



Full wwPDB EM Validation Report ⓘ

Mar 19, 2026 – 10:49 PM UTC

PDB ID : 8T1I / pdb_00008t1i
EMDB ID : EMD-40968
Title : Atomic model of the mammalian Mediator complex with MED26 subunit
Authors : Zhao, H.; Asturias, F.
Deposited on : 2023-06-02
Resolution : 4.68 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

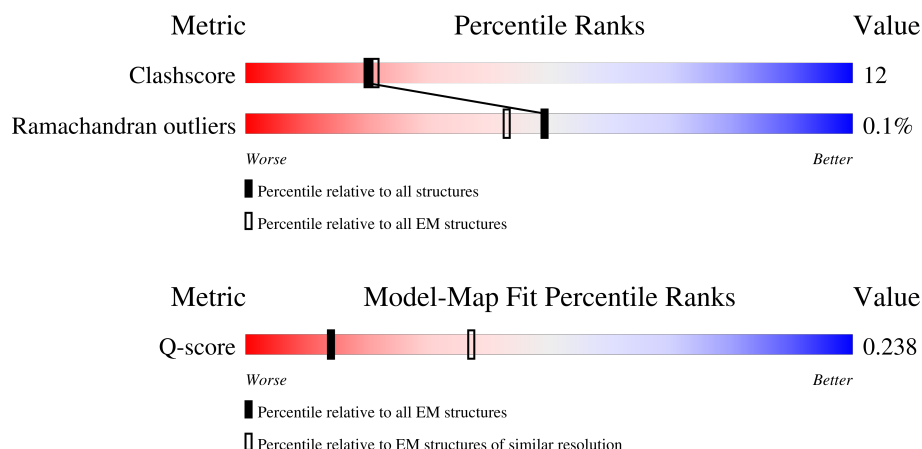
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 4.68 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.



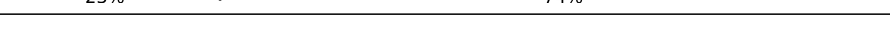
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	1991 (4.18 - 5.18)

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	1575	
2	B	270	
3	C	246	
4	D	233	
5	E	268	

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Mol	Chain	Length	Quality of chain
6	F	142	
7	G	135	
8	H	117	
9	I	1459	
10	J	789	
11	K	828	
12	L	649	
13	M	208	
14	N	240	
15	O	212	
16	P	144	
17	Q	200	
18	R	1367	
19	S	987	
20	T	745	
21	U	588	
22	V	311	
23	W	178	
24	X	199	
25	Y	178	
26	Z	131	
27	a	20	

2 Entry composition

There are 27 unique types of molecules in this entry. The entry contains 49568 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 Mediator of RNA polymerase II transcription subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	467	Total	C	N	O	0	0
			2314	1380	467	467		

- Molecule 2 is a protein called Mediator of RNA polymerase II transcription subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	158	Total	C	N	O	0	0
			784	468	158	158		

- Molecule 3 is a protein called Mediator of RNA polymerase II transcription subunit 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	157	Total	C	N	O	0	0
			785	471	157	157		

- Molecule 4 is a protein called Mediator of RNA polymerase II transcription subunit 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	161	Total	C	N	O	0	0
			801	479	161	161		

- Molecule 5 is a protein called Mediator of RNA polymerase II transcription subunit 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	E	165	Total	C	N	O	0	0
			837	506	166	165		

- Molecule 6 is a protein called Mediator of RNA polymerase II transcription subunit 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	F	73	Total	C	N	O	0	0
			363	217	73	73		

- Molecule 7 is a protein called Mediator of RNA polymerase II transcription subunit 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	G	122	Total	C	N	O	0	0
			605	361	122	122		

- Molecule 8 is a protein called Mediator of RNA polymerase II transcription subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	105	Total	C	N	O	S	0	0
			578	349	116	112	1		

- Molecule 9 is a protein called Mediator of RNA polymerase II transcription subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	1086	Total	C	N	O	S	0	0
			6772	4287	1254	1211	20		

- Molecule 10 is a protein called Mediator of RNA polymerase II transcription subunit 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	167	Total	C	N	O	S	0	0
			1171	748	217	200	6		

- Molecule 11 is a protein called Mediator of RNA polymerase II transcription subunit 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	738	Total	C	N	O	S	0	0
			5085	3283	912	867	23		

- Molecule 12 is a protein called Mediator of RNA polymerase II transcription subunit 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	544	Total	C	N	O	S	0	0
			3335	2093	628	611	3		

- Molecule 13 is a protein called Mediator of RNA polymerase II transcription subunit 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	180	Total	C	N	O	S	0	0
			1140	725	217	197	1		

- Molecule 14 is a protein called Mediator of RNA polymerase II transcription subunit 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	75	Total	C	N	O	S	0	0
			475	293	85	95	2		

- Molecule 15 is a protein called Mediator of RNA polymerase II transcription subunit 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	174	Total	C	N	O	S	0	0
			1013	640	177	192	4		

- Molecule 16 is a protein called Mediator of RNA polymerase II transcription subunit 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	121	Total	C	N	O		0	0
			602	360	121	121			

- Molecule 17 is a protein called Mediator of RNA polymerase II transcription subunit 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	131	Total	C	N	O		0	0
			754	463	145	146			

- Molecule 18 is a protein called Mediator of RNA polymerase II transcription subunit 23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	1295	Total	C	N	O	S	0	0
			9744	6296	1680	1715	53		

- Molecule 19 is a protein called Mediator of RNA polymerase II transcription subunit 24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	901	Total	C	N	O	S	0	0
			5875	3750	1062	1036	27		

- Molecule 20 is a protein called Mediator of RNA polymerase II transcription subunit 25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	192	Total	C	N	O	S	0	0
			1299	837	222	235	5		

- Molecule 21 is a protein called Mediator of RNA polymerase II transcription subunit 26.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	97	Total	C	N	O	0	0
			481	287	97	97		

- Molecule 22 is a protein called Mediator of RNA polymerase II transcription subunit 27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	266	Total	C	N	O	S	0	0
			1657	1053	301	300	3		

- Molecule 23 is a protein called Mediator of RNA polymerase II transcription subunit 28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	118	Total	C	N	O	S	0	0
			773	486	145	140	2		

- Molecule 24 is a protein called Mediator of RNA polymerase II transcription subunit 29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	123	Total	C	N	O	S	0	0
			839	528	150	158	3		

- Molecule 25 is a protein called Mediator of RNA polymerase II transcription subunit 30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	132	Total	C	N	O	S	0	0
			843	527	168	145	3		

- Molecule 26 is a protein called Mediator of RNA polymerase II transcription subunit 31.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	Z	109	Total	C	N	O	0	0
			543	325	109	109		

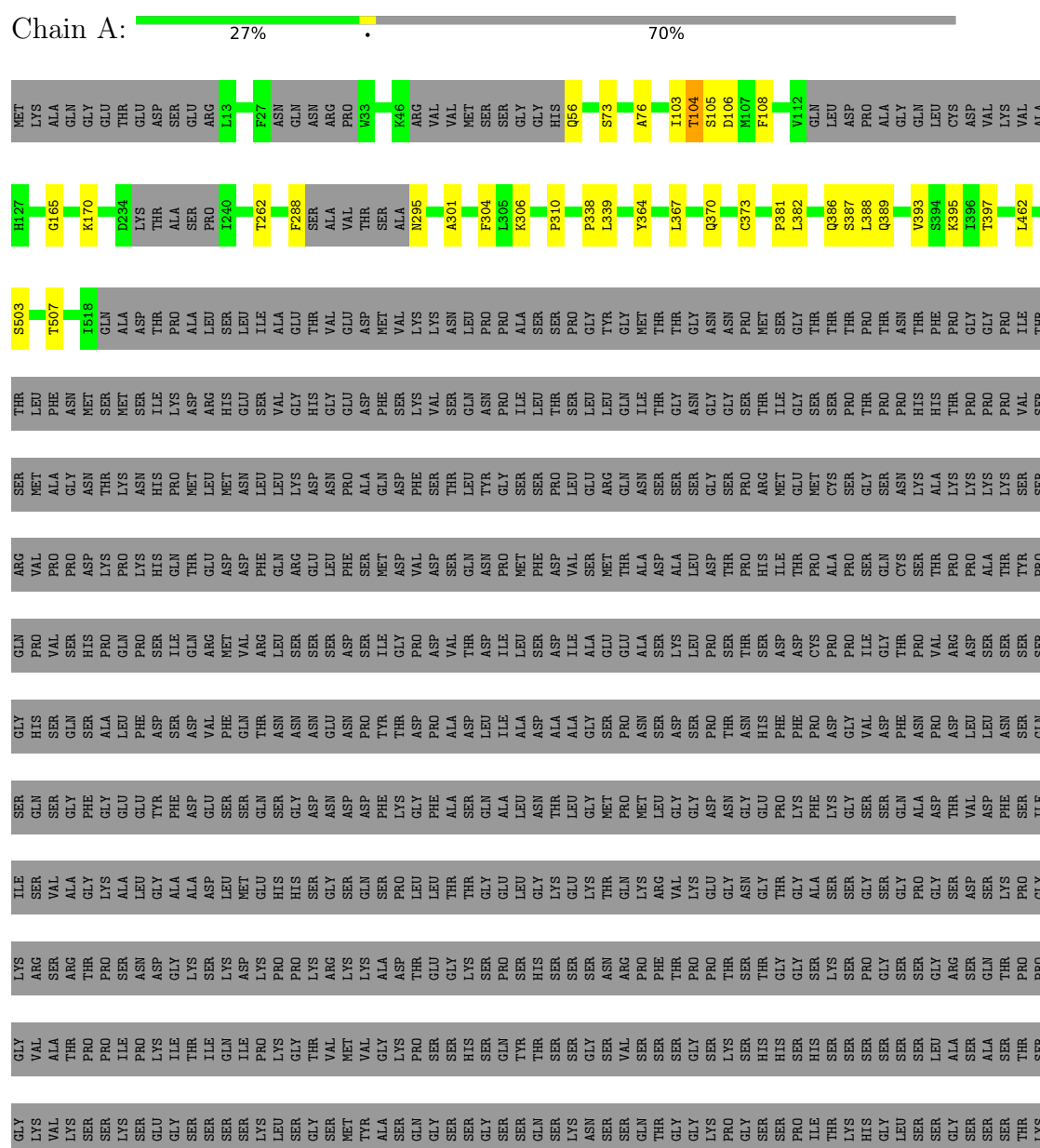
- Molecule 27 is a protein called Unknown Peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	a	20	Total	C	N	O	0	0
			100	60	20	20		

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: Mediator of RNA polymerase II transcription subunit 1



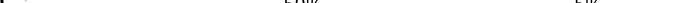
[illegible]

- Molecule 2: Mediator of RNA polymerase II transcription subunit 4

Chain B: 58% 41%

[illegible]

- Molecule 3: Mediator of RNA polymerase II transcription subunit 6

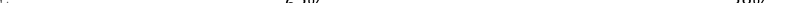
Chain C: 

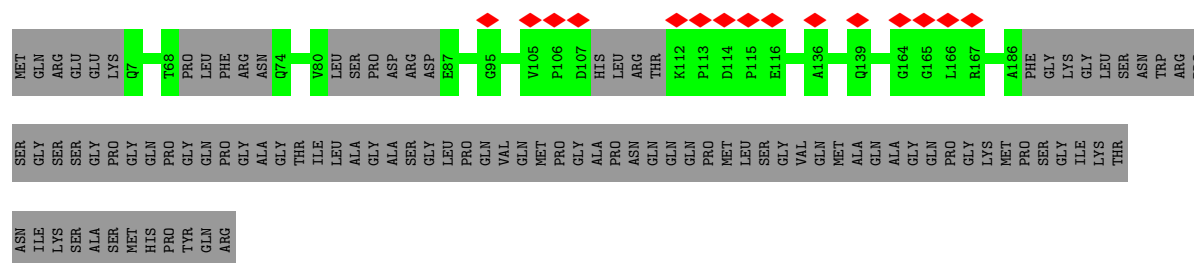
GLU	ALA	GLU	PRO	LEU	PRO	GLU	THR	VAL	LYS	SER	GLU	GLU	LYS	GLU	GLU	LYS	THR	ASN	ILE	GLN	GLN	THR	VAL	SER	THR	LYS	THR	GLU	GLN	PRO	GLU	GLU	LYS	LYS	ARG	LEU	GLN																			
161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199																		
PHE	ALA	VAL	ASP	ILE	ARG	ASP	LYS	L10	L11	GL2	IL3	SL4	LYS	GLY	TVR	TRP	TRP	HIS	PHE	LYS	ASP	HIS	GLU	GLU	GLN	GLU	LYS	VAL	LYS	PRO	LYS	ALA	LYS	ARG	1165	1187	PHE	PRO	PRO	ARG	PHE	VAL	GLN	GLN	LYS	SER	GLY	GLU	LYS	PRO	VAL	ASP	GLN	ALA	LYS	LYS
MET	ALA	VAL	ASP	ILE	ARG	ASP	LYS	L10	L11	GL2	IL3	SL4	LYS	GLY	TVR	TRP	TRP	HIS	PHE	LYS	ASP	HIS	GLU	GLU	GLN	GLU	LYS	VAL	LYS	PRO	LYS	ALA	LYS	ARG	1165	1187	PHE	PRO	PRO	ARG	PHE	VAL	GLN	GLN	LYS	SER	GLY	GLU	LYS	PRO	VAL	ASP	GLN	ALA	LYS	LYS

- Molecule 4: Mediator of RNA polymerase II transcription subunit 7

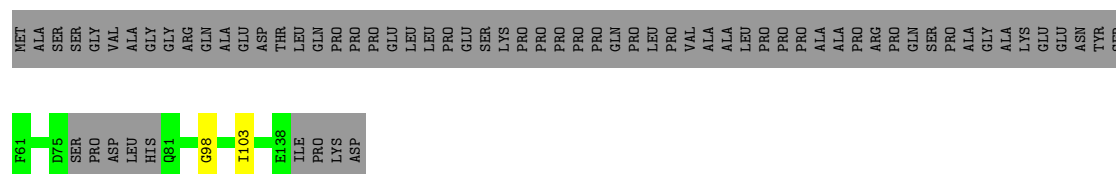
Chain D: 66% 31%

[illegible]

