



Full wwPDB EM Validation Report ⓘ

Jan 27, 2025 – 01:30 PM EST

PDB ID : 8FXY
EMDB ID : EMD-29548
Title : Cryo-EM structure of cowpox virus M2 in complex with human B7.2 (hexameric ring)
Authors : Elliott, J.I.; Adams, L.J.; Nelson, C.A.; Fremont, D.H.
Deposited on : 2023-01-25
Resolution : 3.34 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.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

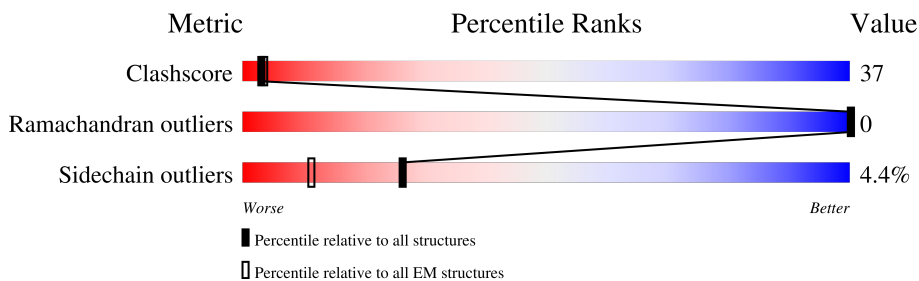
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.34 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	204	
1	B	204	
1	D	204	
1	F	204	
1	I	204	
1	K	204	
2	C	219	
2	E	219	

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Mol	Chain	Length	Quality of chain
2	G	219	
2	H	219	
2	J	219	
2	L	219	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15276 atoms, of which 234 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 CPXV040 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	196	1564	980	258	309	17	0	0
1	B	196	1564	980	258	309	17	0	0
1	D	196	1564	980	258	309	17	0	0
1	F	196	1564	980	258	309	17	0	0
1	I	196	1564	980	258	309	17	0	0
1	K	196	1564	980	258	309	17	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LYS	-	expression tag	UNP Q8QN22
A	-5	PRO	-	expression tag	UNP Q8QN22
A	-4	GLU	-	expression tag	UNP Q8QN22
B	-6	LYS	-	expression tag	UNP Q8QN22
B	-5	PRO	-	expression tag	UNP Q8QN22
B	-4	GLU	-	expression tag	UNP Q8QN22
D	-6	LYS	-	expression tag	UNP Q8QN22
D	-5	PRO	-	expression tag	UNP Q8QN22
D	-4	GLU	-	expression tag	UNP Q8QN22
F	-6	LYS	-	expression tag	UNP Q8QN22
F	-5	PRO	-	expression tag	UNP Q8QN22
F	-4	GLU	-	expression tag	UNP Q8QN22
I	-6	LYS	-	expression tag	UNP Q8QN22
I	-5	PRO	-	expression tag	UNP Q8QN22
I	-4	GLU	-	expression tag	UNP Q8QN22
K	-6	LYS	-	expression tag	UNP Q8QN22
K	-5	PRO	-	expression tag	UNP Q8QN22
K	-4	GLU	-	expression tag	UNP Q8QN22

- Molecule 2 is a protein called T-lymphocyte activation antigen CD86.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	H	110	901	572	155	168	6	0	0
2	C	110	901	572	155	168	6	0	0
2	E	110	901	572	155	168	6	0	0
2	G	110	901	572	155	168	6	0	0
2	J	110	901	572	155	168	6	0	0
2	L	110	901	572	155	168	6	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	0	MET	-	initiating methionine	UNP P42081
H	160	ILE	VAL	variant	UNP P42081
C	0	MET	-	initiating methionine	UNP P42081
C	160	ILE	VAL	variant	UNP P42081
E	0	MET	-	initiating methionine	UNP P42081
E	160	ILE	VAL	variant	UNP P42081
G	0	MET	-	initiating methionine	UNP P42081
G	160	ILE	VAL	variant	UNP P42081
J	0	MET	-	initiating methionine	UNP P42081
J	160	ILE	VAL	variant	UNP P42081
L	0	MET	-	initiating methionine	UNP P42081
L	160	ILE	VAL	variant	UNP P42081

