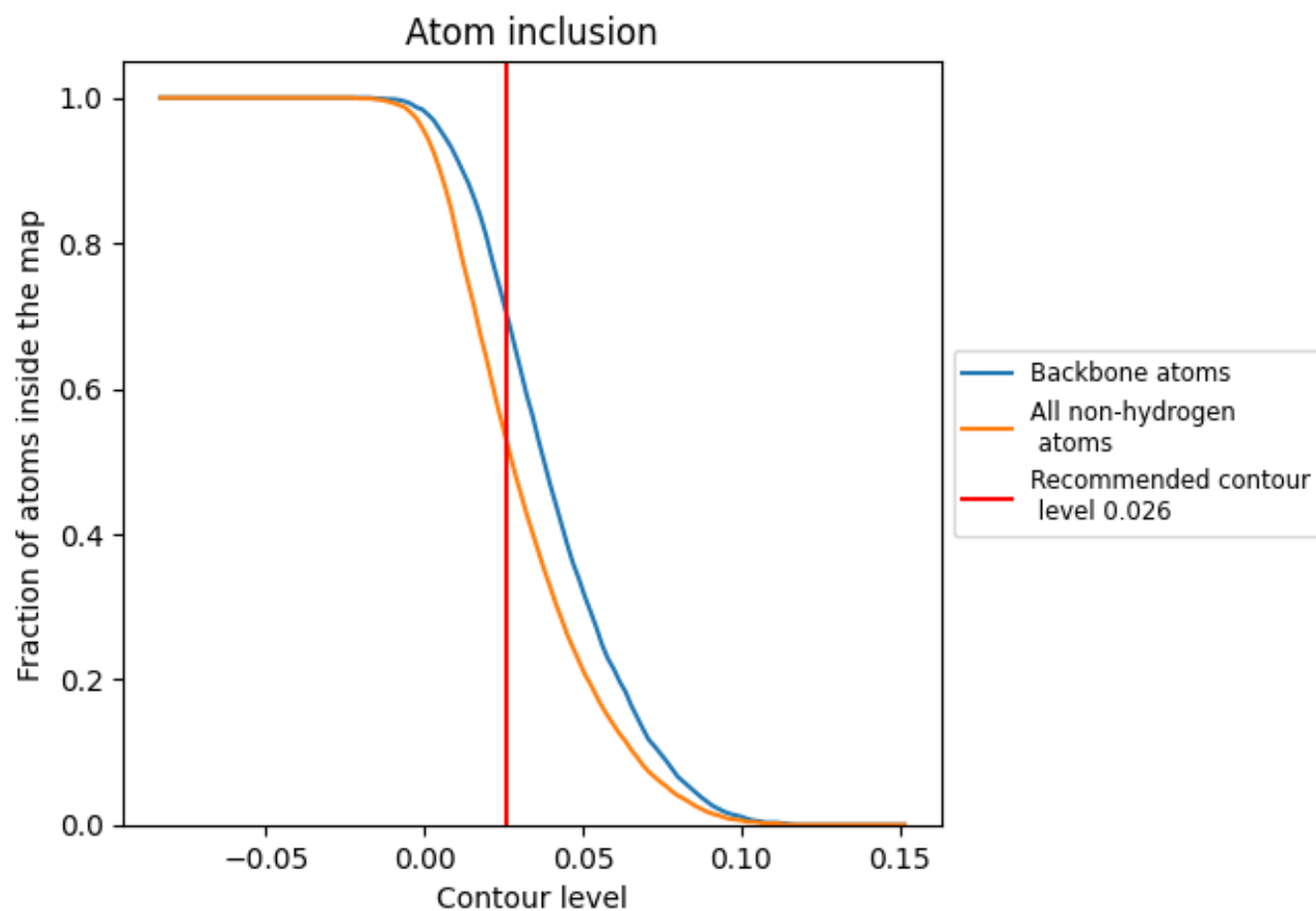
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.026).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 53% 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 (0.026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5270	<div></div> 0.3890
A	<div></div> 0.5340	<div></div> 0.4000
B	<div></div> 0.5610	<div></div> 0.4100
G	<div></div> 0.3970	<div></div> 0.3580
N	<div></div> 0.5630	<div></div> 0.4070
R	<div></div> 0.4920	<div></div> 0.3520