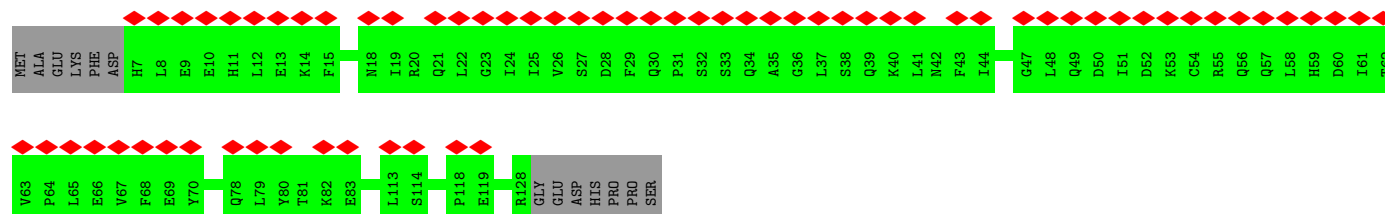
- Chain E:  6% 62% 38%



- Chain F: 50% . 49%

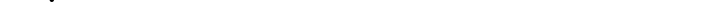


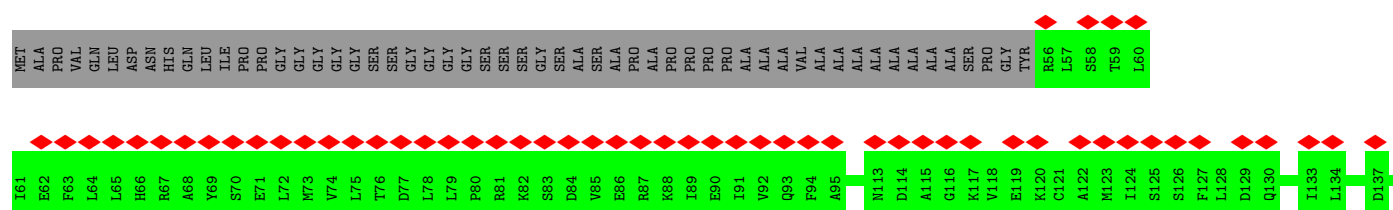
- Chain G:  50% 90% 10%

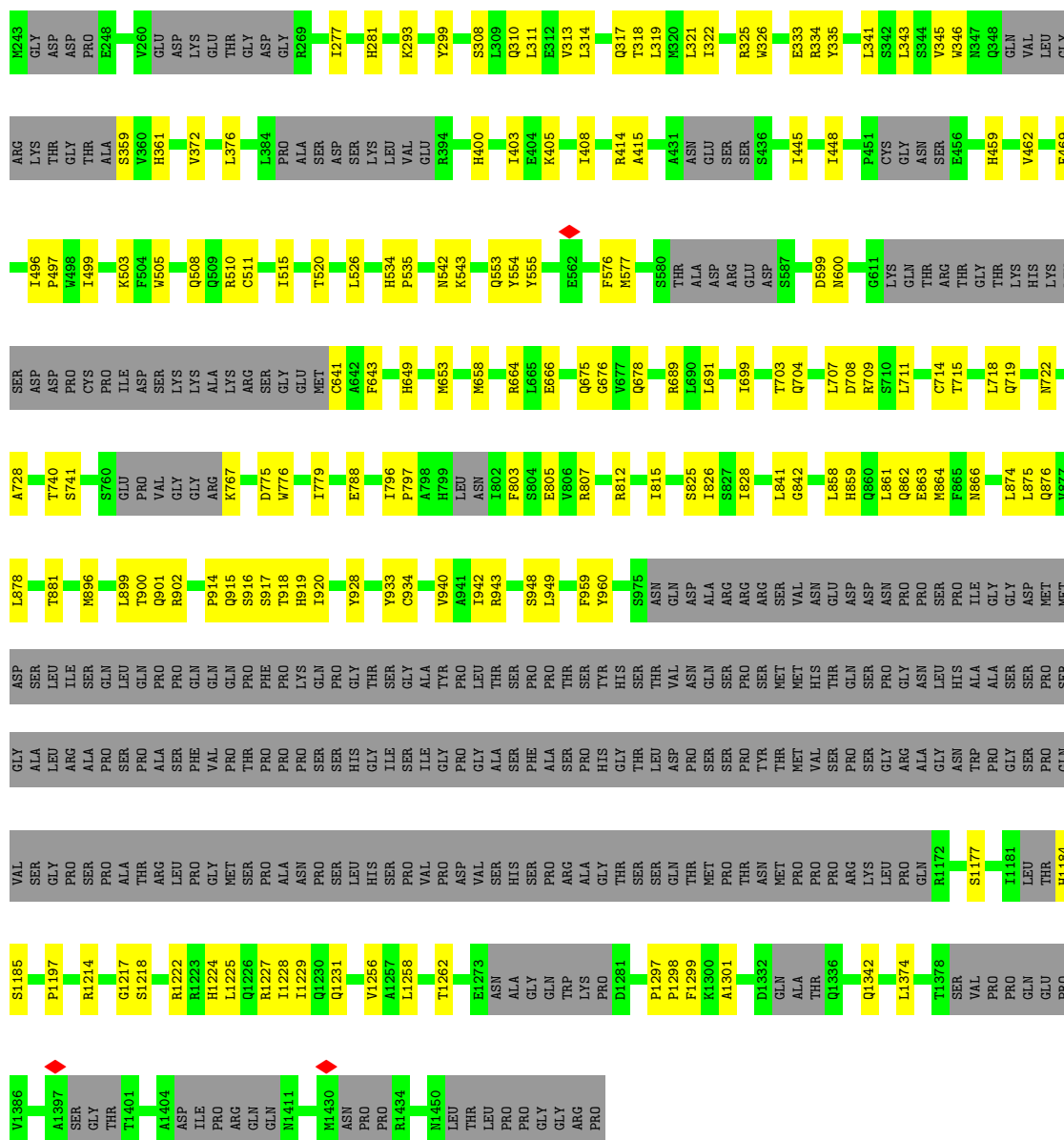


- Chain H: 79% 10% 10%

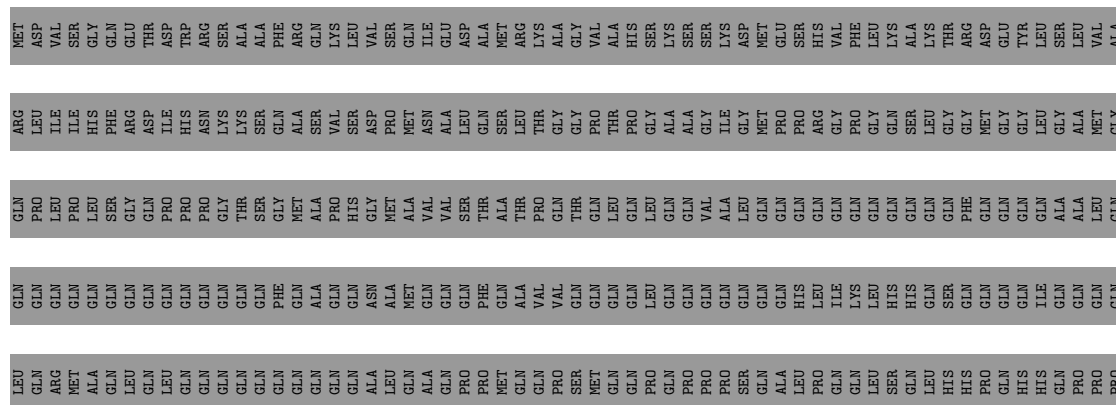


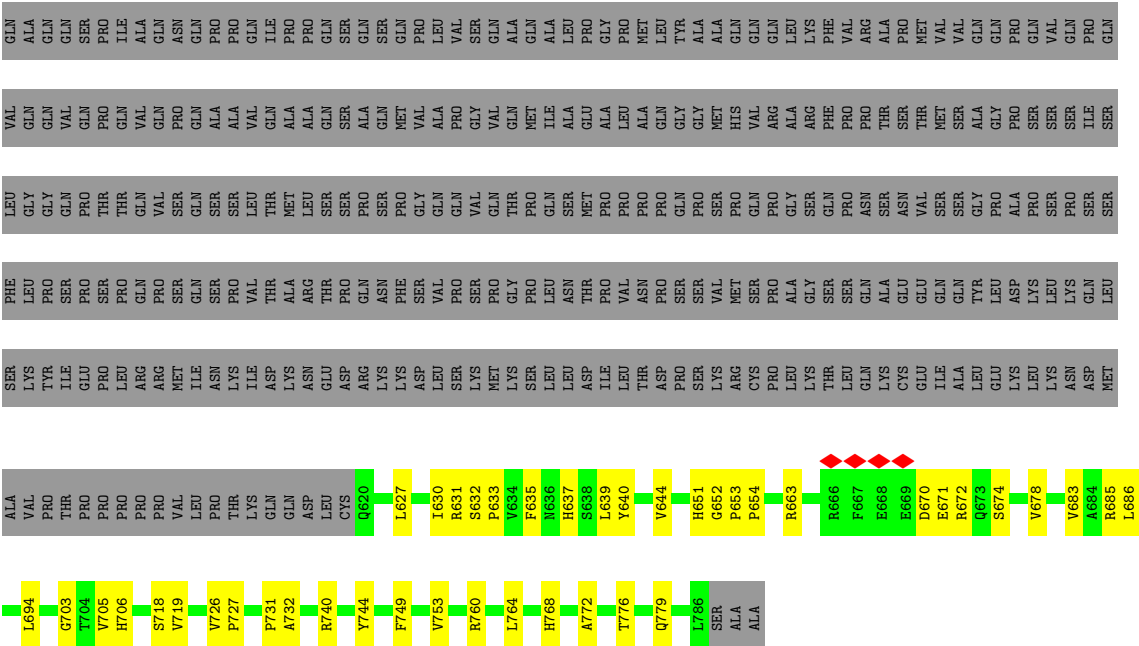
- Chain I:  63% 11% 26%



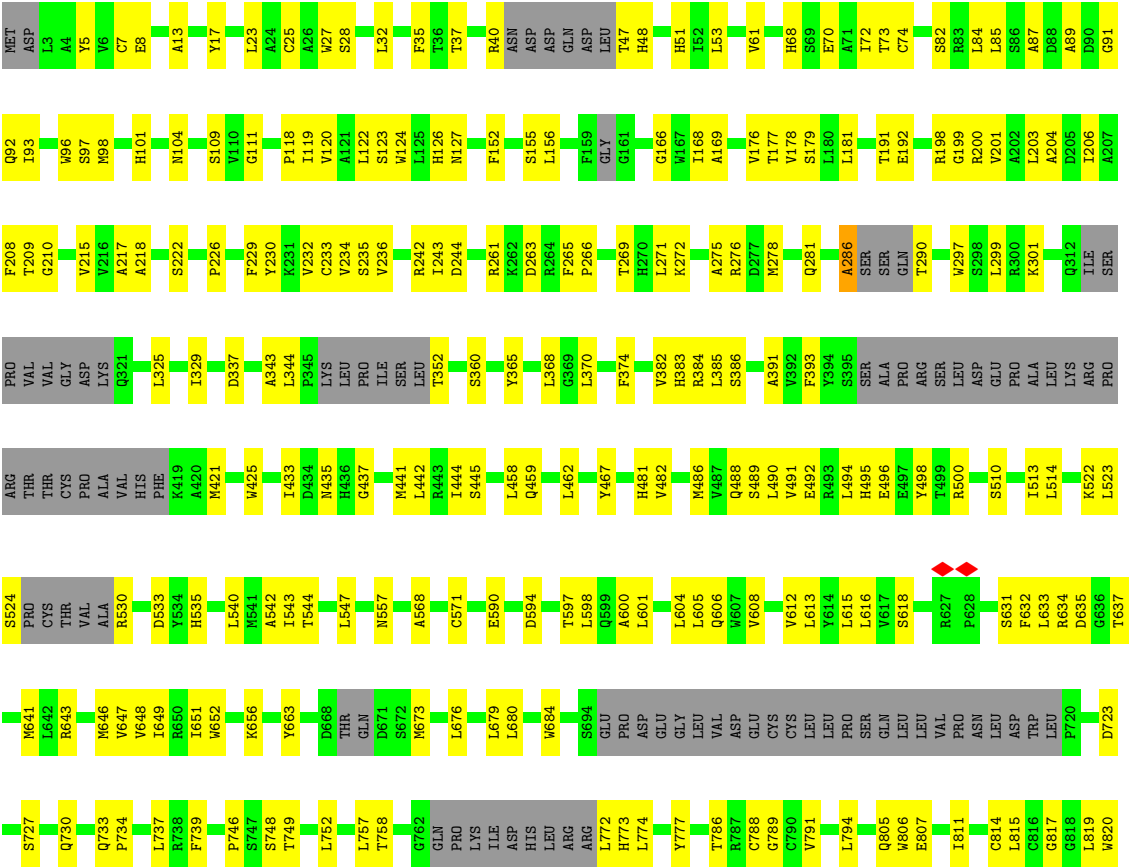


• Molecule 10: Mediator of RNA polymerase II transcription subunit 15



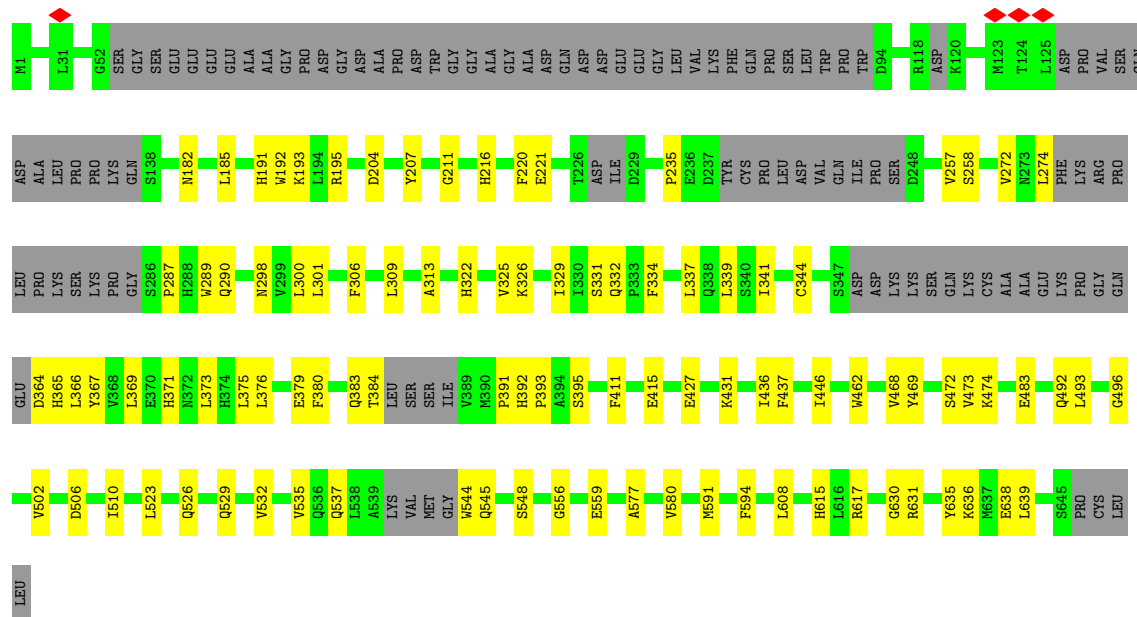


• Molecule 11: Mediator of RNA polymerase II transcription subunit 16

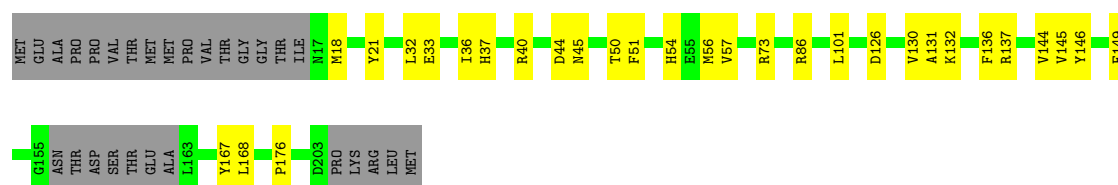


5828

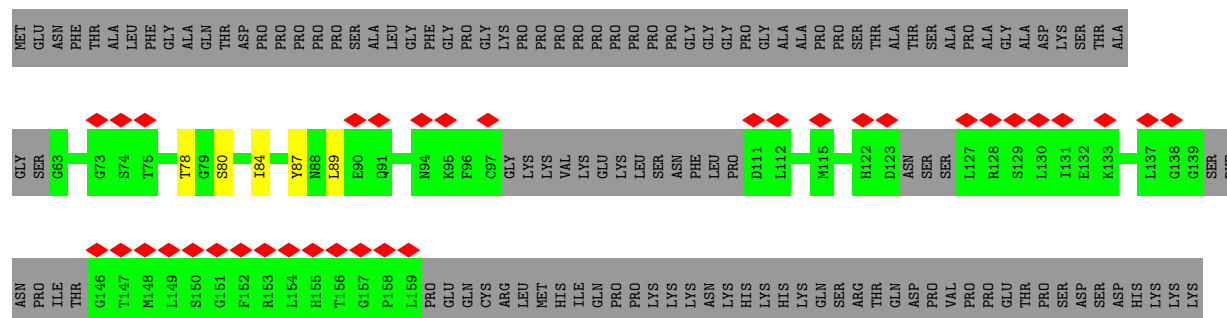
- Molecule 12: Mediator of RNA polymerase II transcription subunit 17

Chain L:  69% 15% 16%

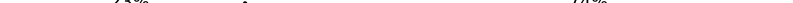
- Molecule 13: Mediator of RNA polymerase II transcription subunit 18

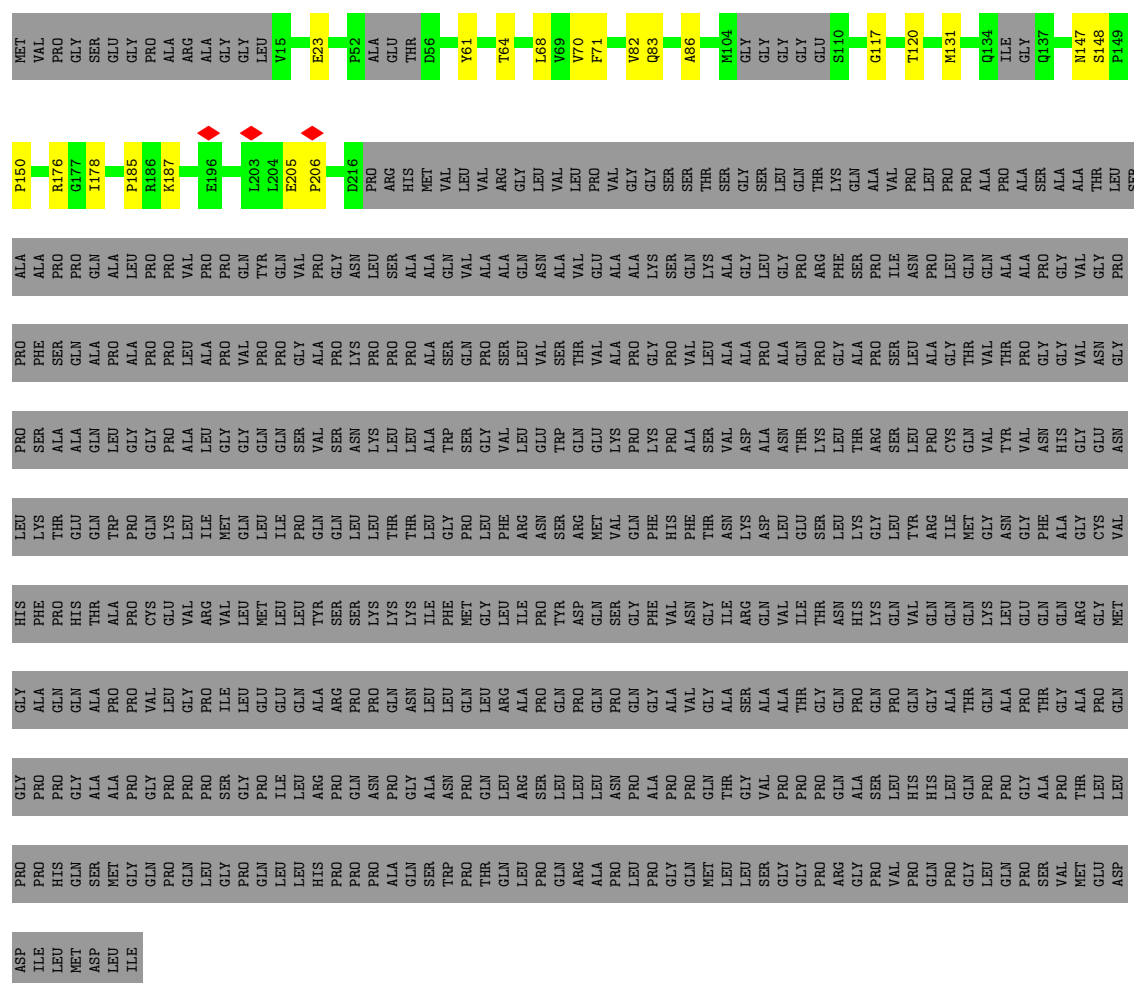
Chain M:  72% 14% 13%

- Molecule 14: Mediator of RNA polymerase II transcription subunit 19

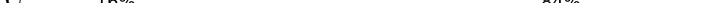
Chain N:  15% 29% 69%

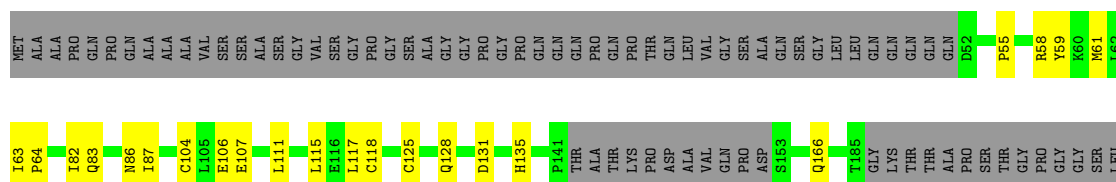
- Molecule 20: Mediator of RNA polymerase II transcription subunit 25

Chain T:  23% 1% 74%



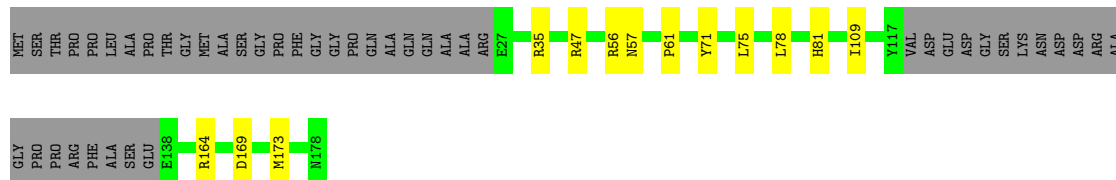
- Molecule 21: Mediator of RNA polymerase II transcription subunit 26

Chain U:  16% 84%



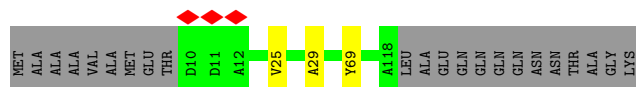
- Molecule 25: Mediator of RNA polymerase II transcription subunit 30

Chain Y: 



- Molecule 26: Mediator of RNA polymerase II transcription subunit 31

Chain Z: 



- Molecule 27: Unknown Peptide

Chain a: 

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	199078	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	22.5	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.308	Depositor
Minimum map value	-0.071	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.054	Depositor
Map size ($\text{\AA}$)	621.60004, 621.60004, 621.60004	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.11, 1.11, 1.11	Depositor

5 Model quality

5.1 Standard geometry

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	0.11	0/2308	0.28	0/3209
2	B	0.12	0/782	0.23	0/1088
3	C	0.13	0/784	0.47	0/1090
4	D	0.12	0/800	0.39	0/1116
5	E	0.10	0/840	0.26	0/1170
6	F	0.09	0/361	0.22	0/501
7	G	0.08	0/604	0.21	0/841
8	H	0.12	0/580	0.30	0/798
9	I	0.13	0/6899	0.36	0/9516
10	J	0.16	0/1207	0.41	0/1668
11	K	0.15	0/5202	0.44	2/7144 (0.0%)
12	L	0.13	0/3385	0.33	0/4658
13	M	0.12	0/1163	0.31	0/1593
14	N	0.09	0/479	0.28	0/648
15	O	1.49	7/1026 (0.7%)	0.44	1/1409 (0.1%)
16	P	0.10	0/600	0.26	0/835
17	Q	0.11	0/758	0.26	0/1046
18	R	0.14	0/9995	0.39	0/13654
19	S	0.14	0/6000	0.34	0/8250
20	T	0.12	0/1336	0.34	0/1836
21	U	0.42	0/480	0.48	0/666
22	V	0.13	0/1694	0.36	0/2338
23	W	0.13	0/785	0.34	0/1076
24	X	0.12	0/852	0.32	0/1169
25	Y	0.13	0/853	0.30	0/1167
26	Z	0.11	0/542	0.36	0/756
All	All	0.25	7/50315 (0.0%)	0.36	3/69242 (0.0%)

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
1	A	0	1
3	C	0	3
All	All	0	4

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	O	46	TYR	CD2-CE2	24.93	2.13	1.38
15	O	46	TYR	CD1-CE1	23.92	2.10	1.38
15	O	46	TYR	CE1-CZ	17.01	1.79	1.38
15	O	46	TYR	CE2-CZ	16.99	1.79	1.38
15	O	46	TYR	CG-CD2	15.24	1.71	1.39
15	O	46	TYR	CG-CD1	14.63	1.70	1.39
15	O	105	ALA	N-CA	6.82	1.54	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	K	286	ALA	CA-C-N	8.64	137.26	121.70
11	K	286	ALA	C-N-CA	8.64	137.26	121.70
15	O	104	SER	CA-C-O	-7.46	111.42	120.89

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	104	THR	Peptide
3	C	46	ASN	Peptide
3	C	50	VAL	Peptide
3	C	58	GLU	Peptide

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	2314	0	992	19	0
2	B	784	0	357	1	0

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Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	785	0	344	10	0
4	D	801	0	327	8	0
5	E	837	0	402	0	0
6	F	363	0	146	1	0
7	G	605	0	256	0	0
8	H	578	0	341	8	0
9	I	6772	0	4972	113	0
10	J	1171	0	1010	34	0
11	K	5085	0	4509	164	0
12	L	3335	0	2395	74	0
13	M	1140	0	832	22	0
14	N	475	0	349	4	0
15	O	1013	0	662	36	0
16	P	602	0	302	7	0
17	Q	754	0	448	4	0
18	R	9744	0	9105	382	0
19	S	5875	0	4690	150	0
20	T	1299	0	1022	12	0
21	U	481	0	202	0	0
22	V	1657	0	1170	25	0
23	W	773	0	607	16	0
24	X	839	0	700	18	0
25	Y	843	0	639	11	0
26	Z	543	0	240	2	0
27	a	100	0	23	0	0
All	All	49568	0	37042	1063	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 12.