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				AltConf	
			Total	C	H	N		O
3	A	1	27	8	13	1	5	0
3	A	1	27	8	13	1	5	0
3	A	1	27	8	13	1	5	0
3	B	1	27	8	13	1	5	0
3	B	1	27	8	13	1	5	0
3	B	1	27	8	13	1	5	0
3	D	1	27	8	13	1	5	0
3	D	1	27	8	13	1	5	0
3	D	1	27	8	13	1	5	0
3	F	1	27	8	13	1	5	0
3	F	1	27	8	13	1	5	0
3	F	1	27	8	13	1	5	0
3	I	1	27	8	13	1	5	0
3	I	1	27	8	13	1	5	0

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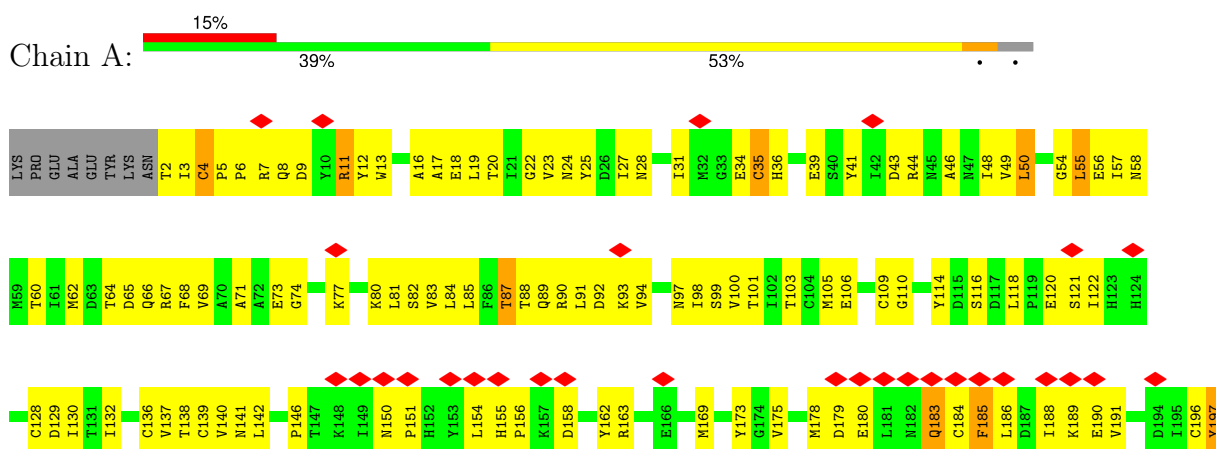
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Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	N	O	
3	I	1	Total 27	C 8	H 13	N 1	O 5	0
3	K	1	Total 27	C 8	H 13	N 1	O 5	0
3	K	1	Total 27	C 8	H 13	N 1	O 5	0
3	K	1	Total 27	C 8	H 13	N 1	O 5	0

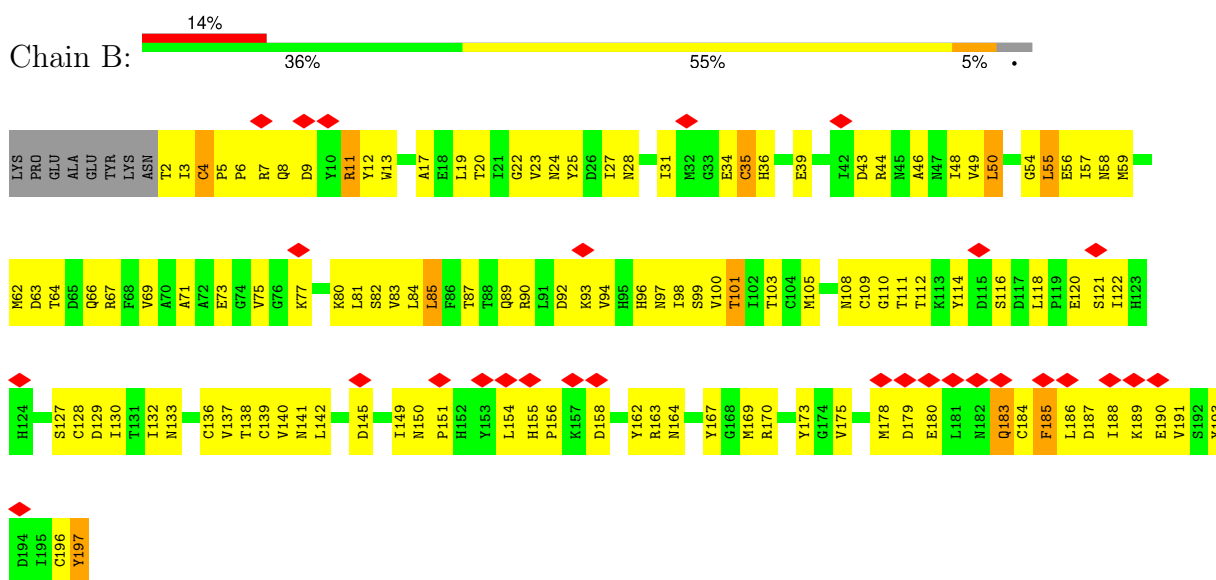
3 Residue-property plots [i](#)

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: CPXV040 protein

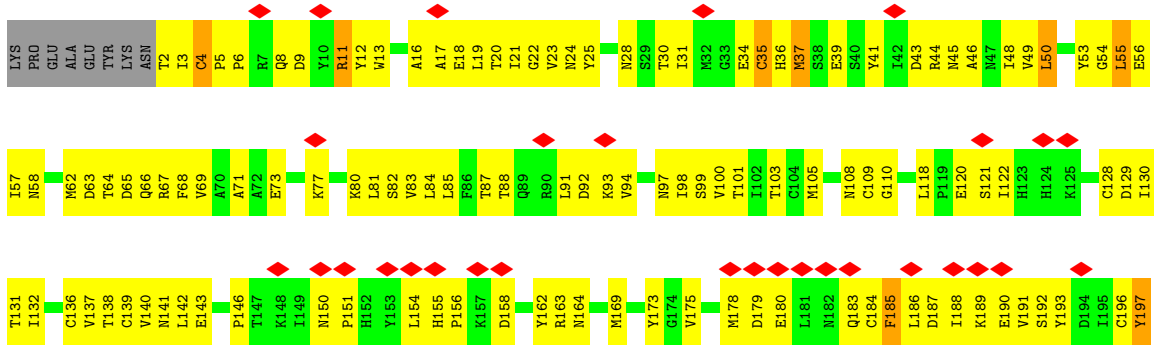


- Molecule 1: CPXV040 protein

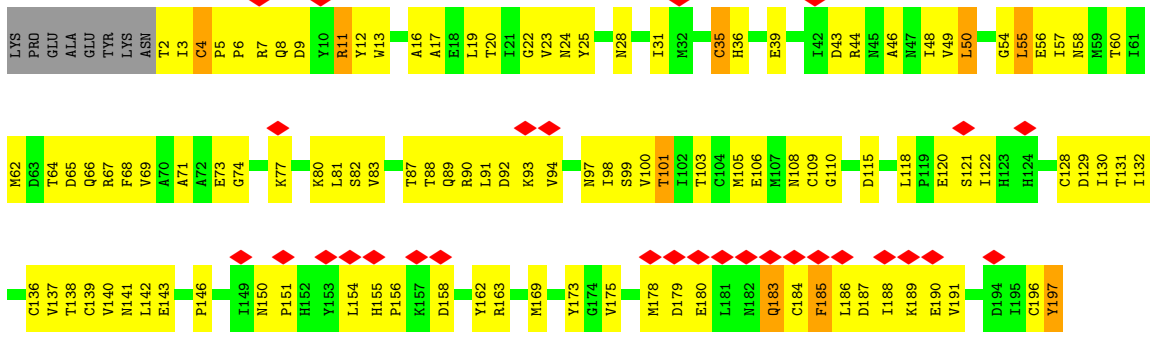


- Molecule 1: CPXV040 protein

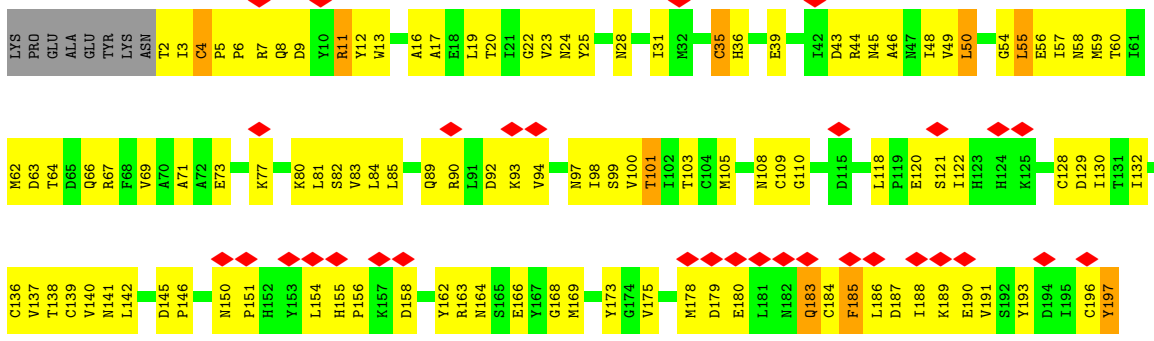