All (1063) 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)
15:O:46:TYR:CZ	15:O:46:TYR:CE1	1.79	1.66
15:O:46:TYR:CZ	15:O:46:TYR:CE2	1.79	1.63
15:O:46:TYR:CE1	15:O:46:TYR:CD1	2.10	1.39
15:O:46:TYR:CE2	15:O:46:TYR:CD2	2.13	1.35
15:O:46:TYR:CD1	15:O:105:ALA:N	1.97	1.33
15:O:46:TYR:CE1	15:O:105:ALA:N	1.96	1.32
15:O:46:TYR:CZ	15:O:105:ALA:N	2.07	1.22
15:O:46:TYR:CD2	15:O:105:ALA:N	2.09	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:46:TYR:CE2	15:O:105:ALA:N	2.10	1.18
15:O:46:TYR:CG	15:O:105:ALA:N	2.13	1.15
15:O:46:TYR:CE2	15:O:104:SER:C	2.35	1.04
15:O:46:TYR:CD2	15:O:104:SER:C	2.36	1.04
15:O:46:TYR:CZ	15:O:104:SER:C	2.43	0.97
19:S:313:ILE:HG13	19:S:314:PRO:HD3	1.48	0.95
15:O:46:TYR:CG	15:O:104:SER:C	2.47	0.93
18:R:1005:LEU:O	18:R:1009:LEU:HB2	1.70	0.91
15:O:46:TYR:CE1	15:O:104:SER:C	2.52	0.88
15:O:46:TYR:CD1	15:O:104:SER:C	2.52	0.87
18:R:1119:GLY:H	18:R:1122:VAL:HG23	1.41	0.86
1:A:310:PRO:HA	1:A:393:VAL:O	1.78	0.82
9:I:815:ILE:O	9:I:825:SER:HA	1.83	0.79
15:O:104:SER:C	15:O:105:ALA:N	2.41	0.79
3:C:48:GLU:H	3:C:61:ASN:H	1.29	0.78
9:I:553:GLN:NE2	9:I:658:MET:SD	2.55	0.76
11:K:72:ILE:HG22	11:K:73:THR:HG23	1.67	0.76
11:K:789:GLY:HA2	11:K:819:LEU:HB2	1.68	0.75
11:K:616:LEU:HD22	11:K:679:LEU:HD11	1.70	0.74
9:I:1342:GLN:HA	9:I:1374:LEU:H	1.53	0.74
4:D:127:ARG:H	16:P:4:ARG:H	1.33	0.74
9:I:319:LEU:HA	9:I:322:ILE:HD12	1.70	0.74
18:R:571:LEU:HD13	18:R:1093:ARG:HD2	1.70	0.73
18:R:975:LEU:HD21	18:R:1019:ARG:HB2	1.71	0.73
11:K:557:ASN:ND2	11:K:590:GLU:O	2.22	0.73
12:L:331:SER:HB2	12:L:339:LEU:HD21	1.71	0.73
18:R:1016:LEU:O	18:R:1020:ASP:N	2.21	0.73
18:R:1182:GLU:HB3	18:R:1184:VAL:HG23	1.71	0.72
15:O:46:TYR:CD2	15:O:104:SER:O	2.42	0.72
13:M:73:ARG:HH22	13:M:131:ALA:H	1.36	0.72
19:S:141:ARG:NH1	19:S:155:GLU:OE2	2.23	0.71
24:X:63:ILE:HG13	24:X:64:PRO:HD3	1.71	0.71
14:N:78:THR:HG22	14:N:80:SER:H	1.56	0.70
1:A:104:THR:O	1:A:106:ASP:N	2.22	0.70
19:S:94:VAL:HG23	19:S:157:GLN:HE22	1.55	0.70
19:S:68:ILE:HA	19:S:71:GLN:HB2	1.73	0.70
11:K:89:ALA:HB2	11:K:118:PRO:HG3	1.74	0.69
18:R:953:PRO:HB2	18:R:954:ILE:HD12	1.75	0.69
9:I:554:TYR:HB2	9:I:577:MET:HB2	1.74	0.69
11:K:772:LEU:N	11:K:791:VAL:O	2.25	0.69
12:L:446:ILE:HD11	25:Y:164:ARG:HH22	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:46:TYR:CE1	15:O:104:SER:CA	2.75	0.69
18:R:911:HIS:O	18:R:914:GLN:NE2	2.26	0.68
18:R:532:THR:O	18:R:573:TYR:OH	2.09	0.68
18:R:664:GLN:HG3	18:R:668:PHE:HE2	1.58	0.68
18:R:1311:LYS:NZ	18:R:1332:ILE:O	2.27	0.68
18:R:1037:ASN:HB3	18:R:1039:PRO:HD3	1.75	0.68
15:O:46:TYR:CD1	15:O:104:SER:HA	2.29	0.68
11:K:492:GLU:O	11:K:495:HIS:ND1	2.24	0.68
18:R:1291:MET:SD	18:R:1328:ARG:NH1	2.67	0.68
9:I:666:GLU:OE2	9:I:767:LYS:N	2.27	0.67
11:K:523:LEU:HD11	11:K:746:PRO:HA	1.74	0.67
18:R:308:VAL:O	18:R:311:ALA:HB3	1.93	0.67
11:K:384:ARG:HG3	11:K:385:LEU:HG	1.76	0.67
18:R:374:TRP:O	18:R:378:GLN:NE2	2.28	0.66
13:M:146:TYR:O	13:M:167:TYR:HA	1.95	0.66
18:R:154:SER:HA	19:S:915:ALA:HB2	1.77	0.66
18:R:123:ARG:O	18:R:123:ARG:NH2	2.28	0.66
18:R:977:LEU:HD21	18:R:980:VAL:HB	1.77	0.66
18:R:1064:GLU:O	18:R:1068:TYR:N	2.24	0.66
18:R:1147:ASN:OD1	18:R:1218:HIS:NE2	2.26	0.66
9:I:1217:GLY:HA3	9:I:1298:PRO:HG2	1.77	0.66
9:I:333:GLU:HA	9:I:343:LEU:HA	1.77	0.66
15:O:46:TYR:CE2	15:O:104:SER:O	2.48	0.66
19:S:587:LEU:O	19:S:592:ASN:N	2.27	0.66
23:W:101:GLN:NE2	25:Y:109:ILE:O	2.29	0.66
18:R:145:ILE:HD13	18:R:201:LEU:HD21	1.78	0.65
18:R:281:ASP:O	18:R:285:ASN:ND2	2.29	0.65
3:C:47:ASN:HA	3:C:59:HIS:H	1.59	0.65
11:K:757:LEU:HG	11:K:758:THR:H	1.62	0.65
18:R:135:ARG:HA	18:R:138:LEU:HD13	1.77	0.65
11:K:360:SER:HG	11:K:365:TYR:HH	1.38	0.65
18:R:810:VAL:O	18:R:813:ARG:NH2	2.26	0.65
18:R:1120:LYS:O	18:R:1124:ASN:ND2	2.28	0.65
24:X:131:ASP:O	24:X:135:HIS:ND1	2.29	0.65
11:K:169:ALA:O	11:K:178:VAL:N	2.28	0.65
10:J:652:GLY:O	10:J:654:PRO:HD3	1.96	0.65
19:S:49:GLN:NE2	19:S:55:SER:O	2.29	0.65
22:V:58:ASP:O	22:V:61:HIS:HB2	1.95	0.65
1:A:381:PRO:HA	1:A:387:SER:HA	1.79	0.65
18:R:1322:LYS:H	18:R:1325:LEU:HD12	1.62	0.65
11:K:232:VAL:HB	11:K:243:ILE:HD11	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:292:LEU:HG	22:V:294:PRO:HD3	1.79	0.64
15:O:127:GLY:O	15:O:136:ARG:HA	1.98	0.64
26:Z:29:ALA:HB3	26:Z:69:TYR:HA	1.79	0.64
19:S:523:PHE:O	19:S:527:MET:N	2.30	0.64
18:R:1169:VAL:O	18:R:1173:SER:OG	2.16	0.64
25:Y:47:ARG:HH21	25:Y:81:HIS:HA	1.62	0.64
11:K:272:LYS:HZ1	11:K:343:ALA:H	1.45	0.64
18:R:122:VAL:HA	18:R:125:ILE:HG22	1.79	0.64
18:R:71:HIS:HA	18:R:111:ARG:HH22	1.63	0.64
18:R:191:TYR:HD2	18:R:194:GLY:H	1.45	0.64
18:R:1023:LYS:HA	18:R:1026:LEU:HB2	1.79	0.64
19:S:118:ILE:O	19:S:121:CYS:HB2	1.97	0.64
11:K:176:VAL:HG22	11:K:177:THR:HG22	1.80	0.64
9:I:788:GLU:O	10:J:663:ARG:NH2	2.30	0.63
18:R:922:MET:HA	18:R:925:HIS:CE1	2.32	0.63
18:R:1031:ILE:HG21	18:R:1049:LEU:HD11	1.80	0.63
22:V:280:PRO:HD2	22:V:299:PHE:HA	1.80	0.63
18:R:690:THR:HA	18:R:693:ARG:HD3	1.80	0.63
19:S:534:GLU:HG3	19:S:536:LYS:H	1.63	0.63
11:K:489:SER:O	11:K:492:GLU:HB3	1.99	0.63
9:I:310:GLN:HE22	9:I:376:LEU:HD11	1.63	0.63
12:L:257:VAL:O	12:L:365:HIS:ND1	2.32	0.63
19:S:282:VAL:HA	19:S:285:ILE:HG12	1.81	0.63
18:R:921:HIS:O	18:R:925:HIS:ND1	2.30	0.62
12:L:272:VAL:HG22	12:L:274:LEU:H	1.64	0.62
18:R:355:SER:O	18:R:359:LYS:N	2.32	0.62
18:R:674:THR:HG23	18:R:675:VAL:HG22	1.80	0.62
11:K:652:TRP:O	11:K:656:LYS:N	2.29	0.62
15:O:46:TYR:CD2	15:O:105:ALA:CA	2.82	0.62
19:S:832:LYS:O	19:S:835:ARG:NH1	2.31	0.62
11:K:788:CYS:HA	11:K:820:TRP:HA	1.79	0.62
11:K:481:HIS:ND1	11:K:482:VAL:O	2.30	0.62
19:S:196:LEU:HD13	19:S:222:ILE:HD11	1.82	0.62
18:R:142:LEU:HD13	18:R:145:ILE:HD12	1.80	0.62
18:R:260:LYS:HA	18:R:263:PHE:HB2	1.81	0.62
18:R:819:LEU:HD22	18:R:864:ARG:HH21	1.64	0.61
11:K:814:CYS:HB3	11:K:817:GLY:HA3	1.81	0.61
18:R:521:THR:HB	18:R:562:ALA:HB3	1.81	0.61
18:R:650:LEU:HD22	18:R:961:LEU:HG	1.82	0.61
8:H:87:ARG:HG3	8:H:91:GLN:HE21	1.65	0.61
11:K:352:THR:N	11:K:467:TYR:HH	1.97	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:192:TRP:HB3	12:L:195:ARG:HH21	1.64	0.61
22:V:49:GLU:O	22:V:52:PHE:HB3	2.00	0.61
11:K:23:LEU:HD22	11:K:37:THR:HA	1.82	0.61
18:R:616:GLN:HE22	18:R:618:HIS:HB3	1.65	0.61
11:K:261:ARG:HG2	11:K:263:ASP:H	1.65	0.60
11:K:789:GLY:HA3	11:K:817:GLY:HA2	1.81	0.60
9:I:902:ARG:NH1	9:I:1301:ALA:O	2.34	0.60
11:K:524:SER:O	11:K:530:ARG:N	2.33	0.60
18:R:681:GLU:HA	18:R:684:ASN:HD22	1.65	0.60
18:R:770:MET:HA	18:R:773:GLU:HG2	1.83	0.60
22:V:178:ILE:HG22	22:V:192:VAL:HG23	1.84	0.60
1:A:56:GLN:N	2:B:52:ARG:O	2.35	0.60
11:K:514:LEU:HD22	11:K:542:ALA:HB2	1.83	0.60
11:K:814:CYS:SG	11:K:815:LEU:N	2.75	0.60
15:O:186:PRO:O	15:O:189:THR:OG1	2.19	0.60
18:R:257:PRO:O	19:S:755:ARG:NH2	2.35	0.60
18:R:1075:LEU:O	18:R:1078:THR:OG1	2.18	0.60
23:W:74:ARG:HA	23:W:77:VAL:HG12	1.81	0.60
12:L:332:GLN:HE22	12:L:337:LEU:H	1.49	0.60
18:R:161:LEU:HD11	18:R:164:ARG:HE	1.65	0.60
11:K:458:LEU:HD22	11:K:490:LEU:HD21	1.84	0.60
18:R:156:VAL:HG12	18:R:160:LEU:HB2	1.83	0.60
18:R:615:ILE:O	18:R:620:ARG:NH1	2.35	0.60
19:S:358:ASP:O	19:S:362:PHE:CB	2.49	0.60
18:R:458:LEU:HD12	18:R:459:GLN:HG2	1.84	0.60
18:R:857:TYR:OH	18:R:930:GLU:N	2.34	0.60
19:S:243:THR:HG22	19:S:764:GLN:HB3	1.83	0.60
1:A:338:PRO:HA	1:A:389:GLN:HA	1.82	0.59
18:R:45:ARG:HA	18:R:48:TRP:CD1	2.36	0.59
18:R:380:ILE:HG21	18:R:428:ILE:HD13	1.85	0.59
18:R:819:LEU:HD11	18:R:860:VAL:HA	1.83	0.59
18:R:1212:ALA:C	18:R:1216:TRP:HD1	2.10	0.59
9:I:405:LYS:HA	9:I:408:ILE:HD12	1.84	0.59
10:J:631:ARG:HE	10:J:639:LEU:HD21	1.66	0.59
11:K:676:LEU:O	11:K:680:LEU:HG	2.01	0.59
25:Y:169:ASP:O	25:Y:173:MET:HG2	2.02	0.59
1:A:339:LEU:N	1:A:388:LEU:O	2.32	0.59
18:R:399:PHE:O	18:R:403:TYR:N	2.33	0.59
9:I:510:ARG:NH2	9:I:641:CYS:O	2.36	0.59
18:R:819:LEU:HA	18:R:822:HIS:HB2	1.82	0.59
19:S:723:ASP:O	19:S:726:SER:N	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:35:PHE:HB2	11:K:51:HIS:HB2	1.84	0.59
15:O:46:TYR:CE2	15:O:105:ALA:CA	2.85	0.59
19:S:169:LEU:HA	19:S:174:ASN:HD21	1.67	0.59
22:V:198:LEU:HA	22:V:216:GLY:HA2	1.84	0.59
9:I:334:ARG:NH1	9:I:335:TYR:O	2.36	0.59
11:K:594:ASP:O	11:K:597:THR:OG1	2.21	0.59
15:O:46:TYR:HA	15:O:107:ALA:HB3	1.85	0.59
18:R:613:HIS:H	18:R:1094:PHE:HE1	1.50	0.59
18:R:1143:THR:HA	18:R:1146:MET:HG2	1.84	0.59
20:T:82:VAL:HG11	20:T:120:THR:HG21	1.85	0.58
6:F:98:GLY:O	6:F:103:ILE:N	2.33	0.58
9:I:511:CYS:HB3	9:I:643:PHE:HZ	1.67	0.58
18:R:616:GLN:OE1	18:R:619:TYR:N	2.34	0.58
18:R:726:ASN:HD22	18:R:747:ASN:HA	1.68	0.58
18:R:1302:LYS:NZ	18:R:1307:GLY:O	2.30	0.58
9:I:515:ILE:O	9:I:520:THR:OG1	2.22	0.58
15:O:46:TYR:CD1	15:O:104:SER:CA	2.86	0.58
18:R:785:PHE:HB3	18:R:788:LEU:HD13	1.84	0.58
9:I:543:LYS:N	9:I:555:TYR:O	2.36	0.58
9:I:943:ARG:HH12	9:I:949:LEU:HA	1.67	0.58
11:K:123:SER:OG	11:K:166:GLY:O	2.21	0.58
18:R:787:PRO:HD2	18:R:788:LEU:HD12	1.85	0.58
11:K:421:MET:HG2	11:K:433:ILE:HG22	1.86	0.58
18:R:686:ALA:O	18:R:690:THR:HG23	2.03	0.58
18:R:685:ARG:HH12	18:R:726:ASN:H	1.52	0.58
18:R:225:CYS:HG	18:R:1143:THR:HG1	1.51	0.58
18:R:719:ILE:HB	18:R:724:PRO:HB3	1.86	0.58
18:R:1203:MET:O	18:R:1206:SER:OG	2.19	0.58
9:I:775:ASP:O	9:I:779:ILE:HG12	2.04	0.58
10:J:749:PHE:O	10:J:753:VAL:HG23	2.04	0.58
11:K:17:TYR:HB2	19:S:905:LEU:HD11	1.86	0.58
12:L:207:TYR:HB3	12:L:211:GLY:HA3	1.84	0.58
12:L:379:GLU:OE2	12:L:383:GLN:NE2	2.37	0.58
18:R:871:MET:HB3	18:R:872:ARG:HD3	1.86	0.58
22:V:180:LEU:HB3	22:V:190:LEU:HD13	1.85	0.58
11:K:96:TRP:CE2	11:K:104:ASN:HA	2.39	0.57
12:L:332:GLN:NE2	12:L:334:PHE:O	2.37	0.57
9:I:741:SER:OG	9:I:807:ARG:NH2	2.32	0.57
3:C:48:GLU:N	3:C:61:ASN:H	2.01	0.57
18:R:119:PHE:HA	18:R:122:VAL:HG22	1.87	0.57
18:R:651:ARG:HH21	18:R:961:LEU:HD22	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:23:GLU:OE1	20:T:71:PHE:HB3	2.05	0.57
18:R:350:PRO:O	18:R:354:LEU:N	2.30	0.57
8:H:84:TYR:OH	12:L:191:HIS:O	2.22	0.57
18:R:972:HIS:HD2	18:R:1008:THR:HA	1.69	0.57
19:S:588:ASN:O	19:S:594:VAL:N	2.38	0.57
19:S:674:ASP:OD2	19:S:696:TRP:NE1	2.33	0.57
19:S:338:PHE:HA	19:S:341:LEU:HD12	1.87	0.57
9:I:896:MET:HE3	24:X:125:CYS:HA	1.87	0.57
19:S:703:ARG:HH11	19:S:704:PRO:HD2	1.68	0.57
19:S:731:ASP:OD1	19:S:829:ARG:NH1	2.38	0.57
19:S:250:LEU:HD12	19:S:727:ILE:HG23	1.86	0.56
9:I:553:GLN:HA	9:I:577:MET:O	2.05	0.56
9:I:740:THR:HG22	9:I:741:SER:H	1.71	0.56
11:K:85:LEU:HD22	11:K:91:GLY:HA3	1.86	0.56
4:D:124:ASN:N	16:P:5:LEU:H	2.03	0.56
18:R:537:MET:SD	18:R:537:MET:N	2.75	0.56
12:L:427:GLU:OE2	12:L:469:TYR:OH	2.24	0.56
9:I:676:GLY:O	9:I:678:GLN:NE2	2.37	0.56
19:S:761:ARG:O	19:S:765:LEU:HG	2.05	0.56
12:L:615:HIS:O	12:L:617:ARG:NH2	2.38	0.56
18:R:272:TYR:O	18:R:276:GLN:NE2	2.38	0.56
9:I:1222:ARG:NH2	9:I:1256:VAL:O	2.39	0.56
18:R:109:TRP:HH2	18:R:149:PRO:HD2	1.71	0.56
18:R:1158:GLU:HA	18:R:1161:TRP:CE2	2.40	0.56
12:L:638:GLU:HG2	23:W:100:LEU:HD21	1.87	0.56
18:R:1216:TRP:CZ3	18:R:1227:ILE:HG13	2.40	0.56
11:K:643:ARG:NH2	11:K:684:TRP:HB2	2.21	0.55
11:K:737:LEU:HD23	11:K:739:PHE:H	1.70	0.55
11:K:74:CYS:HA	11:K:84:LEU:HB3	1.89	0.55
15:O:4:THR:H	15:O:184:TYR:HB3	1.71	0.55
18:R:1019:ARG:HH12	18:R:1023:LYS:HE2	1.71	0.55
18:R:1009:LEU:HA	18:R:1012:TYR:HB2	1.88	0.55
19:S:358:ASP:O	19:S:362:PHE:HB2	2.06	0.55
19:S:500:HIS:HA	19:S:668:LEU:HD11	1.87	0.55
11:K:176:VAL:HG13	11:K:177:THR:H	1.70	0.55
18:R:427:CYS:O	18:R:431:HIS:ND1	2.39	0.55
19:S:138:SER:O	19:S:141:ARG:NH1	2.27	0.55
19:S:164:CYS:O	19:S:168:THR:HG23	2.06	0.55
12:L:258:SER:OG	12:L:365:HIS:ND1	2.38	0.55
19:S:712:ILE:HG21	19:S:730:LEU:HD21	1.89	0.55
18:R:613:HIS:HB3	18:R:1094:PHE:HD1	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:868:CYS:HA	18:R:871:MET:HG2	1.86	0.55
18:R:158:GLN:NE2	19:S:956:VAL:O	2.38	0.55
20:T:61:TYR:OH	20:T:131:MET:SD	2.54	0.55
12:L:364:ASP:N	12:L:367:TYR:HB3	2.22	0.55
19:S:122:ARG:O	19:S:125:LEU:HB3	2.06	0.55
18:R:115:TRP:HH2	18:R:144:LYS:HB3	1.72	0.55
18:R:1061:TRP:CE2	18:R:1115:LEU:HB2	2.41	0.55
9:I:948:SER:OG	24:X:106:GLU:OE1	2.23	0.54
18:R:790:LEU:H	18:R:822:HIS:CD2	2.26	0.54
18:R:1246:LEU:HD21	18:R:1294:ILE:HD11	1.89	0.54
1:A:503:SER:O	1:A:507:THR:N	2.35	0.54
9:I:317:GLN:NE2	9:I:403:ILE:H	2.05	0.54
11:K:5:TYR:HA	11:K:752:LEU:HD13	1.89	0.54
11:K:737:LEU:HB3	11:K:739:PHE:CE2	2.43	0.54
9:I:796:ILE:HG21	9:I:875:LEU:HD21	1.89	0.54
10:J:683:VAL:HA	10:J:686:LEU:HD23	1.90	0.54
18:R:185:THR:HA	18:R:188:ARG:HD3	1.89	0.54
18:R:113:GLN:O	18:R:117:LEU:HG	2.08	0.54
18:R:613:HIS:CD2	18:R:1000:ARG:HH21	2.26	0.54
18:R:617:PRO:O	18:R:620:ARG:HG2	2.07	0.54
18:R:1130:VAL:HG21	18:R:1211:LEU:HD21	1.89	0.54
18:R:1288:LEU:HB3	18:R:1291:MET:HB3	1.89	0.54
19:S:765:LEU:O	19:S:769:ILE:HG13	2.08	0.54
9:I:689:ARG:HD3	10:J:685:ARG:HD3	1.88	0.54
18:R:521:THR:HG21	18:R:563:LEU:HD22	1.90	0.54
20:T:185:PRO:HG2	20:T:187:LYS:HZ1	1.72	0.54
9:I:313:VAL:HG13	9:I:400:HIS:HE1	1.73	0.54
9:I:859:HIS:O	9:I:862:GLN:HG3	2.07	0.54
18:R:1200:TYR:HA	19:S:347:LEU:HD21	1.88	0.54
9:I:959:PHE:CZ	24:X:117:LEU:HD21	2.42	0.54
11:K:222:SER:H	11:K:265:PHE:HA	1.73	0.53
12:L:502:VAL:HB	12:L:510:ILE:HD11	1.89	0.53
4:D:121:HIS:HA	16:P:5:LEU:HA	1.91	0.53
8:H:88:LYS:O	8:H:92:MET:HG2	2.07	0.53
9:I:415:ALA:HB1	9:I:462:VAL:HG21	1.90	0.53
11:K:215:VAL:HB	11:K:229:PHE:HB3	1.90	0.53
18:R:685:ARG:HH11	18:R:727:TRP:NE1	2.06	0.53
18:R:1266:CYS:O	18:R:1269:GLU:HB2	2.07	0.53
19:S:243:THR:OG1	19:S:244:ILE:N	2.41	0.53
11:K:632:PHE:HD2	11:K:634:ARG:H	1.56	0.53
18:R:717:GLN:O	18:R:721:ASN:ND2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:600:ALA:O	11:K:605:LEU:N	2.25	0.53
18:R:331:TRP:CH2	18:R:371:HIS:HB3	2.43	0.53
8:H:46:ASP:O	8:H:49:ALA:HB3	2.08	0.53
19:S:280:LEU:HD23	19:S:283:LEU:HD12	1.91	0.53
19:S:311:LEU:HD13	19:S:455:ALA:O	2.08	0.53
19:S:385:ARG:HH22	19:S:389:ARG:HH22	1.55	0.53
3:C:47:ASN:HA	3:C:59:HIS:N	2.23	0.53
10:J:694:LEU:HA	10:J:706:HIS:CE1	2.43	0.53
18:R:543:ILE:H	18:R:543:ILE:HD12	1.73	0.53
19:S:119:GLY:HA2	19:S:122:ARG:HH11	1.73	0.53
18:R:766:LYS:HG2	18:R:770:MET:HE3	1.90	0.53
18:R:1177:LEU:H	18:R:1181:THR:HG23	1.73	0.53
18:R:1314:VAL:O	18:R:1318:ILE:HG12	2.09	0.53
19:S:286:TRP:HA	19:S:289:CYS:SG	2.49	0.53
18:R:135:ARG:O	18:R:138:LEU:HB2	2.07	0.53
18:R:152:VAL:HG13	18:R:153:SER:H	1.73	0.53
18:R:1153:ILE:HG23	18:R:1161:TRP:HB3	1.91	0.53
11:K:27:TRP:HB2	11:K:32:LEU:HA	1.92	0.52
18:R:1189:ARG:NH1	19:S:239:THR:O	2.42	0.52
18:R:1279:LEU:HD21	18:R:1317:ILE:HG12	1.90	0.52
19:S:179:HIS:O	19:S:183:LEU:HG	2.09	0.52
9:I:359:SER:O	9:I:414:ARG:NH2	2.42	0.52
11:K:601:LEU:HA	11:K:605:LEU:HB2	1.91	0.52
18:R:570:LEU:HD22	18:R:573:TYR:HD2	1.74	0.52
18:R:1121:ASP:HA	18:R:1124:ASN:HD22	1.74	0.52
20:T:117:GLY:O	20:T:120:THR:OG1	2.16	0.52
10:J:740:ARG:HB2	10:J:744:TYR:CD2	2.44	0.52
11:K:615:LEU:HD13	11:K:633:LEU:HD21	1.91	0.52
18:R:756:LEU:HA	18:R:759:ASN:HD21	1.74	0.52
11:K:13:ALA:O	11:K:40:ARG:N	2.38	0.52
17:Q:98:ILE:O	17:Q:102:ASN:ND2	2.36	0.52
18:R:570:LEU:HB3	18:R:573:TYR:HB2	1.92	0.52
18:R:1168:ILE:HG13	18:R:1169:VAL:HG13	1.91	0.52
18:R:1327:LEU:O	18:R:1330:ARG:NH1	2.42	0.52
19:S:724:SER:HA	19:S:727:ILE:HB	1.91	0.52
19:S:945:MET:N	19:S:946:PRO:HD2	2.24	0.52
10:J:760:ARG:HH11	10:J:779:GLN:HE22	1.57	0.52
18:R:849:ILE:O	18:R:853:MET:HB2	2.09	0.52
11:K:600:ALA:HB1	11:K:604:LEU:HB2	1.92	0.52
19:S:785:ILE:O	19:S:789:LEU:N	2.34	0.52
22:V:96:PRO:HG2	22:V:106:GLN:HE22	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:337:ASP:HA	11:K:374:PHE:HE1	1.75	0.52
11:K:613:LEU:HD13	11:K:734:PRO:HD2	1.92	0.52
12:L:431:LYS:NZ	12:L:468:VAL:O	2.43	0.52
1:A:262:THR:H	1:A:301:ALA:HA	1.75	0.52
4:D:123:ILE:C	16:P:4:ARG:HA	2.34	0.52
9:I:863:GLU:HA	9:I:866:ASN:HD22	1.74	0.52
9:I:896:MET:HE2	24:X:128:GLN:OE1	2.09	0.52
10:J:627:LEU:HD11	24:X:82:ILE:HB	1.92	0.52
10:J:631:ARG:HH21	10:J:639:LEU:HG	1.75	0.52
15:O:143:GLU:N	15:O:143:GLU:OE1	2.43	0.52
18:R:963:PHE:HB3	18:R:994:LEU:HD13	1.92	0.52
9:I:1258:LEU:O	9:I:1262:THR:N	2.40	0.52
11:K:7:CYS:SG	11:K:8:GLU:N	2.83	0.52
11:K:272:LYS:NZ	11:K:344:LEU:H	2.08	0.52
11:K:730:GLN:H	11:K:733:GLN:NE2	2.08	0.52
15:O:154:TRP:HA	15:O:157:LEU:HB3	1.92	0.52
18:R:229:PRO:HG3	18:R:1151:LEU:HD21	1.92	0.52
18:R:672:PRO:HB3	18:R:676:LEU:HD12	1.91	0.52
11:K:613:LEU:HA	11:K:616:LEU:HG	1.92	0.51
12:L:192:TRP:CD1	12:L:193:LYS:H	2.28	0.51
12:L:204:ASP:HB3	12:L:220:PHE:HB3	1.91	0.51
3:C:48:GLU:H	3:C:60:LEU:H	1.58	0.51
9:I:462:VAL:HA	9:I:469:PHE:HB2	1.91	0.51
9:I:919:HIS:HA	9:I:933:TYR:HB3	1.92	0.51
11:K:47:THR:HG23	11:K:70:GLU:HA	1.91	0.51
18:R:1061:TRP:CD2	18:R:1115:LEU:HD22	2.45	0.51
18:R:1184:VAL:HG22	19:S:340:PHE:CD2	2.44	0.51
1:A:104:THR:C	1:A:106:ASP:H	2.13	0.51
8:H:63:LEU:O	8:H:67:ILE:N	2.41	0.51
11:K:92:GLN:NE2	11:K:111:GLY:H	2.09	0.51
11:K:635:ASP:CG	11:K:637:THR:HG1	2.18	0.51
15:O:165:LEU:HD21	15:O:169:ALA:HB2	1.92	0.51
18:R:685:ARG:NH1	18:R:726:ASN:H	2.08	0.51
18:R:1005:LEU:HB3	18:R:1113:MET:HE3	1.91	0.51
18:R:1126:LEU:HD13	18:R:1149:ILE:HG23	1.93	0.51
10:J:768:HIS:H	10:J:772:ALA:HB3	1.75	0.51
18:R:866:ILE:HD12	18:R:966:VAL:HG13	1.93	0.51
9:I:1224:HIS:O	9:I:1228:ILE:HG12	2.11	0.51
13:M:32:LEU:O	13:M:36:ILE:HG12	2.10	0.51
18:R:241:TRP:HA	18:R:1258:ARG:HH12	1.75	0.51
18:R:857:TYR:H	18:R:936:GLY:HA3	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:1329:LEU:HB3	18:R:1332:ILE:HB	1.93	0.51
19:S:182:LYS:NZ	19:S:226:PRO:O	2.44	0.51
11:K:47:THR:OG1	11:K:48:HIS:N	2.44	0.51
19:S:130:TRP:HA	19:S:133:ARG:HG3	1.92	0.51
19:S:385:ARG:HH22	19:S:389:ARG:HH12	1.58	0.51
24:X:83:GLN:O	24:X:87:ILE:HG12	2.11	0.51
9:I:917:SER:OG	9:I:918:THR:N	2.43	0.51
9:I:901:GLN:O	9:I:902:ARG:NH2	2.44	0.51
18:R:1268:ILE:HG22	18:R:1310:VAL:HB	1.93	0.51
20:T:70:VAL:HG13	20:T:83:GLN:HG2	1.92	0.51
18:R:202:GLY:HA2	19:S:920:GLN:HE22	1.76	0.51
18:R:1051:HIS:HD2	18:R:1060:PRO:HA	1.76	0.51
18:R:1205:CYS:HB2	18:R:1247:TYR:CE2	2.46	0.51
9:I:505:TRP:HA	9:I:508:GLN:HE21	1.77	0.50
9:I:649:HIS:NE2	12:L:556:GLY:HA3	2.26	0.50
9:I:812:ARG:HA	9:I:828:ILE:O	2.10	0.50
11:K:612:VAL:O	11:K:616:LEU:HG	2.11	0.50
11:K:773:HIS:CE1	11:K:774:LEU:HD22	2.45	0.50
18:R:622:GLN:O	18:R:626:HIS:ND1	2.25	0.50
18:R:1259:PHE:O	18:R:1263:ARG:N	2.44	0.50
19:S:117:CYS:O	19:S:120:LEU:HB3	2.11	0.50
11:K:748:SER:OG	11:K:749:THR:N	2.45	0.50
11:K:786:THR:N	11:K:794:LEU:O	2.44	0.50
18:R:301:GLU:O	18:R:304:LEU:HG	2.12	0.50
24:X:59:TYR:HD1	24:X:115:LEU:HD11	1.75	0.50
9:I:345:VAL:HG22	9:I:346:TRP:H	1.76	0.50
10:J:718:SER:OG	10:J:719:VAL:N	2.41	0.50
11:K:805:GLN:H	11:K:805:GLN:CD	2.18	0.50
18:R:807:GLY:O	18:R:811:LEU:N	2.44	0.50
18:R:866:ILE:HG22	18:R:962:ARG:NH1	2.27	0.50
19:S:160:LEU:O	19:S:163:GLN:HG2	2.11	0.50
18:R:173:ARG:O	18:R:177:LEU:N	2.45	0.50
18:R:447:ILE:HG21	20:T:64:THR:HG21	1.93	0.50
22:V:290:ASP:OD1	22:V:301:THR:N	2.42	0.50
9:I:335:TYR:HB2	9:I:341:LEU:HA	1.93	0.50
9:I:948:SER:OG	9:I:948:SER:O	2.29	0.50
12:L:371:HIS:O	12:L:375:LEU:HG	2.12	0.50
18:R:1047:THR:O	18:R:1050:LYS:HG3	2.12	0.50
18:R:754:PHE:HA	18:R:757:LYS:HE2	1.92	0.50
19:S:755:ARG:O	19:S:759:THR:HG23	2.12	0.50
11:K:643:ARG:HH21	11:K:680:LEU:C	2.20	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:373:MET:O	18:R:377:LEU:HD23	2.10	0.50
18:R:732:LEU:HD21	18:R:740:GLN:HE21	1.77	0.50
18:R:1128:ASN:O	18:R:1132:LYS:N	2.44	0.50
11:K:236:VAL:HG11	11:K:242:ARG:HB2	1.94	0.50
13:M:18:MET:HA	13:M:176:PRO:HA	1.93	0.50
13:M:32:LEU:HD22	13:M:167:TYR:HE2	1.77	0.50
18:R:804:SER:O	18:R:805:GLN:HG3	2.12	0.50
4:D:124:ASN:H	16:P:5:LEU:H	1.58	0.50
11:K:269:THR:HA	11:K:281:GLN:HA	1.93	0.50
12:L:287:PRO:HB2	12:L:290:GLN:HB2	1.93	0.50
12:L:462:TRP:HA	12:L:473:VAL:HG22	1.93	0.50
18:R:620:ARG:HD2	18:R:656:LEU:HB3	1.94	0.50
18:R:967:PHE:HA	18:R:970:VAL:HG12	1.94	0.50
18:R:1014:MET:SD	18:R:1014:MET:N	2.84	0.50
9:I:861:LEU:HD13	9:I:874:LEU:HD11	1.93	0.49
18:R:141:ILE:HG21	18:R:167:ILE:HD11	1.93	0.49
18:R:1071:LEU:HD11	18:R:1108:THR:HG22	1.95	0.49
18:R:1164:LEU:HA	18:R:1167:ARG:HB2	1.94	0.49
19:S:283:LEU:HD21	19:S:337:ALA:HA	1.93	0.49
20:T:68:LEU:H	20:T:86:ALA:HB3	1.77	0.49
11:K:198:ARG:NE	11:K:199:GLY:H	2.10	0.49
19:S:603:ILE:C	19:S:642:ARG:HH11	2.19	0.49
26:Z:25:VAL:HA	26:Z:69:TYR:O	2.12	0.49
9:I:1225:LEU:O	9:I:1229:ILE:HG12	2.12	0.49
11:K:53:LEU:HD22	11:K:61:VAL:HG22	1.95	0.49
11:K:301:LYS:HD2	11:K:325:LEU:HG	1.94	0.49
18:R:833:GLU:HB3	18:R:843:LEU:HD13	1.94	0.49
18:R:844:ASN:O	18:R:848:GLU:HG2	2.12	0.49
11:K:488:GLN:HE21	11:K:530:ARG:HH12	1.59	0.49
19:S:280:LEU:HA	19:S:283:LEU:HD12	1.95	0.49
18:R:685:ARG:HH11	18:R:727:TRP:HE1	1.61	0.49
18:R:1036:ASP:OD1	18:R:1036:ASP:N	2.46	0.49
18:R:1278:LEU:HA	18:R:1281:VAL:HG22	1.93	0.49
9:I:718:LEU:HD21	9:I:722:ASN:HA	1.93	0.49
18:R:754:PHE:HB3	18:R:758:LYS:HE3	1.94	0.49
18:R:831:VAL:HG11	18:R:873:SER:HB3	1.93	0.49
24:X:55:PRO:HA	24:X:58:ARG:HE	1.78	0.49
9:I:496:ILE:N	9:I:497:PRO:HD2	2.27	0.49
15:O:46:TYR:CE1	15:O:104:SER:HA	2.48	0.49
18:R:81:ASP:O	18:R:85:MET:HG2	2.12	0.49
11:K:383:HIS:CD2	11:K:386:SER:HB3	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:1198:GLN:HB3	19:S:721:TRP:CE3	2.48	0.49
20:T:176:ARG:HG3	20:T:178:ILE:H	1.77	0.49
22:V:200:VAL:HG22	22:V:214:VAL:HG23	1.94	0.49
13:M:145:VAL:HA	13:M:168:LEU:O	2.12	0.49
18:R:1024:ARG:NH2	18:R:1057:GLU:OE1	2.45	0.49
18:R:1149:ILE:HA	18:R:1152:ILE:HG12	1.95	0.49
18:R:1182:GLU:CD	18:R:1183:TRP:H	2.20	0.49
11:K:441:MET:SD	11:K:441:MET:N	2.84	0.49
11:K:647:VAL:O	11:K:651:ILE:HG13	2.12	0.49
18:R:613:HIS:HB3	18:R:1094:PHE:CD1	2.48	0.49
18:R:1241:THR:HG23	18:R:1244:GLN:H	1.78	0.49
9:I:826:ILE:HA	9:I:841:LEU:HA	1.95	0.48
11:K:120:VAL:HG12	11:K:122:LEU:HG	1.95	0.48
11:K:222:SER:N	11:K:266:PRO:HD2	2.27	0.48
12:L:289:TRP:CE2	12:L:290:GLN:HG2	2.48	0.48
18:R:786:PRO:HB2	18:R:787:PRO:HD3	1.95	0.48
18:R:1117:VAL:N	18:R:1118:PRO:HD2	2.27	0.48
11:K:676:LEU:O	11:K:679:LEU:HG	2.14	0.48
12:L:537:GLN:O	23:W:89:ARG:NH2	2.46	0.48
18:R:875:GLU:O	18:R:879:ALA:N	2.46	0.48
18:R:1168:ILE:HG13	18:R:1169:VAL:N	2.27	0.48
19:S:500:HIS:HB2	19:S:668:LEU:HD21	1.96	0.48
9:I:526:LEU:N	9:I:542:ASN:HD21	2.10	0.48
10:J:635:PHE:CE2	10:J:637:HIS:HB3	2.48	0.48
18:R:351:HIS:O	18:R:355:SER:N	2.42	0.48
18:R:799:GLU:HG2	18:R:802:HIS:HB2	1.95	0.48
18:R:891:LEU:HD22	18:R:987:LEU:HD12	1.95	0.48
19:S:297:PRO:HG2	19:S:354:ARG:HH21	1.78	0.48
22:V:109:GLN:HE22	23:W:65:VAL:H	1.62	0.48
11:K:168:ILE:HD11	11:K:181:LEU:HB3	1.96	0.48
12:L:373:LEU:HD23	12:L:376:LEU:HD21	1.95	0.48
18:R:449:HIS:HA	18:R:452:LYS:HB3	1.94	0.48
19:S:426:HIS:CD2	19:S:426:HIS:H	2.32	0.48
9:I:797:PRO:HA	9:I:803:PHE:CD1	2.49	0.48
11:K:101:HIS:NE2	11:K:820:TRP:HB2	2.27	0.48
11:K:209:THR:HA	11:K:275:ALA:HB3	1.95	0.48
18:R:999:ASP:OD1	18:R:999:ASP:N	2.47	0.48
22:V:269:TRP:HE1	22:V:294:PRO:HA	1.79	0.48
24:X:59:TYR:O	24:X:63:ILE:HG12	2.13	0.48
9:I:878:LEU:HA	9:I:881:THR:HG22	1.95	0.48
12:L:367:TYR:HB2	25:Y:173:MET:SD	2.53	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:646:MET:HA	11:K:649:ILE:HG12	1.96	0.48
13:M:57:VAL:O	13:M:126:ASP:N	2.44	0.48
18:R:354:LEU:O	18:R:358:GLN:N	2.35	0.48
18:R:725:HIS:CE1	18:R:735:PHE:HE2	2.31	0.48
18:R:972:HIS:CD2	18:R:1008:THR:HA	2.47	0.48
18:R:1247:TYR:O	18:R:1251:LEU:HG	2.13	0.48
19:S:412:GLU:HG2	19:S:413:PRO:HD3	1.96	0.48
4:D:112:LEU:O	4:D:116:PHE:N	2.41	0.48
11:K:648:VAL:HA	11:K:651:ILE:HD12	1.96	0.48
1:A:304:PHE:HA	1:A:397:THR:HA	1.96	0.48
18:R:72:SER:O	18:R:76:ILE:HG12	2.14	0.48
18:R:109:TRP:CH2	18:R:149:PRO:HD2	2.48	0.48
9:I:899:LEU:HD12	9:I:900:THR:H	1.77	0.48
10:J:703:GLY:O	10:J:705:VAL:HG12	2.14	0.48
11:K:491:VAL:O	11:K:494:LEU:HB3	2.14	0.48
18:R:732:LEU:HD11	18:R:740:GLN:NE2	2.28	0.48
18:R:1023:LYS:NZ	18:R:1026:LEU:HB3	2.29	0.48
23:W:139:TRP:HA	23:W:142:VAL:HG22	1.94	0.48
10:J:640:TYR:O	10:J:644:VAL:HG22	2.14	0.47
12:L:635:TYR:HB3	12:L:638:GLU:HB3	1.96	0.47
15:O:46:TYR:CD2	15:O:105:ALA:HA	2.49	0.47
18:R:226:SER:O	18:R:1147:ASN:ND2	2.47	0.47
18:R:377:LEU:HA	18:R:380:ILE:HG22	1.96	0.47
19:S:603:ILE:O	19:S:642:ARG:NH1	2.46	0.47
19:S:607:ILE:CB	19:S:642:ARG:HH12	2.27	0.47
22:V:106:GLN:CD	22:V:106:GLN:H	2.21	0.47
18:R:449:HIS:CD2	18:R:452:LYS:HD2	2.49	0.47
19:S:245:HIS:HA	19:S:288:ALA:HB2	1.97	0.47
19:S:623:VAL:HA	19:S:676:LEU:HD11	1.96	0.47
1:A:382:LEU:N	1:A:386:GLN:O	2.37	0.47
3:C:48:GLU:N	3:C:60:LEU:H	2.12	0.47
9:I:699:ILE:O	9:I:703:THR:OG1	2.25	0.47
11:K:206:ILE:HD12	11:K:271:LEU:HG	1.95	0.47
11:K:444:ILE:HG13	11:K:445:SER:H	1.78	0.47
18:R:834:PHE:HE2	18:R:885:ILE:HD11	1.78	0.47
18:R:1205:CYS:HB2	18:R:1247:TYR:HE2	1.79	0.47
18:R:1329:LEU:HD22	18:R:1332:ILE:HG13	1.96	0.47
9:I:691:LEU:HB2	10:J:685:ARG:HH22	1.80	0.47
11:K:540:LEU:HA	11:K:543:ILE:HG22	1.96	0.47
12:L:630:GLY:HA2	12:L:635:TYR:HD2	1.78	0.47
18:R:855:TRP:HE1	18:R:893:PRO:HB3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:PHE:H	1:A:295:ASN:HA	1.79	0.47
10:J:637:HIS:CE1	11:K:777:TYR:H	2.33	0.47
18:R:255:LEU:O	18:R:257:PRO:HD3	2.13	0.47
18:R:855:TRP:NE1	18:R:893:PRO:HB3	2.30	0.47
18:R:907:ASN:HB3	18:R:996:LYS:NZ	2.29	0.47
18:R:958:ASN:OD1	18:R:959:VAL:N	2.48	0.47
19:S:782:LEU:HA	19:S:786:LEU:HG	1.96	0.47
20:T:148:SER:O	20:T:150:PRO:HD3	2.15	0.47
8:H:92:MET:O	8:H:96:ARG:HG3	2.14	0.47
18:R:755:ASN:O	18:R:759:ASN:ND2	2.48	0.47
18:R:1064:GLU:HB3	18:R:1068:TYR:CZ	2.49	0.47
9:I:325:ARG:NH2	12:L:325:VAL:O	2.41	0.47
9:I:553:GLN:HG2	9:I:576:PHE:CZ	2.50	0.47
9:I:1197:PRO:HA	9:I:1214:ARG:CZ	2.45	0.47
13:M:45:ASN:HA	13:M:137:ARG:NE	2.30	0.47
18:R:553:THR:OG1	18:R:554:LYS:N	2.47	0.47
18:R:951:TYR:CE2	18:R:953:PRO:HB3	2.50	0.47
18:R:1068:TYR:O	18:R:1071:LEU:HB3	2.14	0.47
19:S:358:ASP:O	19:S:362:PHE:HB3	2.15	0.47
19:S:363:LEU:HD21	19:S:386:THR:HG21	1.96	0.47
19:S:817:SER:O	19:S:820:SER:OG	2.30	0.47
24:X:107:GLU:O	24:X:111:LEU:HG	2.15	0.47
8:H:87:ARG:HG3	8:H:91:GLN:NE2	2.29	0.47
11:K:540:LEU:O	11:K:544:THR:HG23	2.15	0.47
13:M:50:THR:OG1	13:M:51:PHE:N	2.48	0.47
18:R:80:TYR:CD1	18:R:121:LEU:HD22	2.50	0.47
19:S:220:THR:HA	19:S:223:ARG:HG2	1.96	0.47
19:S:698:LEU:HB2	19:S:729:ILE:HD11	1.97	0.47
19:S:721:TRP:HD1	19:S:723:ASP:H	1.63	0.47
9:I:858:LEU:O	9:I:861:LEU:HG	2.15	0.47
11:K:191:THR:OG1	11:K:192:GLU:N	2.45	0.47
11:K:200:ARG:NH2	19:S:737:GLY:O	2.47	0.47
12:L:332:GLN:NE2	12:L:337:LEU:H	2.13	0.47
18:R:377:LEU:HD21	18:R:428:ILE:HB	1.97	0.47
12:L:257:VAL:HG23	12:L:365:HIS:HA	1.97	0.47
12:L:371:HIS:CE1	12:L:375:LEU:HD11	2.50	0.47
18:R:520:VAL:HG21	18:R:559:LEU:O	2.15	0.47
18:R:606:GLU:O	18:R:610:HIS:ND1	2.28	0.47
18:R:682:GLU:CD	18:R:682:GLU:H	2.23	0.47
18:R:738:PRO:HA	18:R:740:GLN:NE2	2.29	0.47
18:R:1314:VAL:HA	18:R:1317:ILE:HG22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:816:LEU:HD21	19:S:934:GLU:HA	1.97	0.47
23:W:134:THR:N	23:W:137:ARG:HH11	2.13	0.47
1:A:367:LEU:N	1:A:370:GLN:O	2.47	0.46
10:J:652:GLY:N	10:J:653:PRO:HD3	2.30	0.46
18:R:718:THR:OG1	18:R:719:ILE:N	2.48	0.46
18:R:1115:LEU:HD23	18:R:1117:VAL:HG22	1.97	0.46
18:R:1270:ILE:O	18:R:1273:ALA:HB3	2.15	0.46
11:K:168:ILE:HD11	11:K:181:LEU:HD22	1.97	0.46
11:K:337:ASP:HA	11:K:374:PHE:CE1	2.51	0.46
11:K:632:PHE:O	11:K:634:ARG:NH2	2.46	0.46
11:K:673:MET:HA	11:K:676:LEU:HD12	1.98	0.46
18:R:1014:MET:O	18:R:1017:ARG:NH1	2.39	0.46
22:V:96:PRO:HG2	22:V:106:GLN:NE2	2.30	0.46
22:V:292:LEU:O	22:V:294:PRO:HD3	2.16	0.46
10:J:674:SER:OG	12:L:608:LEU:O	2.33	0.46
18:R:53:GLN:O	18:R:56:HIS:HB3	2.15	0.46
18:R:641:LEU:N	18:R:933:TYR:OH	2.48	0.46
18:R:1062:VAL:HB	18:R:1063:PRO:HD3	1.97	0.46
18:R:1076:VAL:HG11	18:R:1145:TRP:CD1	2.51	0.46
18:R:1130:VAL:HG21	18:R:1211:LEU:HD11	1.98	0.46
19:S:696:TRP:CG	19:S:697:ASN:H	2.33	0.46
9:I:649:HIS:CE1	12:L:559:GLU:HA	2.51	0.46
11:K:206:ILE:HB	11:K:271:LEU:HD21	1.97	0.46
18:R:136:ASP:OD1	18:R:137:LEU:N	2.48	0.46
19:S:97:LEU:HD23	19:S:98:LEU:HD23	1.97	0.46
19:S:161:CYS:HA	19:S:164:CYS:SG	2.56	0.46
19:S:176:ALA:O	19:S:180:ILE:HG13	2.15	0.46
19:S:638:LEU:O	19:S:642:ARG:HB3	2.15	0.46
12:L:392:HIS:O	12:L:392:HIS:ND1	2.49	0.46
19:S:85:PHE:O	19:S:89:SER:N	2.41	0.46
19:S:185:GLU:OE2	19:S:188:SER:OG	2.31	0.46
12:L:446:ILE:HD11	25:Y:164:ARG:NH2	2.28	0.46
18:R:60:VAL:O	18:R:63:ILE:HB	2.16	0.46
1:A:165:GLY:HA3	1:A:170:LYS:N	2.31	0.46
12:L:437:PHE:CE2	12:L:496:GLY:HA2	2.50	0.46
12:L:532:VAL:HA	12:L:535:VAL:HG12	1.98	0.46
12:L:636:LYS:O	12:L:639:LEU:HG	2.16	0.46
18:R:617:PRO:HB2	18:R:660:GLU:HG2	1.97	0.46
18:R:738:PRO:HA	18:R:740:GLN:HE22	1.79	0.46
18:R:1249:TYR:HE1	18:R:1274:PHE:CG	2.34	0.46
19:S:473:THR:HB	19:S:491:PHE:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:632:SER:N	10:J:633:PRO:HD2	2.31	0.46
18:R:79:LEU:HA	18:R:82:CYS:SG	2.56	0.46
18:R:816:ALA:O	18:R:820:VAL:HG13	2.15	0.46
24:X:55:PRO:HA	24:X:58:ARG:NE	2.31	0.46
9:I:825:SER:O	9:I:842:GLY:N	2.49	0.46
11:K:441:MET:O	11:K:442:LEU:HD23	2.16	0.46
11:K:643:ARG:HA	11:K:646:MET:HG2	1.98	0.46
11:K:649:ILE:HA	11:K:652:TRP:HD1	1.80	0.46
18:R:1257:GLN:O	18:R:1261:GLN:HG2	2.16	0.46
19:S:722:VAL:O	19:S:726:SER:OG	2.33	0.46
9:I:321:LEU:HG	9:I:325:ARG:HB2	1.98	0.46
9:I:709:ARG:HH22	10:J:670:ASP:HA	1.81	0.46
12:L:306:PHE:O	12:L:309:LEU:HG	2.16	0.46
18:R:152:VAL:HG13	18:R:153:SER:N	2.31	0.46
18:R:213:ARG:HD3	19:S:755:ARG:HH11	1.80	0.46
18:R:527:LEU:HD23	18:R:529:ASP:H	1.80	0.46
11:K:459:GLN:O	11:K:462:LEU:HG	2.16	0.45
12:L:313:ALA:O	12:L:322:HIS:NE2	2.47	0.45
18:R:166:VAL:O	18:R:170:ILE:HG12	2.16	0.45
18:R:182:PHE:HA	18:R:185:THR:HG22	1.96	0.45
8:H:62:GLU:O	8:H:66:GLN:N	2.46	0.45
9:I:310:GLN:HE21	9:I:400:HIS:HB3	1.80	0.45
12:L:380:PHE:O	12:L:384:THR:HG23	2.15	0.45
18:R:773:GLU:O	18:R:777:ILE:N	2.40	0.45
18:R:844:ASN:HA	18:R:847:ILE:HD12	1.97	0.45
22:V:273:TYR:CZ	22:V:293:PRO:HD2	2.51	0.45
1:A:306:LYS:HA	1:A:395:LYS:HA	1.97	0.45
9:I:299:TYR:OH	9:I:372:VAL:O	2.34	0.45
9:I:345:VAL:HG12	9:I:361:HIS:H	1.81	0.45
11:K:286:ALA:HB3	11:K:290:THR:CB	2.47	0.45
11:K:613:LEU:HD11	11:K:733:GLN:HA	1.97	0.45
11:K:723:ASP:O	11:K:727:SER:OG	2.28	0.45
18:R:765:ARG:HH12	18:R:769:SER:HB3	1.80	0.45
18:R:981:SER:O	18:R:984:LEU:HG	2.16	0.45
18:R:1012:TYR:HB3	18:R:1016:LEU:HD13	1.97	0.45
18:R:1088:PRO:HB3	18:R:1097:PHE:CZ	2.52	0.45
19:S:175:ARG:O	19:S:178:LEU:HG	2.16	0.45
19:S:311:LEU:O	19:S:314:PRO:HD2	2.15	0.45
17:Q:120:ARG:O	17:Q:124:SER:OG	2.27	0.45
18:R:298:PRO:HG2	18:R:300:LEU:HG	1.99	0.45
18:R:964:LEU:HD13	18:R:994:LEU:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:1065:ASP:OD1	18:R:1066:SER:N	2.44	0.45
23:W:89:ARG:O	23:W:92:GLU:HG2	2.16	0.45
1:A:103:ILE:HA	1:A:108:PHE:HA	1.98	0.45
9:I:815:ILE:O	9:I:825:SER:CA	2.60	0.45
12:L:594:PHE:HD2	12:L:617:ARG:HB2	1.80	0.45
18:R:571:LEU:HD21	18:R:1094:PHE:CE2	2.52	0.45
18:R:1263:ARG:HD2	18:R:1265:ARG:CZ	2.47	0.45
22:V:290:ASP:HB3	22:V:300:ARG:HA	1.98	0.45
24:X:104:CYS:O	24:X:107:GLU:HG3	2.17	0.45
9:I:707:LEU:HD21	9:I:776:TRP:HZ2	1.81	0.45
9:I:803:PHE:HD2	23:W:33:ALA:HB3	1.82	0.45
11:K:96:TRP:O	11:K:98:MET:N	2.50	0.45
11:K:730:GLN:H	11:K:733:GLN:HE22	1.64	0.45
15:O:38:THR:HA	15:O:115:THR:HA	1.99	0.45
18:R:754:PHE:O	18:R:758:LYS:HG3	2.17	0.45
18:R:1158:GLU:HA	18:R:1161:TRP:NE1	2.31	0.45
19:S:426:HIS:CG	19:S:427:SER:H	2.35	0.45
11:K:119:ILE:HG13	11:K:120:VAL:HG23	1.97	0.45
18:R:655:ALA:HB2	18:R:1000:ARG:CZ	2.47	0.45
18:R:1130:VAL:HG11	18:R:1211:LEU:HD11	1.98	0.45
19:S:279:PRO:O	19:S:283:LEU:HG	2.17	0.45
23:W:79:GLN:HG2	23:W:82:GLN:HE21	1.81	0.45
12:L:506:ASP:OD1	12:L:506:ASP:N	2.49	0.45
18:R:945:VAL:HG12	18:R:947:ILE:HG12	1.99	0.45
18:R:1051:HIS:CD2	18:R:1060:PRO:HA	2.51	0.45
19:S:539:ASN:O	19:S:543:PRO:HD2	2.17	0.45
22:V:197:VAL:HB	22:V:217:TYR:HA	1.98	0.45
9:I:796:ILE:HD11	9:I:876:GLN:HE22	1.82	0.45
11:K:127:ASN:ND2	11:K:152:PHE:H	2.15	0.45
11:K:297:TRP:CE2	11:K:329:ILE:HG22	2.52	0.45
18:R:975:LEU:HD11	18:R:1019:ARG:HD3	1.99	0.45
18:R:1024:ARG:NE	18:R:1057:GLU:HB3	2.32	0.45
19:S:169:LEU:HD12	19:S:218:CYS:HB3	1.98	0.45
19:S:642:ARG:O	19:S:642:ARG:NH2	2.41	0.45
12:L:325:VAL:HG12	12:L:326:LYS:N	2.32	0.45
12:L:411:PHE:HB3	12:L:415:GLU:H	1.82	0.45
12:L:493:LEU:HD12	12:L:493:LEU:O	2.17	0.45
13:M:44:ASP:O	13:M:137:ARG:HG3	2.17	0.45
18:R:66:PHE:HZ	18:R:75:ARG:HH21	1.64	0.45
18:R:1260:GLN:HE22	18:R:1305:PHE:C	2.24	0.45
19:S:94:VAL:O	19:S:98:LEU:HG	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:763:VAL:HG11	19:S:806:ALA:HB1	1.99	0.45
11:K:124:TRP:HB2	11:K:208:PHE:CE2	2.52	0.44
18:R:374:TRP:CG	18:R:378:GLN:HE22	2.35	0.44
18:R:549:LYS:HE3	18:R:549:LYS:HB3	1.87	0.44
18:R:584:PHE:CZ	18:R:588:LEU:HD11	2.51	0.44
18:R:1064:GLU:O	18:R:1067:TYR:HB3	2.17	0.44
18:R:1216:TRP:HZ3	18:R:1227:ILE:HG13	1.81	0.44
9:I:805:GLU:HA	9:I:815:ILE:HA	2.00	0.44
10:J:651:HIS:C	10:J:653:PRO:HD3	2.43	0.44
10:J:706:HIS:O	10:J:706:HIS:ND1	2.49	0.44
11:K:47:THR:N	11:K:70:GLU:H	2.15	0.44
11:K:510:SER:HA	11:K:513:ILE:HG22	1.98	0.44
12:L:272:VAL:HG21	12:L:344:CYS:SG	2.58	0.44
18:R:587:GLN:C	18:R:590:PRO:HD2	2.42	0.44
18:R:1321:LEU:HB3	18:R:1325:LEU:HB2	1.98	0.44
11:K:547:LEU:HD13	11:K:806:TRP:HZ2	1.83	0.44
13:M:32:LEU:HD22	13:M:167:TYR:CE2	2.52	0.44
14:N:87:TYR:HE2	14:N:89:LEU:HD13	1.82	0.44
19:S:75:CYS:HA	19:S:78:VAL:HG12	1.99	0.44
3:C:37:SER:HA	3:C:38:ASN:HA	1.67	0.44
9:I:649:HIS:CE1	12:L:556:GLY:HA3	2.52	0.44
18:R:790:LEU:HD13	18:R:822:HIS:HB3	1.98	0.44
18:R:1167:ARG:HA	18:R:1167:ARG:HD3	1.68	0.44
18:R:1275:TYR:CE1	18:R:1298:LEU:HD11	2.52	0.44
18:R:1294:ILE:HD12	18:R:1294:ILE:H	1.82	0.44
18:R:1302:LYS:HA	18:R:1306:THR:HG1	1.82	0.44