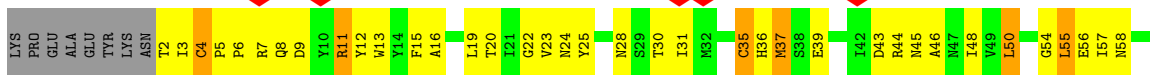
• Molecule 1: CPXV040 protein

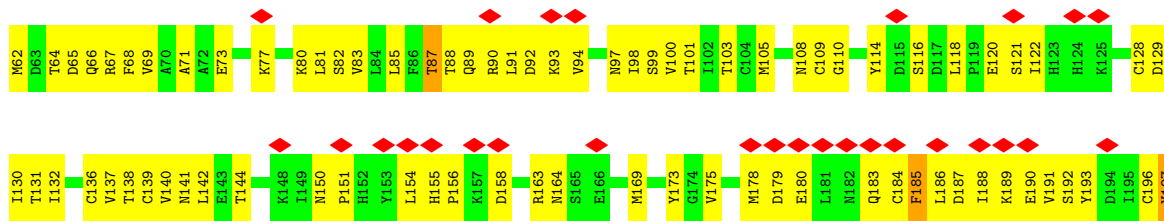


• Molecule 1: CPXV040 protein

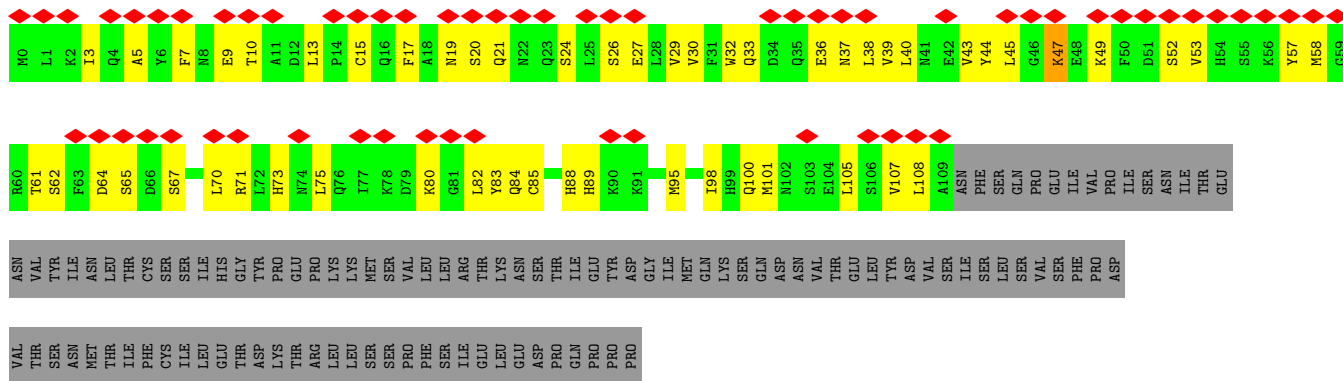
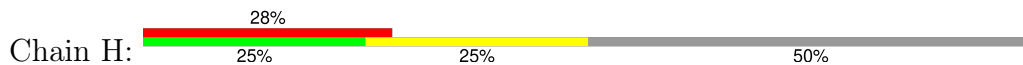