19:S:808:ALA:O	19:S:812:VAL:HG22	2.18	0.44
9:I:714:CYS:SG	9:I:715:THR:N	2.90	0.44
12:L:472:SER:HA	12:L:492:GLN:O	2.18	0.44
13:M:37:HIS:HA	13:M:40:ARG:HG2	1.99	0.44
17:Q:124:SER:O	17:Q:127:LEU:HG	2.18	0.44
18:R:156:VAL:HG13	18:R:159:GLN:HB3	1.99	0.44
18:R:305:VAL:O	18:R:309:VAL:N	2.43	0.44
18:R:603:THR:HG23	18:R:951:TYR:CG	2.53	0.44
19:S:311:LEU:C	19:S:314:PRO:HD2	2.43	0.44
10:J:776:THR:O	10:J:779:GLN:HG3	2.17	0.44
11:K:276:ARG:O	11:K:299:LEU:HB2	2.17	0.44
12:L:221:GLU:HA	12:L:235:PRO:HG2	1.99	0.44
18:R:693:ARG:NH2	18:R:1003:THR:OG1	2.49	0.44
18:R:1019:ARG:NH1	18:R:1023:LYS:HE2	2.33	0.44
18:R:1074:ARG:O	18:R:1078:THR:HG23	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:707:LEU:O	9:I:711:LEU:N	2.51	0.44
9:I:1227:ARG:O	9:I:1231:GLN:HB2	2.18	0.44
10:J:637:HIS:O	10:J:640:TYR:HB3	2.18	0.44
10:J:726:VAL:HB	10:J:727:PRO:HD2	2.00	0.44
11:K:598:LEU:H	11:K:598:LEU:HD23	1.82	0.44
18:R:480:ALA:HB1	18:R:491:PRO:HB3	1.98	0.44
18:R:1231:LEU:HA	18:R:1235:LEU:HD23	2.00	0.44
18:R:1241:THR:HG21	18:R:1243:PHE:CZ	2.52	0.44
19:S:174:ASN:HA	19:S:177:LEU:HD12	2.00	0.44
24:X:115:LEU:HA	24:X:118:CYS:SG	2.58	0.44
9:I:314:LEU:HD13	9:I:400:HIS:NE2	2.33	0.44
12:L:329:ILE:HG13	12:L:341:ILE:HG13	1.99	0.44
18:R:202:GLY:HA2	19:S:920:GLN:NE2	2.32	0.44
18:R:581:ILE:HA	18:R:584:PHE:HB3	1.98	0.44
19:S:218:CYS:O	19:S:222:ILE:HG12	2.18	0.44
9:I:277:ILE:HG23	9:I:281:HIS:HB2	2.00	0.44
11:K:126:HIS:ND1	11:K:127:ASN:O	2.39	0.44
11:K:496:GLU:O	11:K:500:ARG:N	2.50	0.44
13:M:136:PHE:CD2	13:M:144:VAL:HA	2.53	0.44
18:R:171:LEU:HD12	18:R:208:PHE:CZ	2.53	0.44
18:R:536:LYS:HB3	18:R:573:TYR:CE1	2.53	0.44
18:R:714:ASP:N	18:R:714:ASP:OD1	2.49	0.44
22:V:120:HIS:ND1	23:W:59:LEU:HD21	2.33	0.44
9:I:345:VAL:CG1	9:I:361:HIS:H	2.31	0.43
9:I:942:ILE:O	9:I:1177:SER:HA	2.18	0.43
11:K:124:TRP:NE1	11:K:126:HIS:O	2.51	0.43
18:R:696:HIS:HD2	18:R:1010:HIS:CE1	2.36	0.43
18:R:890:LEU:HD11	18:R:987:LEU:HD11	2.00	0.43
18:R:1145:TRP:O	18:R:1149:ILE:HG13	2.18	0.43
18:R:1228:PRO:HG3	18:R:1270:ILE:HD11	1.99	0.43
19:S:521:PRO:HG2	19:S:523:PHE:CD2	2.53	0.43
19:S:642:ARG:HH21	19:S:642:ARG:C	2.25	0.43
9:I:505:TRP:HA	9:I:508:GLN:NE2	2.33	0.43
11:K:25:CYS:HB3	11:K:35:PHE:H	1.83	0.43
11:K:226:PRO:HB3	19:S:534:GLU:CD	2.44	0.43
11:K:271:LEU:HD12	11:K:278:MET:O	2.16	0.43
11:K:637:THR:O	11:K:641:MET:HG3	2.18	0.43
11:K:807:GLU:O	11:K:811:ILE:HG12	2.18	0.43
18:R:416:LYS:N	18:R:417:PRO:HD2	2.33	0.43
9:I:934:CYS:HA	9:I:940:VAL:HA	1.99	0.43
11:K:92:GLN:HE21	11:K:111:GLY:H	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:1004:TYR:O	18:R:1008:THR:OG1	2.33	0.43
18:R:1198:GLN:HE21	18:R:1201:SER:HB3	1.83	0.43
19:S:275:HIS:CE1	19:S:277:PRO:HG3	2.52	0.43
9:I:691:LEU:HD21	10:J:678:VAL:HG12	2.01	0.43
9:I:803:PHE:CE2	23:W:34:PRO:HG3	2.52	0.43
11:K:523:LEU:HD12	11:K:523:LEU:HA	1.77	0.43
18:R:259:ASP:O	18:R:261:ASP:N	2.51	0.43
18:R:581:ILE:HD12	18:R:581:ILE:H	1.82	0.43
12:L:437:PHE:HE2	12:L:496:GLY:HA2	1.83	0.43
12:L:483:GLU:N	22:V:134:LYS:O	2.47	0.43
9:I:740:THR:HG22	9:I:741:SER:N	2.32	0.43
11:K:176:VAL:HG13	11:K:177:THR:N	2.33	0.43
11:K:643:ARG:O	11:K:646:MET:HG2	2.18	0.43
13:M:21:TYR:HA	13:M:101:LEU:H	1.83	0.43
18:R:732:LEU:HD11	18:R:740:GLN:HE21	1.84	0.43
22:V:81:SER:O	22:V:81:SER:OG	2.29	0.43
14:N:84:ILE:H	14:N:84:ILE:HD12	1.84	0.43
18:R:696:HIS:HB3	18:R:1006:TYR:CE1	2.54	0.43
18:R:1061:TRP:NE1	18:R:1115:LEU:HB2	2.33	0.43
18:R:1279:LEU:HD11	18:R:1317:ILE:HD11	2.01	0.43
19:S:738:GLY:N	19:S:741:TRP:HE1	2.17	0.43
9:I:448:ILE:HG13	9:I:503:LYS:HD3	2.01	0.43
9:I:902:ARG:HA	9:I:902:ARG:HD3	1.79	0.43
18:R:867:LEU:HD12	18:R:868:CYS:N	2.34	0.43
18:R:1072:ILE:O	18:R:1076:VAL:HG13	2.19	0.43
18:R:1177:LEU:HG	18:R:1243:PHE:HE1	1.83	0.43
11:K:155:SER:C	11:K:156:LEU:HD23	2.43	0.43
11:K:370:LEU:HG	11:K:382:VAL:O	2.19	0.43
13:M:45:ASN:HA	13:M:137:ARG:HE	1.83	0.43
13:M:130:VAL:O	13:M:149:PHE:N	2.46	0.43
18:R:527:LEU:HD23	18:R:528:LEU:N	2.34	0.43
18:R:696:HIS:NE2	18:R:734:CYS:O	2.52	0.43
18:R:1165:HIS:O	18:R:1169:VAL:HG22	2.18	0.43
19:S:309:THR:O	19:S:313:ILE:HG12	2.18	0.43
19:S:582:ALA:HB3	19:S:621:TRP:HE1	1.84	0.43
9:I:664:ARG:HD2	9:I:675:GLN:HB2	2.01	0.43
18:R:429:TRP:HZ2	18:R:446:PRO:O	2.02	0.43
18:R:682:GLU:HB2	18:R:867:LEU:HD22	2.01	0.43
18:R:985:GLU:O	18:R:988:LEU:HG	2.19	0.43
18:R:1074:ARG:NH2	18:R:1107:VAL:HG21	2.34	0.43
9:I:653:MET:HE2	9:I:653:MET:HB2	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:915:GLN:HE22	9:I:919:HIS:CG	2.37	0.42
9:I:1297:PRO:O	9:I:1299:PHE:N	2.52	0.42
11:K:435:ASN:ND2	11:K:437:GLY:O	2.52	0.42
18:R:618:HIS:O	18:R:622:GLN:HG2	2.18	0.42
18:R:1090:CYS:N	18:R:1091:ASP:HA	2.33	0.42
19:S:245:HIS:NE2	19:S:291:VAL:HG11	2.34	0.42
23:W:115:VAL:O	23:W:119:ARG:HG2	2.19	0.42
11:K:272:LYS:NZ	11:K:343:ALA:H	2.14	0.42
12:L:474:LYS:HE2	12:L:474:LYS:HB3	1.88	0.42
12:L:577:ALA:HB3	12:L:594:PHE:CZ	2.54	0.42
18:R:928:TYR:HB3	18:R:929:PRO:HD3	2.01	0.42
18:R:1189:ARG:CZ	19:S:240:GLY:HA2	2.49	0.42
9:I:534:HIS:N	9:I:535:PRO:HD2	2.34	0.42
12:L:216:HIS:HD2	12:L:300:LEU:HD11	1.83	0.42
18:R:674:THR:HG23	18:R:675:VAL:N	2.34	0.42
18:R:1191:PHE:HE2	18:R:1243:PHE:HB2	1.84	0.42
19:S:903:PHE:HB3	19:S:946:PRO:HG3	2.01	0.42
11:K:92:GLN:HB2	11:K:109:SER:O	2.20	0.42
12:L:182:ASN:HA	12:L:185:LEU:HD12	2.01	0.42
12:L:366:LEU:O	12:L:369:LEU:HG	2.19	0.42
18:R:756:LEU:O	18:R:760:VAL:HG22	2.18	0.42
18:R:1262:GLU:CD	18:R:1263:ARG:HE	2.26	0.42
18:R:1273:ALA:O	18:R:1277:MET:HG2	2.20	0.42
22:V:292:LEU:C	22:V:294:PRO:HD3	2.43	0.42
11:K:631:SER:OG	11:K:632:PHE:N	2.52	0.42
12:L:339:LEU:O	12:L:339:LEU:HD12	2.19	0.42
18:R:138:LEU:HD21	18:R:170:ILE:HG21	2.02	0.42
18:R:697:VAL:HG22	18:R:1006:TYR:CD2	2.55	0.42
19:S:804:GLY:HA2	19:S:807:LEU:HG	2.00	0.42
9:I:914:PRO:HA	9:I:920:ILE:HA	2.01	0.42
11:K:201:VAL:HG12	11:K:218:ALA:H	1.85	0.42
18:R:664:GLN:HG3	18:R:668:PHE:CE2	2.47	0.42
19:S:484:ALA:HA	19:S:487:ARG:HE	1.85	0.42
19:S:760:LEU:HA	19:S:763:VAL:HG12	2.02	0.42
20:T:205:GLU:HB2	20:T:206:PRO:HD3	2.01	0.42
9:I:321:LEU:HD21	9:I:326:TRP:CE3	2.55	0.42
11:K:203:LEU:HD22	11:K:218:ALA:HB3	2.02	0.42
19:S:189:TRP:CZ2	19:S:226:PRO:HG3	2.55	0.42
19:S:732:THR:HG23	19:S:735:HIS:HE1	1.83	0.42
23:W:48:LEU:HD12	23:W:49:GLU:N	2.34	0.42
11:K:522:LYS:HD3	11:K:535:HIS:ND1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:33:GLU:CD	13:M:33:GLU:H	2.27	0.42
18:R:617:PRO:HA	18:R:620:ARG:HE	1.84	0.42
18:R:758:LYS:O	18:R:762:GLU:HG2	2.20	0.42
18:R:859:ILE:HD12	18:R:859:ILE:H	1.83	0.42
18:R:918:HIS:HA	18:R:921:HIS:CD2	2.55	0.42
20:T:147:ASN:O	20:T:187:LYS:NZ	2.40	0.42
25:Y:56:ARG:NH2	25:Y:57:ASN:HB3	2.35	0.42
9:I:293:LYS:HD2	9:I:293:LYS:HA	1.82	0.42
9:I:308:SER:O	9:I:311:LEU:HG	2.19	0.42
9:I:314:LEU:O	9:I:318:THR:HG23	2.20	0.42
11:K:217:ALA:HB2	11:K:230:TYR:CE2	2.54	0.42
11:K:533:ASP:N	11:K:533:ASP:OD1	2.51	0.42
18:R:869:LEU:HD21	18:R:882:CYS:HB3	2.00	0.42
18:R:1120:LYS:HA	18:R:1163:VAL:HG11	2.02	0.42
18:R:1165:HIS:HB3	18:R:1230:PHE:CE1	2.55	0.42
18:R:1260:GLN:HB2	18:R:1267:MET:HE2	2.00	0.42
19:S:283:LEU:HD21	19:S:340:PHE:HB3	2.02	0.42
11:K:606:GLN:HA	11:K:663:TYR:CZ	2.55	0.42
18:R:205:VAL:O	18:R:209:VAL:HG22	2.20	0.42
18:R:283:VAL:HA	18:R:286:MET:HB2	2.02	0.42
18:R:643:LEU:O	18:R:646:GLU:HB2	2.20	0.42
18:R:1061:TRP:HE1	18:R:1114:ALA:HB3	1.85	0.42
19:S:802:PRO:N	19:S:803:PRO:HD2	2.35	0.42
9:I:704:GLN:NE2	9:I:708:ASP:OD2	2.53	0.41
9:I:1184:HIS:CG	9:I:1185:SER:H	2.38	0.41
11:K:368:LEU:HA	11:K:384:ARG:CZ	2.50	0.41
11:K:391:ALA:HB3	11:K:393:PHE:CZ	2.55	0.41
12:L:529:GLN:O	12:L:532:VAL:HG12	2.20	0.41
12:L:580:VAL:HA	12:L:591:MET:HA	2.01	0.41
18:R:163:ALA:O	18:R:167:ILE:HG12	2.20	0.41
18:R:280:ARG:NH2	18:R:575:GLU:OE2	2.53	0.41
18:R:455:HIS:CD2	18:R:456:GLU:HG2	2.55	0.41
18:R:577:GLU:O	18:R:581:ILE:HD12	2.20	0.41
18:R:692:ALA:O	18:R:696:HIS:ND1	2.36	0.41
18:R:857:TYR:N	18:R:936:GLY:HA3	2.35	0.41
18:R:1024:ARG:HE	18:R:1057:GLU:HB3	1.85	0.41
18:R:1302:LYS:HZ3	18:R:1310:VAL:HG12	1.84	0.41
18:R:1324:ALA:O	18:R:1328:ARG:HG2	2.20	0.41
19:S:721:TRP:HD1	19:S:723:ASP:N	2.18	0.41
24:X:166:GLN:HG3	25:Y:61:PRO:HD2	2.02	0.41
1:A:364:TYR:HA	1:A:373:CYS:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:719:GLN:HA	12:L:548:SER:O	2.20	0.41
11:K:35:PHE:CE1	11:K:433:ILE:HD13	2.55	0.41
11:K:119:ILE:HD12	11:K:204:ALA:HA	2.01	0.41
11:K:232:VAL:HG12	11:K:244:ASP:O	2.20	0.41
15:O:35:LYS:HA	15:O:117:TYR:CE1	2.55	0.41
18:R:521:THR:OG1	18:R:560:ALA:O	2.37	0.41
18:R:828:ASP:HA	18:R:831:VAL:HG22	2.02	0.41
18:R:1066:SER:O	18:R:1069:CYS:HB3	2.20	0.41
19:S:131:LEU:HD13	19:S:165:LEU:HG	2.01	0.41
19:S:269:MET:HE3	19:S:269:MET:HB3	1.88	0.41
19:S:288:ALA:O	19:S:291:VAL:HG12	2.20	0.41
19:S:623:VAL:HA	19:S:626:VAL:HG12	2.02	0.41
4:D:127:ARG:H	16:P:4:ARG:N	2.10	0.41
9:I:864:MET:HE3	9:I:864:MET:HB3	1.93	0.41
11:K:608:VAL:O	11:K:612:VAL:HG13	2.21	0.41
12:L:298:ASN:O	12:L:301:LEU:HG	2.21	0.41
12:L:436:ILE:HD12	12:L:436:ILE:HA	1.95	0.41
12:L:523:LEU:HA	12:L:526:GLN:HG2	2.01	0.41
18:R:22:PHE:O	18:R:24:GLY:N	2.49	0.41
18:R:377:LEU:HG	18:R:424:ALA:HB1	2.01	0.41
18:R:656:LEU:HD23	18:R:656:LEU:H	1.84	0.41
19:S:278:THR:O	19:S:282:VAL:HG22	2.19	0.41
19:S:385:ARG:NH2	19:S:389:ARG:HH22	2.17	0.41
19:S:940:SER:O	19:S:944:PHE:HB2	2.20	0.41
23:W:99:ARG:HH12	25:Y:35:ARG:HH11	1.67	0.41
9:I:496:ILE:HD12	9:I:499:ILE:HB	2.02	0.41
10:J:640:TYR:CE1	10:J:644:VAL:HG21	2.55	0.41
11:K:233:CYS:O	11:K:243:ILE:HD12	2.21	0.41
18:R:713:LYS:O	18:R:717:GLN:N	2.40	0.41
18:R:862:LEU:HD11	18:R:959:VAL:HG23	2.02	0.41
18:R:954:ILE:CG2	18:R:957:GLY:H	2.32	0.41
18:R:1005:LEU:HD12	18:R:1113:MET:SD	2.61	0.41
18:R:1227:ILE:HD13	18:R:1227:ILE:HA	1.91	0.41
18:R:1297:PHE:HA	18:R:1300:HIS:HD1	1.86	0.41
19:S:83:SER:O	19:S:83:SER:OG	2.32	0.41
3:C:47:ASN:N	3:C:62:GLN:H	2.19	0.41
10:J:630:ILE:O	10:J:632:SER:N	2.49	0.41
11:K:72:ILE:HD12	11:K:72:ILE:H	1.86	0.41
14:N:87:TYR:CE2	14:N:89:LEU:HD13	2.55	0.41
18:R:374:TRP:HH2	18:R:534:HIS:HB2	1.86	0.41
18:R:429:TRP:NE1	18:R:448:PRO:HB3	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:240:GLY:C	19:S:242:PRO:HD3	2.45	0.41
19:S:311:LEU:HB2	19:S:455:ALA:HA	2.02	0.41
19:S:385:ARG:HH22	19:S:389:ARG:NH2	2.18	0.41
24:X:82:ILE:HG13	24:X:86:ASN:HD21	1.86	0.41
1:A:73:SER:N	1:A:76:ALA:HB3	2.35	0.41
4:D:125:GLU:H	16:P:5:LEU:CB	2.32	0.41
11:K:498:TYR:CD1	11:K:513:ILE:HG21	2.55	0.41
18:R:646:GLU:O	18:R:649:ALA:HB3	2.20	0.41
18:R:667:ARG:O	18:R:667:ARG:NE	2.54	0.41
18:R:880:GLN:H	18:R:880:GLN:CD	2.29	0.41
19:S:79:LEU:HA	19:S:82:ILE:HG22	2.02	0.41
23:W:143:LEU:HA	23:W:143:LEU:HD23	1.86	0.41
1:A:462:LEU:O	19:S:51:MET:HE2	2.21	0.41
3:C:47:ASN:H	3:C:62:GLN:H	1.68	0.41
3:C:54:ARG:C	3:C:56:THR:H	2.28	0.41
9:I:715:THR:O	9:I:728:ALA:HA	2.21	0.41
18:R:1148:ALA:O	18:R:1152:ILE:HG23	2.21	0.41
19:S:317:LEU:HD21	19:S:372:LEU:CB	2.50	0.41
19:S:346:PRO:HA	19:S:349:ASP:HB3	2.02	0.41
19:S:495:PHE:HE1	19:S:526:TRP:CD1	2.38	0.41
25:Y:71:TYR:O	25:Y:75:LEU:HG	2.21	0.41
9:I:916:SER:OG	9:I:919:HIS:HB3	2.21	0.41
10:J:764:LEU:HD23	10:J:764:LEU:HA	1.89	0.41
12:L:391:PRO:HG2	12:L:393:PRO:HD3	2.03	0.41
12:L:395:SER:HA	13:M:86:ARG:NH1	2.35	0.41
18:R:221:ILE:HG23	18:R:1213:HIS:HB3	2.03	0.41
18:R:766:LYS:HB3	18:R:766:LYS:HE2	1.81	0.41
18:R:1167:ARG:HH11	18:R:1171:VAL:HG21	1.86	0.41
19:S:537:ILE:O	19:S:540:PRO:HD2	2.20	0.41
22:V:204:MET:HA	22:V:209:ILE:HA	2.03	0.41
9:I:314:LEU:HD13	9:I:400:HIS:CD2	2.56	0.41
9:I:599:ASP:HA	9:I:600:ASN:HA	1.66	0.41
10:J:726:VAL:HG21	10:J:731:PRO:HD2	2.02	0.41
11:K:68:HIS:HB2	11:K:87:ALA:HB3	2.03	0.41
11:K:82:SER:HB3	11:K:93:ILE:HG23	2.03	0.41
11:K:200:ARG:HD2	19:S:736:MET:HA	2.02	0.41
11:K:234:VAL:HG23	11:K:235:SER:N	2.36	0.41
11:K:646:MET:HE2	11:K:646:MET:HB3	1.81	0.41
12:L:366:LEU:HD12	12:L:369:LEU:HD21	2.03	0.41
12:L:544:TRP:HB3	12:L:545:GLN:H	1.51	0.41
13:M:51:PHE:O	13:M:132:LYS:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:54:HIS:HA	13:M:73:ARG:HH21	1.85	0.41
18:R:576:ILE:HD12	18:R:576:ILE:HA	1.95	0.41
18:R:1027:VAL:HG23	18:R:1028:HIS:H	1.86	0.41
18:R:1151:LEU:HA	18:R:1154:THR:HG22	2.03	0.41
18:R:1292:ASP:HA	18:R:1295:CYS:SG	2.61	0.41
19:S:292:GLY:O	19:S:294:ILE:HG12	2.20	0.41
19:S:389:ARG:HG2	19:S:392:GLN:HA	2.03	0.41
19:S:579:ILE:O	19:S:583:ILE:HG13	2.20	0.41
19:S:766:LEU:HD23	19:S:810:LEU:HD13	2.03	0.41
25:Y:78:LEU:HA	25:Y:81:HIS:HB2	2.02	0.41
10:J:732:ALA:HA	18:R:71:HIS:HB3	2.02	0.41
11:K:215:VAL:HG12	11:K:230:TYR:C	2.45	0.41
11:K:486:MET:O	11:K:489:SER:OG	2.24	0.41
11:K:488:GLN:O	11:K:491:VAL:HG12	2.21	0.41
11:K:615:LEU:O	11:K:618:SER:OG	2.39	0.41
12:L:635:TYR:O	12:L:638:GLU:HB3	2.21	0.41
18:R:583:GLY:HA2	18:R:586:SER:OG	2.21	0.41
18:R:1016:LEU:HD12	18:R:1016:LEU:HA	1.92	0.41
19:S:228:MET:HG2	19:S:230:SER:H	1.86	0.41
19:S:333:ASP:OD1	19:S:334:VAL:N	2.53	0.41
24:X:58:ARG:HA	24:X:61:MET:HG3	2.03	0.41
9:I:928:TYR:CE2	9:I:960:TYR:HD2	2.39	0.40
11:K:568:ALA:HA	11:K:571:CYS:SG	2.61	0.40
13:M:56:MET:N	13:M:56:MET:SD	2.94	0.40
17:Q:127:LEU:HA	17:Q:130:LEU:HG	2.02	0.40
18:R:377:LEU:HD11	18:R:428:ILE:N	2.36	0.40
19:S:100:ILE:HD12	19:S:100:ILE:HA	1.90	0.40
18:R:286:MET:C	18:R:287:LEU:HD22	2.46	0.40
18:R:311:ALA:HB1	18:R:331:TRP:CZ2	2.57	0.40
18:R:337:GLN:HA	18:R:340:PHE:HB2	2.03	0.40
18:R:1240:LYS:HA	18:R:1240:LYS:HD3	1.98	0.40
9:I:445:ILE:HD12	9:I:459:HIS:ND1	2.36	0.40
9:I:825:SER:N	9:I:842:GLY:H	2.19	0.40
10:J:671:GLU:O	10:J:672:ARG:HG2	2.22	0.40
11:K:28:SER:O	11:K:425:TRP:NE1	2.55	0.40
11:K:203:LEU:HD23	11:K:203:LEU:H	1.86	0.40
11:K:210:GLY:HA2	11:K:276:ARG:CZ	2.50	0.40
12:L:631:ARG:HA	12:L:631:ARG:HD2	1.88	0.40
18:R:160:LEU:HD12	18:R:160:LEU:HA	1.92	0.40
18:R:672:PRO:HB2	18:R:718:THR:HG21	2.03	0.40
18:R:756:LEU:HA	18:R:759:ASN:ND2	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:72:MET:HE3	19:S:72:MET:HB3	1.96	0.40
19:S:750:LEU:HD23	19:S:751:LEU:HD23	2.04	0.40
11:K:35:PHE:O	11:K:51:HIS:ND1	2.52	0.40
11:K:168:ILE:HD13	11:K:179:SER:HA	2.04	0.40
11:K:272:LYS:HA	11:K:272:LYS:HD3	1.80	0.40
12:L:577:ALA:HB3	12:L:594:PHE:CE2	2.56	0.40
13:M:136:PHE:HD2	13:M:144:VAL:HA	1.85	0.40
18:R:62:TRP:O	18:R:65:LYS:HB3	2.22	0.40
18:R:98:CYS:HA	18:R:101:LEU:HG	2.03	0.40
18:R:452:LYS:HE3	18:R:452:LYS:HB2	1.86	0.40
18:R:661:VAL:HA	18:R:664:GLN:CD	2.46	0.40
18:R:710:THR:HA	18:R:713:LYS:HB2	2.02	0.40
18:R:765:ARG:NH1	18:R:765:ARG:O	2.54	0.40
18:R:1073:GLY:O	18:R:1076:VAL:HG22	2.22	0.40
18:R:1211:LEU:O	18:R:1215:VAL:HG13	2.21	0.40
18:R:1228:PRO:O	18:R:1232:THR:HG23	2.22	0.40
19:S:755:ARG:HG2	19:S:758:HIS:HD2	1.86	0.40
19:S:920:GLN:HG2	19:S:924:TRP:NE1	2.37	0.40
9:I:1218:SER:O	9:I:1222:ARG:HG3	2.21	0.40
15:O:189:THR:HB	15:O:193:TYR:CZ	2.57	0.40
18:R:1026:LEU:HD23	18:R:1029:ALA:HB3	2.03	0.40
18:R:1224:LEU:HA	18:R:1227:ILE:HG12	2.04	0.40
18:R:1248:VAL:O	18:R:1252:VAL:HG23	2.22	0.40
18:R:1260:GLN:NE2	18:R:1305:PHE:O	2.52	0.40
18:R:1302:LYS:HB3	18:R:1302:LYS:HE3	1.94	0.40
19:S:189:TRP:HZ2	19:S:226:PRO:HG3	1.87	0.40
19:S:196:LEU:HD22	19:S:222:ILE:HG13	2.04	0.40
19:S:579:ILE:HG13	19:S:621:TRP:NE1	2.36	0.40
22:V:79:LYS:O	22:V:81:SER:N	2.55	0.40
22:V:108:LEU:HA	22:V:111:TYR:CD2	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	455/1575 (29%)	426 (94%)	28 (6%)	1 (0%)	43	78
2	B	154/270 (57%)	150 (97%)	4 (3%)	0	100	100
3	C	153/246 (62%)	123 (80%)	30 (20%)	0	100	100
4	D	159/233 (68%)	147 (92%)	12 (8%)	0	100	100
5	E	157/268 (59%)	144 (92%)	13 (8%)	0	100	100
6	F	69/142 (49%)	66 (96%)	3 (4%)	0	100	100
7	G	120/135 (89%)	119 (99%)	1 (1%)	0	100	100
8	H	101/117 (86%)	94 (93%)	7 (7%)	0	100	100
9	I	1050/1459 (72%)	901 (86%)	149 (14%)	0	100	100
10	J	165/789 (21%)	135 (82%)	30 (18%)	0	100	100
11	K	718/828 (87%)	574 (80%)	143 (20%)	1 (0%)	48	83
12	L	524/649 (81%)	457 (87%)	67 (13%)	0	100	100
13	M	176/208 (85%)	160 (91%)	16 (9%)	0	100	100
14	N	67/240 (28%)	63 (94%)	4 (6%)	0	100	100
15	O	162/212 (76%)	134 (83%)	28 (17%)	0	100	100
16	P	117/144 (81%)	107 (92%)	10 (8%)	0	100	100
17	Q	129/200 (64%)	126 (98%)	3 (2%)	0	100	100
18	R	1285/1367 (94%)	1105 (86%)	179 (14%)	1 (0%)	48	83
19	S	889/987 (90%)	790 (89%)	99 (11%)	0	100	100
20	T	184/745 (25%)	163 (89%)	21 (11%)	0	100	100
21	U	93/588 (16%)	84 (90%)	8 (9%)	1 (1%)	11	45
22	V	258/311 (83%)	216 (84%)	42 (16%)	0	100	100
23	W	116/178 (65%)	109 (94%)	7 (6%)	0	100	100
24	X	119/199 (60%)	116 (98%)	3 (2%)	0	100	100
25	Y	128/178 (72%)	112 (88%)	16 (12%)	0	100	100
26	Z	107/131 (82%)	96 (90%)	11 (10%)	0	100	100
All	All	7655/12399 (62%)	6717 (88%)	934 (12%)	4 (0%)	49	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	105	SER
18	R	1177	LEU
21	U	528	LEU
11	K	97	SER