• Molecule 1: CPXV040 protein

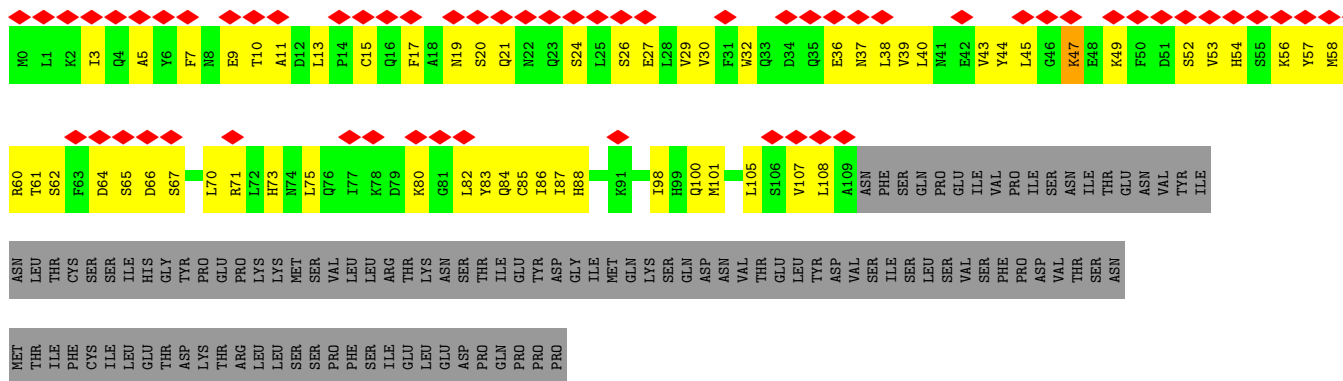




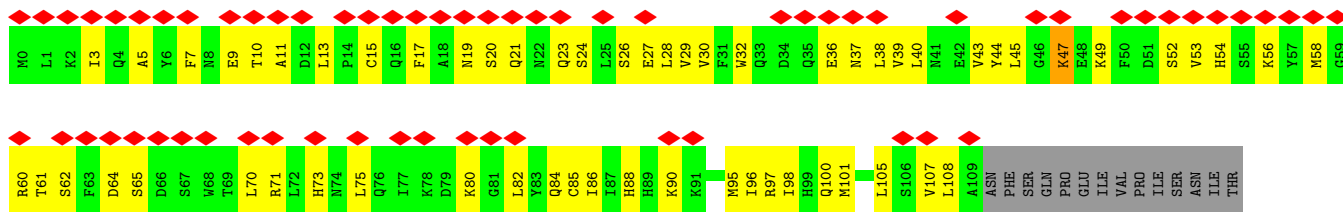
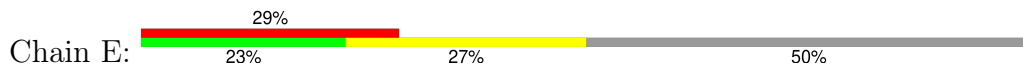
• Molecule 2: T-lymphocyte activation antigen CD86



• Molecule 2: T-lymphocyte activation antigen CD86



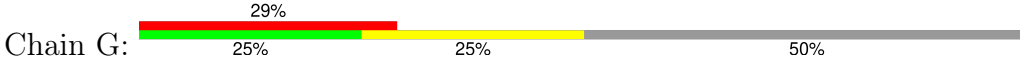
• Molecule 2: T-lymphocyte activation antigen CD86



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

ASP VAL THR SER MET ILE PHE CYS ILE LEU THR ASP LYS THR ARG PRO PHE SER LEU ILE GLU LEU PRO PRO

● Molecule 2: T-lymphocyte activation antigen CD86



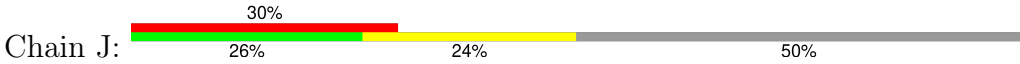
M0 L1 K2 I3 Q4 A5 Y6 F7 N8 E9 T10 A11 D12 L13 P14 C15 Q16 F17 A18 N19 S20 Q21 N22 Q23 S24 L25 S26 E27 L28 V29 V30 F31 W32 Q33 D34 Q35 E36 N37 L38 V39 L40 M41 M42 V43 Y44 L45 G46 K47 E48 K49 F50 D51 S52 V53 H54 S55 K56 Y57 M58 G59

R60 T61 S62 F63 D64 S65 D66 S67 W68 T69 L70 R71 L72 H73 H74 N74 L75 Q76 I77 K78 D79 K80 G81 L82 Y83 Q84 C85 I86 I87 H88 H89 K90 K91 M95 I98 H99 Q100 M101 L105 S106 V107 L108 A109 ASN PHE SER GLN PRO GLU ILE VAL SER ASP

ASN VAL TYR ASN ILE LEU THR CYS SER ILE SER HIS TYR PRO GLU PRO LYS MET SER VAL LEU ARG THR LYS ASN SER THR ILE GLU PRO PRO