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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
15	O	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	O	104:SER	C	105:ALA	N	2.41

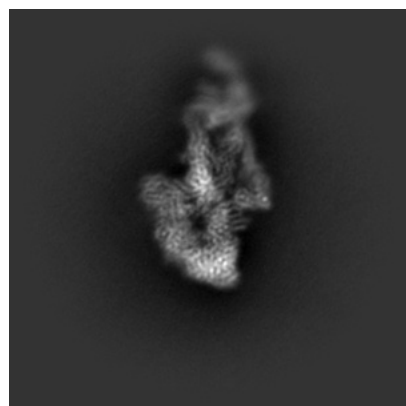
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40968. These allow visual inspection of the internal detail of the map and identification of artifacts.

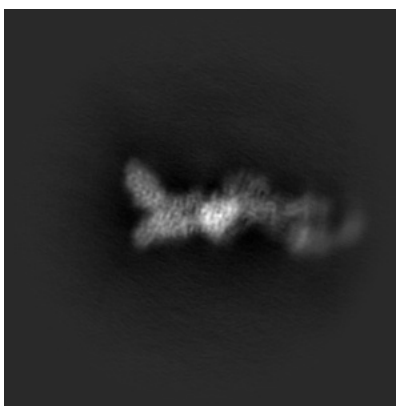
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

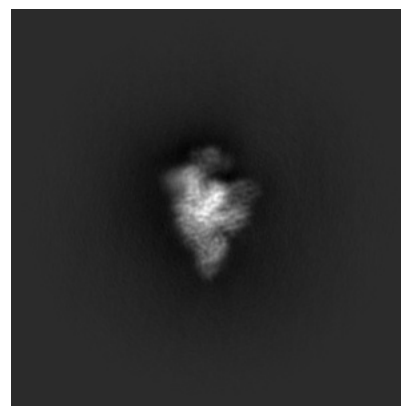
6.1.1 Primary map



X

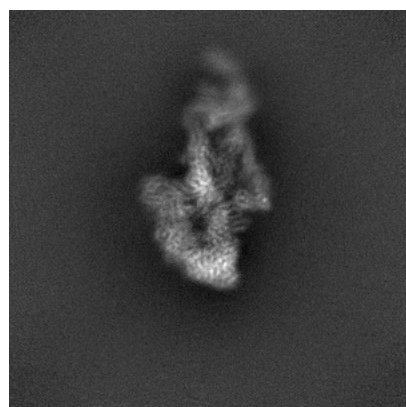


Y

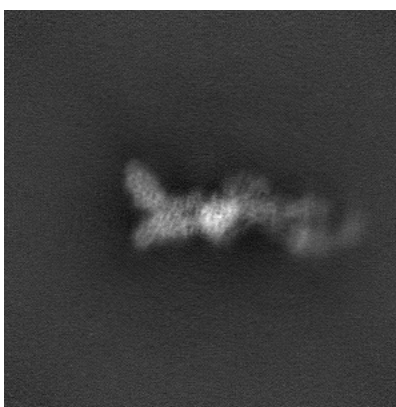


Z

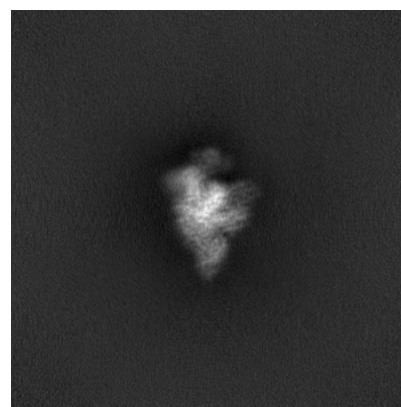
6.1.2 Raw map



X



Y

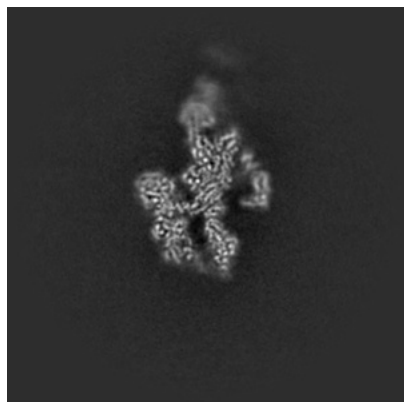


Z

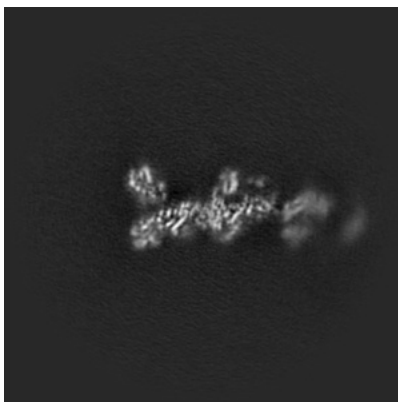
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

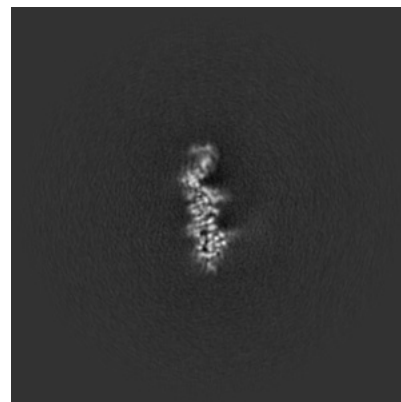
6.2.1 Primary map



X Index: 280

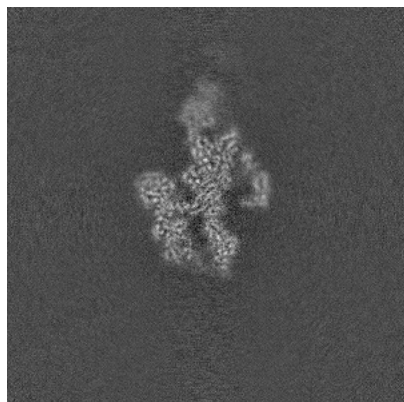


Y Index: 280

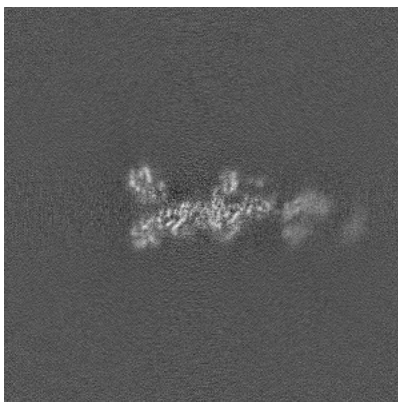


Z Index: 280

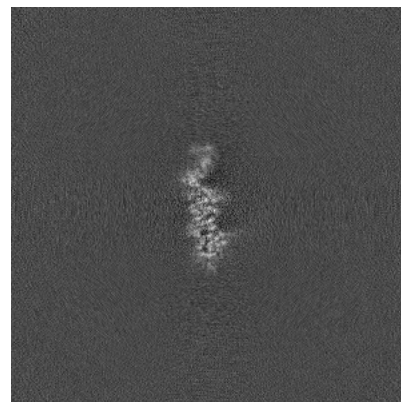
6.2.2 Raw map



X Index: 280



Y Index: 280

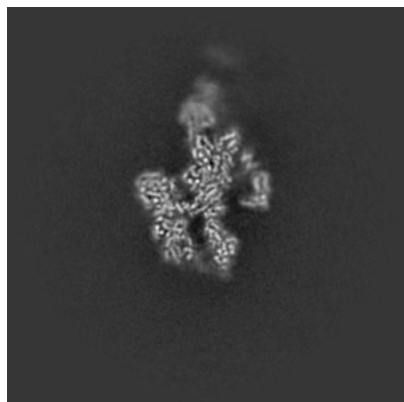


Z Index: 280

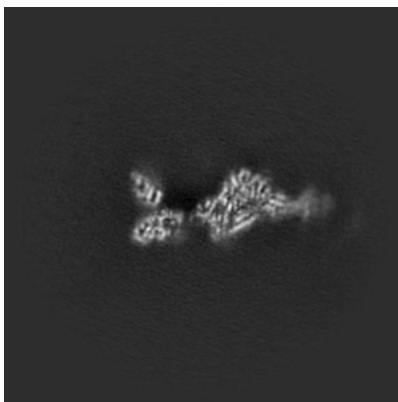
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

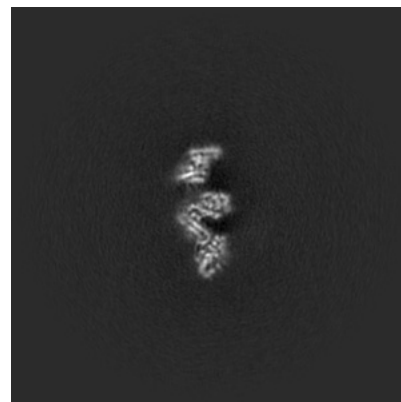
6.3.1 Primary map



X Index: 279

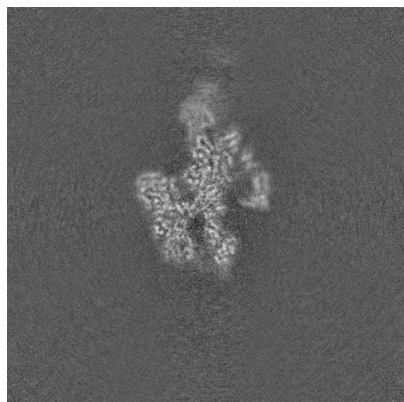


Y Index: 266



Z Index: 296

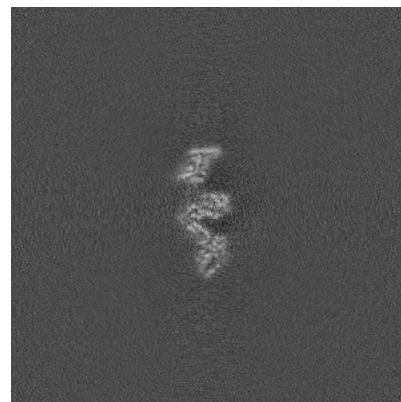
6.3.2 Raw map



X Index: 278



Y Index: 267



Z Index: 295

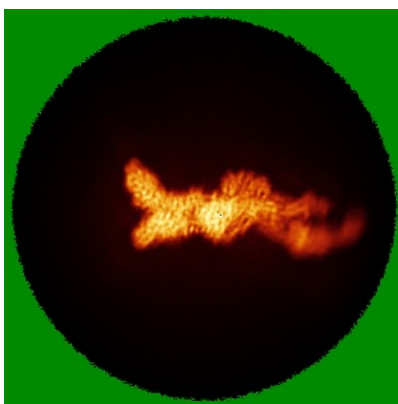
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

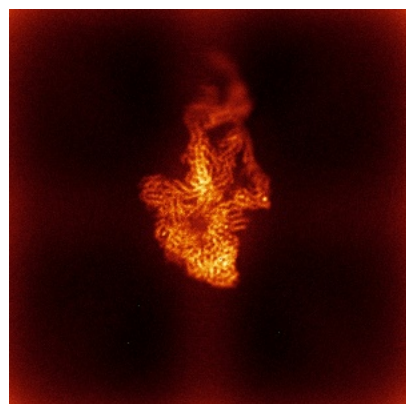


Y

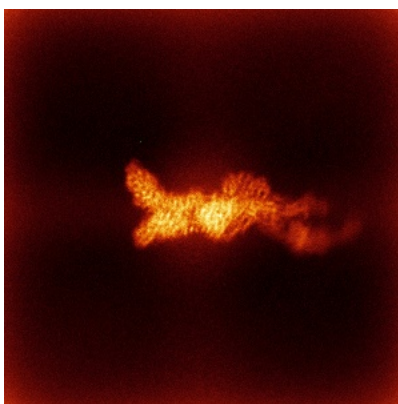


Z

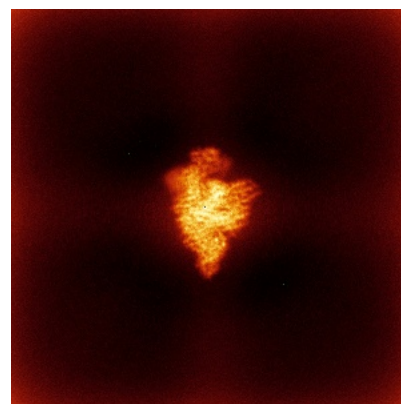
6.4.2 Raw map



X



Y

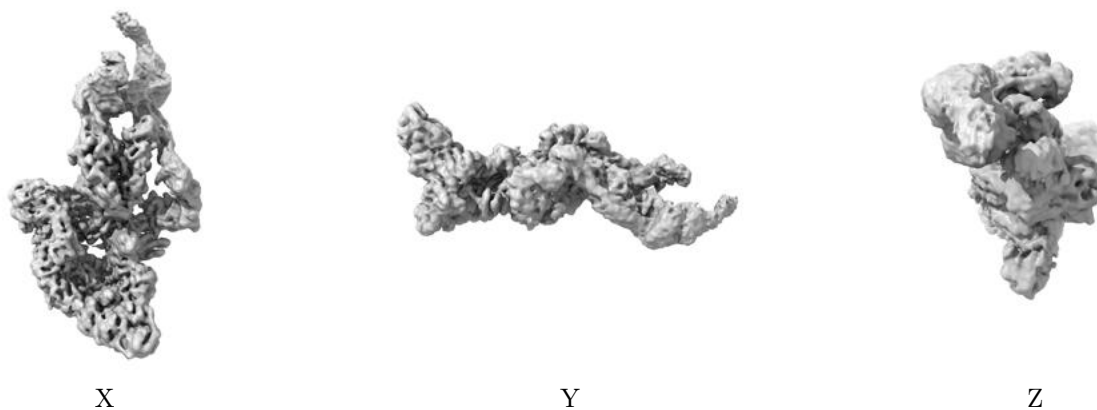


Z

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

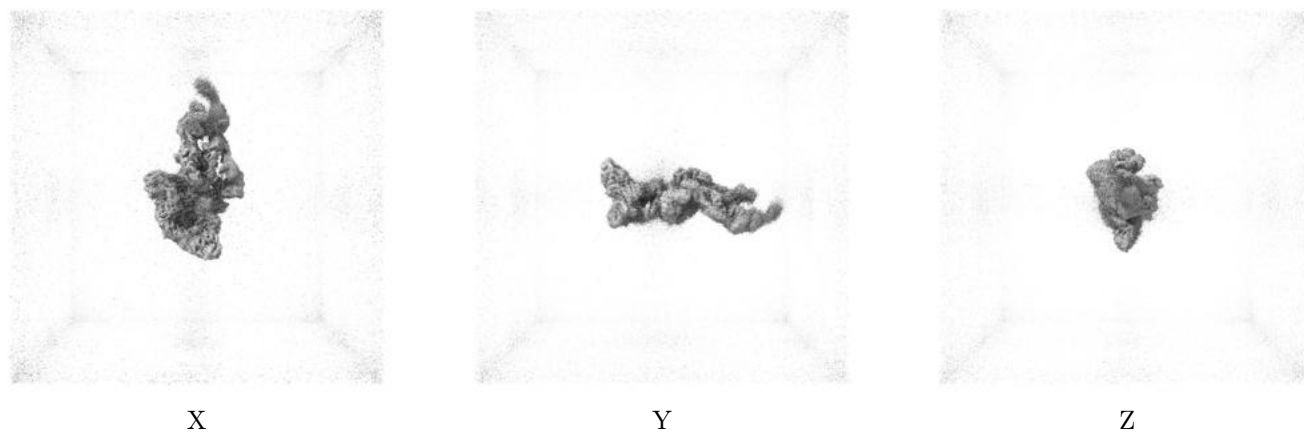
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.054. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

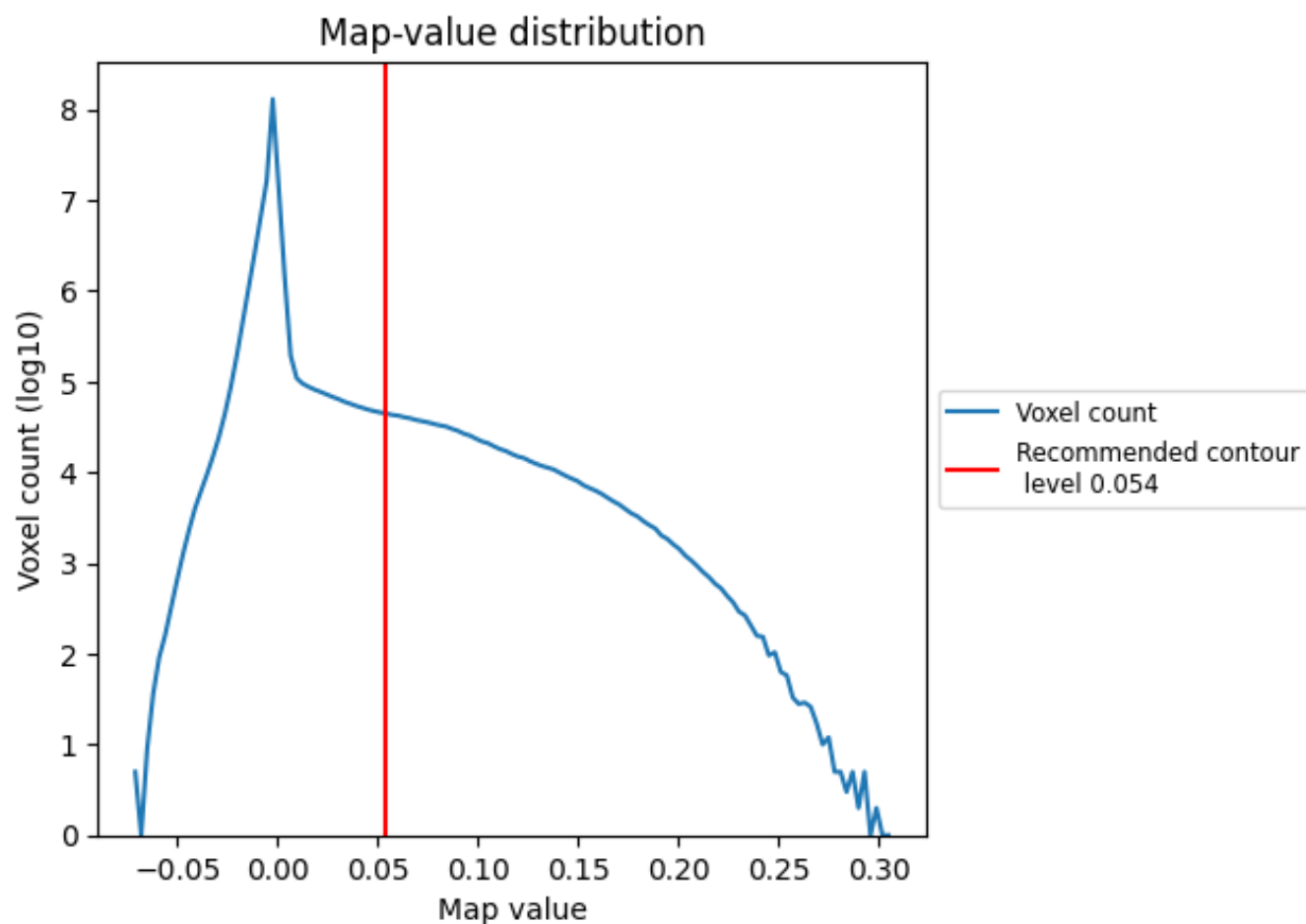
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

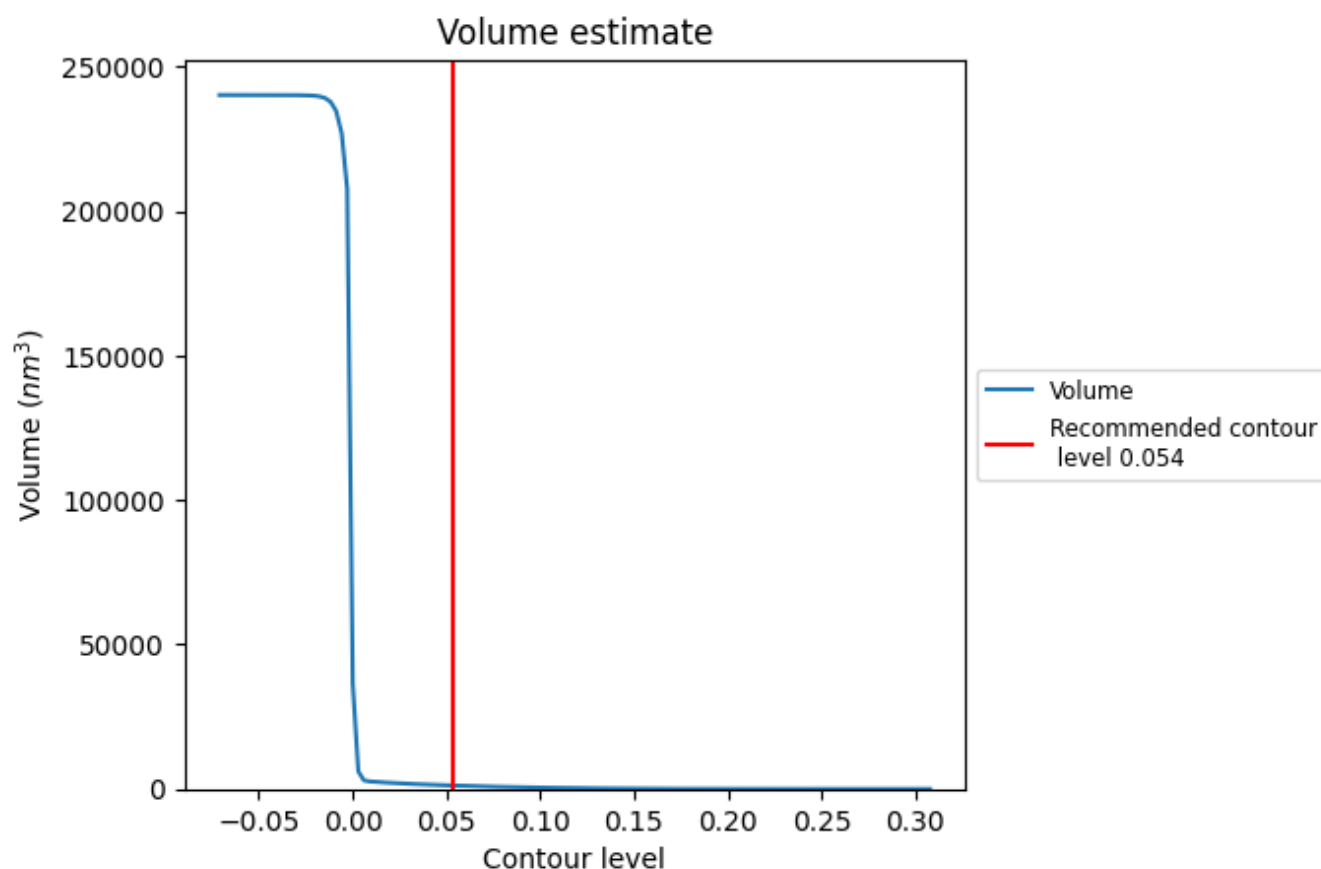
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

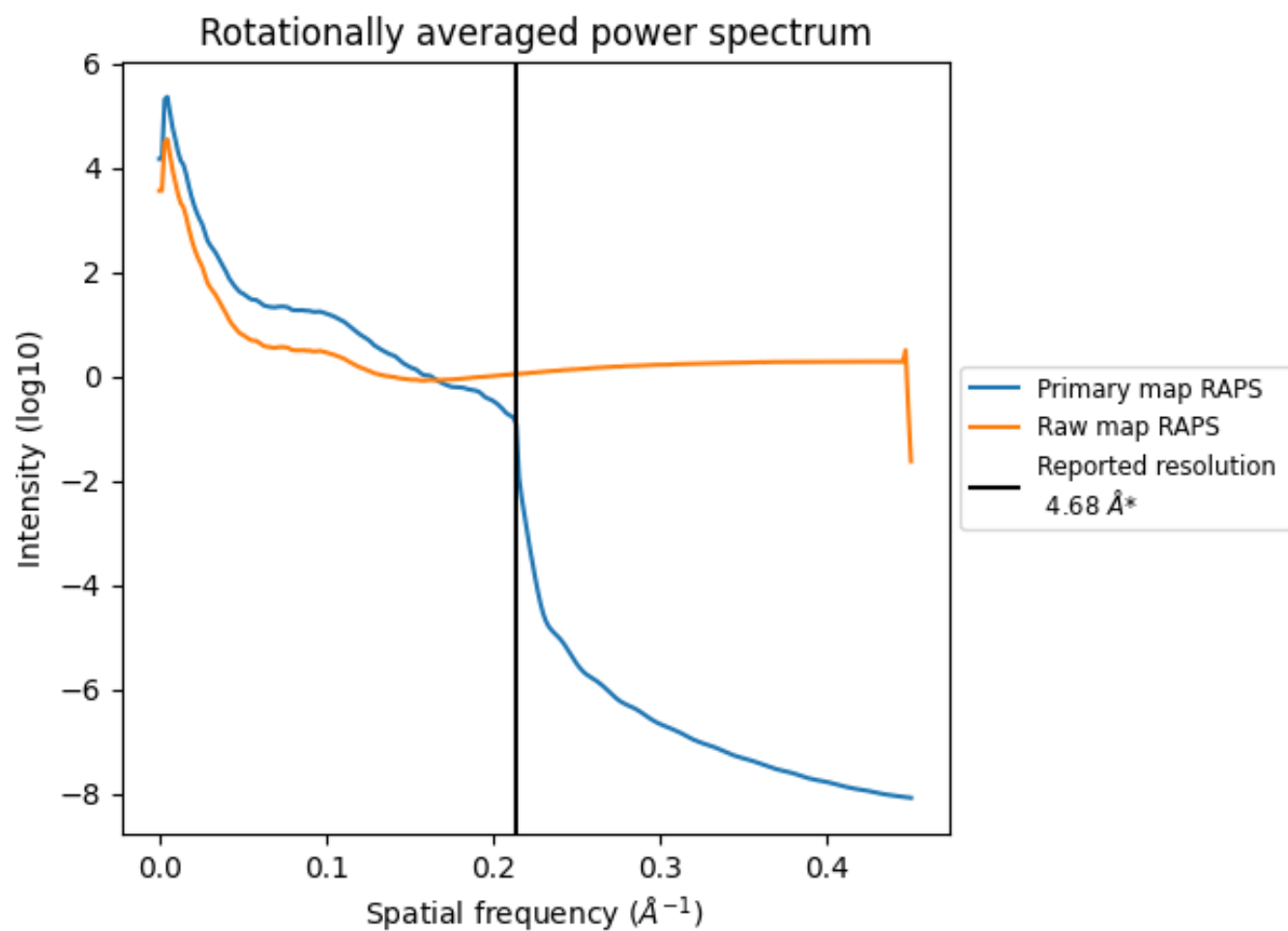
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1192 nm^3 ; this corresponds to an approximate mass of 1076 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 ⓘ

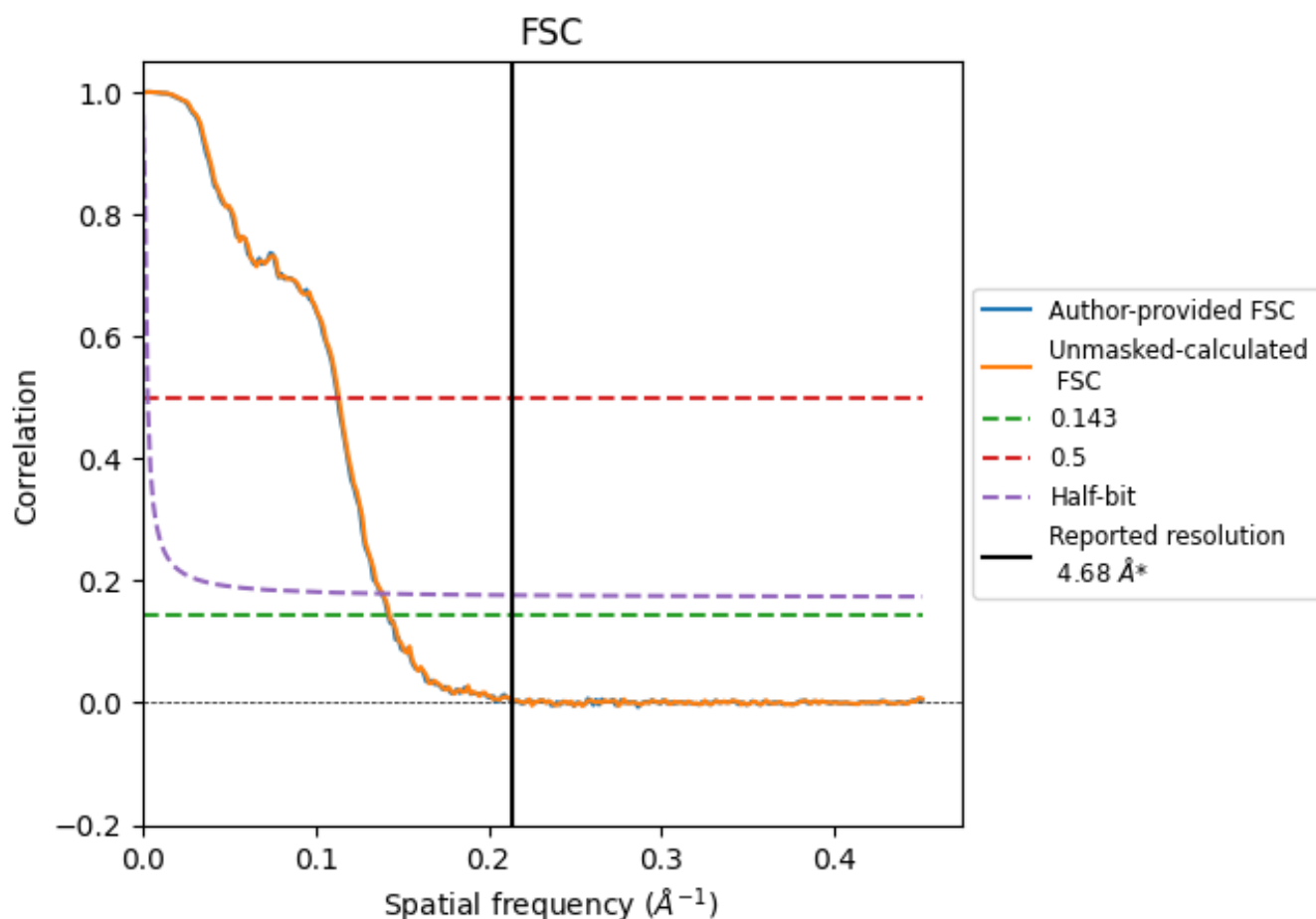


*Reported resolution corresponds to spatial frequency of 0.214 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.214 Å⁻¹

8.2 Resolution estimates

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.68	-	-
Author-provided FSC curve	7.04	8.87	7.24
Unmasked-calculated*	7.00	8.80	7.20

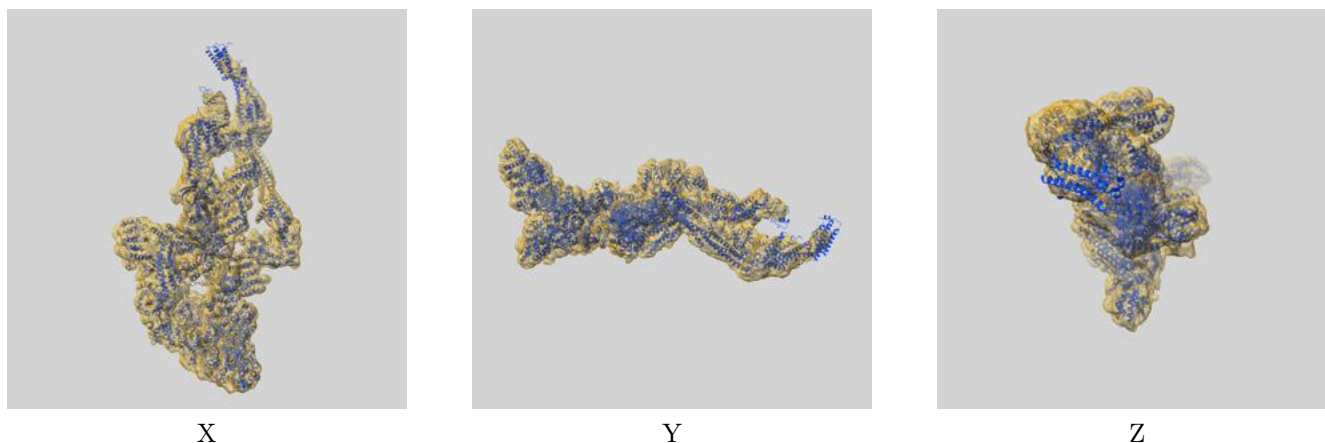
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 7.04 differs from the reported value 4.68 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.00 differs from the reported value 4.68 by more than 10 %

9 Map-model fit [i](#)

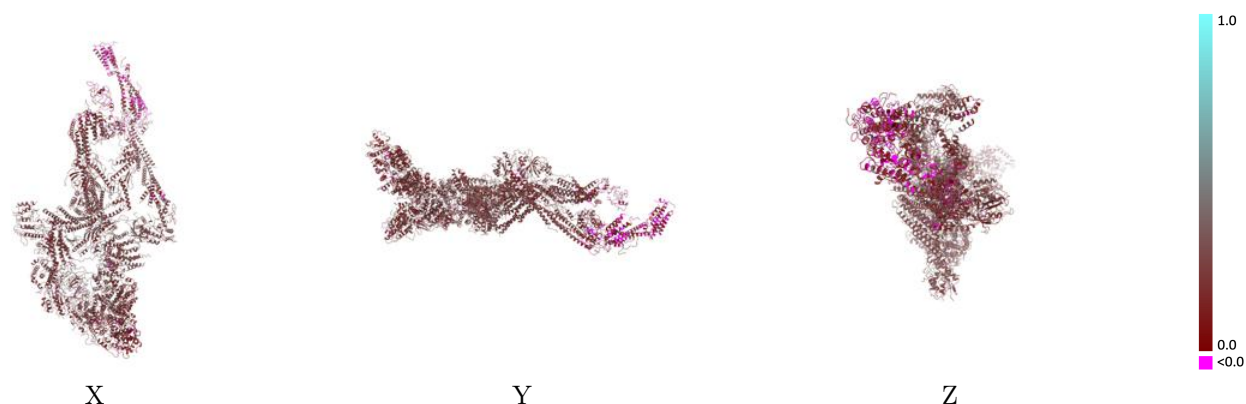
This section contains information regarding the fit between EMDB map EMD-40968 and PDB model 8T1I. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



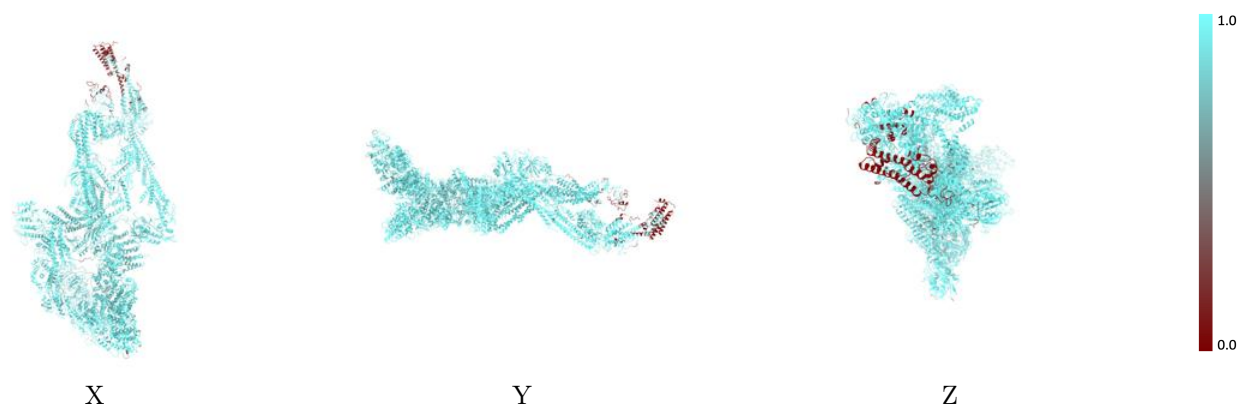
The images above show the 3D surface view of the map at the recommended contour level 0.054 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



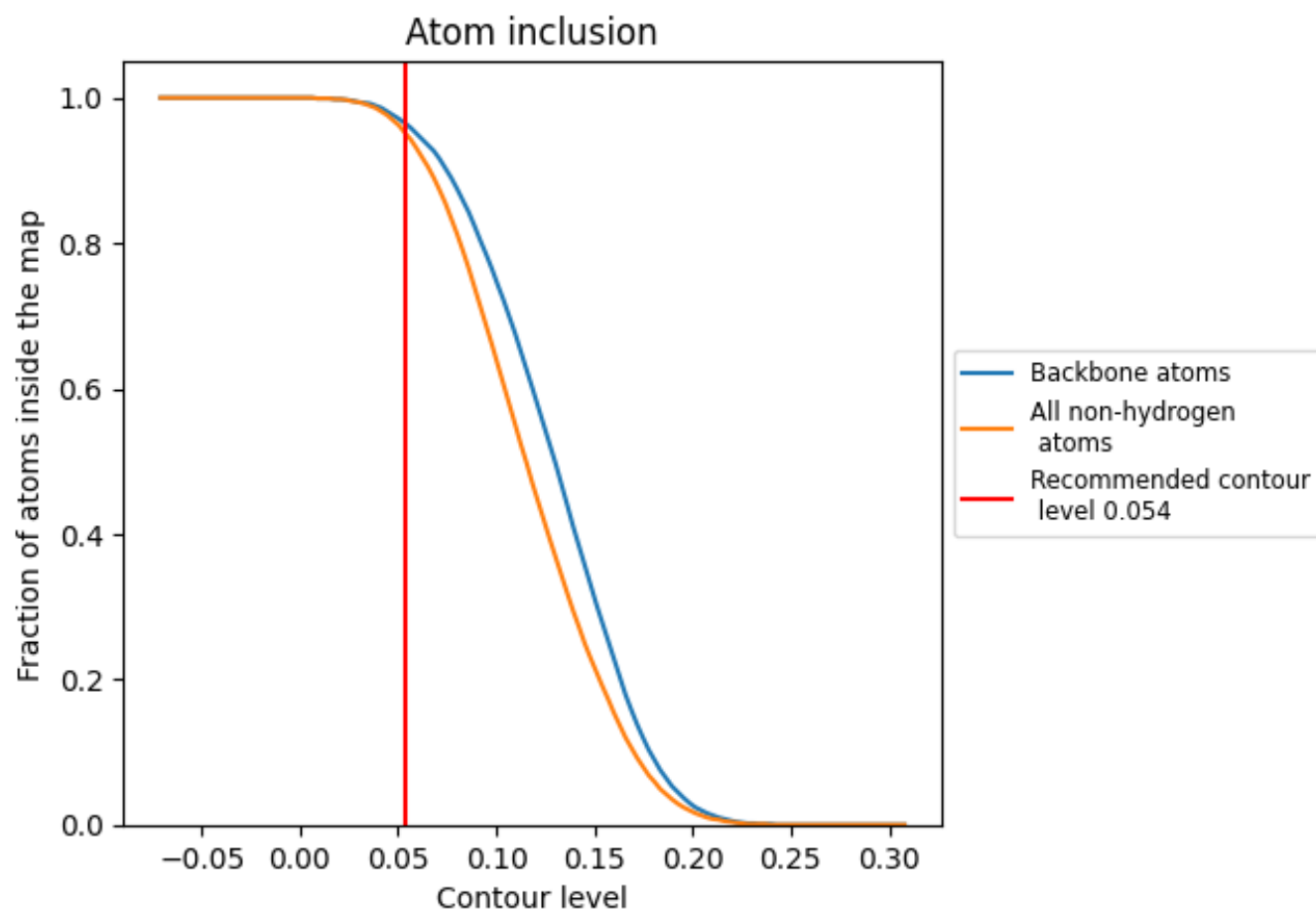
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.054).

9.4 Atom inclusion ⓘ



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.054) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9500	 0.2380
A	 0.9950	 0.2750
B	 0.9940	 0.1950
C	 0.6480	 0.1630
D	 0.9760	 0.1820
E	 0.8900	 0.2080
F	 0.9970	 0.2470
G	 0.4300	 0.0860
H	 0.9970	 0.2420
I	 0.9340	 0.2580
J	 0.9390	 0.2720
K	 0.9820	 0.2550
L	 0.9700	 0.2640
M	 0.9900	 0.2400
N	 0.5570	 0.0880
O	 0.9940	 0.2680
P	 0.9000	 0.1290
Q	 0.9840	 0.2220
R	 0.9650	 0.2220
S	 0.9760	 0.2530
T	 0.9200	 0.2340
U	 0.9540	 0.1250
V	 0.9880	 0.2870
W	 0.9670	 0.2440
X	 0.9890	 0.2470
Y	 0.9820	 0.2480
Z	 0.9760	 0.1780
a	 1.0000	 0.3010