VAL THR ASN MET ILE PHE CYS ILE LEU THR ASP LYS THR ARG LEU SER SER PHE ILE GLU LEU PRO PRO

● Molecule 2: T-lymphocyte activation antigen CD86



M0 L1 F2 I3 Q4 A5 Y6 N8 E9 T10 A11 D12 L13 P14 C15 Q16 F17 A18 N19 S20 Q21 N22 Q23 S24 L25 S26 E27 L28 V29 V30 F31 W32 Q33 D34 Q35 E36 N37 L38 V39 L40 M41 M42 V43 Y44 L45 G46 K47 E48 K49 F50 D51 S52 V53 H54 S55 K56 Y57 M58 G59

R60 T61 S62 F63 D64 S65 D66 S67 W68 T69 L70 R71 L72 H73 H74 N74 L75 Q76 I77 K78 D79 K80 G81 L82 Y83 Q84 C85 I86 I87 H88 K91 P92 T93 M95 I98 H99 Q100 M101 L105 S106 V107 L108 A109 ASN PHE SER GLN PRO GLU ILE VAL SER ASP

THR GLU ASN VAL TYR ILE ASN LEU THR CYS SER ILE SER HIS GLY TYR PRO GLU PRO ARG PRO LYS MET SER VAL LEU ARG THR THR ASN SER THR ILE GLU LEU PRO PRO

PRO ASP VAL THR SER MET ILE PHE CYS ILE LEU THR ASP LYS THR ARG LEU SER SER PHE ILE GLU LEU PRO PRO

● Molecule 2: T-lymphocyte activation antigen CD86



M0 L1 K2 I3 Q4 A5 Y6 F7 N8 E9 T10 A11 D12 L13 P14 C15 Q16 F17 A18 N19 S20 Q21 N22 Q23 S24 L25 S26 E27 L28 V29 V30 F31 W32 Q33 D34 Q35 E36 N37 L38 V39 L40 M41 M42 V43 Y44 L45 G46 K47 E48 K49 F50 D51 S52 V53 H54 S55 K56 Y57 M58 G59

R60 T61 S62 F63 D64 S65 D66 S67 W68 T69 L70 R71 L72 H73 H74 N74 L75 Q76 I77 K78 D79 K80 G81 L82 Y83 Q84 C85 I86 I87 H88 H89 K90 K91 M95 I98 H99 Q100 M101 L105 S106 V107 L108 A109 ASN PHE SER GLN PRO GLU ILE VAL SER ASP

GLU ASN VAL TYR ILE ASN LEU THR CYS SER ILE SER HIS GLY TYR PRO GLU PRO ARG PRO LYS MET SER VAL LEU ARG THR THR ASN SER THR ILE GLU LEU PRO PRO

ASP
VAL
THR
SER
ASN
MET
THR
ILE
PHE
CYS
ILE
LEU
GLU
THR
ASP
LYS
THR
ARG
LEU
LEU
SER
SER
PRO
PHE
SER
ILE
GLU
LEU
GLU
ASP
PRO
GLN
PRO
PRO
PRO

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75929	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 ($e^-/\text{\AA}^2$)	66	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.850	Depositor
Minimum map value	-0.017	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.25	Depositor
Map size (\AA)	308.0, 308.0, 308.0	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	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: NAG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.26	0/1597	0.50	0/2166
1	B	0.26	0/1597	0.50	0/2166
1	D	0.26	0/1597	0.50	0/2166
1	F	0.26	0/1597	0.50	0/2166
1	I	0.26	0/1597	0.50	0/2166
1	K	0.26	0/1597	0.49	0/2166
2	C	0.25	0/920	0.46	0/1240
2	E	0.25	0/920	0.46	0/1240
2	G	0.25	0/920	0.46	0/1240
2	H	0.25	0/920	0.46	0/1240
2	J	0.25	0/920	0.46	0/1240
2	L	0.25	0/920	0.46	0/1240
All	All	0.26	0/15102	0.48	0/20436

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	1564	0	1487	139	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1564	0	1487	137	0
1	D	1564	0	1487	138	0
1	F	1564	0	1487	134	0
1	I	1564	0	1487	133	0
1	K	1564	0	1487	140	0
2	C	901	0	886	58	0
2	E	901	0	886	53	0
2	G	901	0	886	54	0
2	H	901	0	886	52	0
2	J	901	0	886	54	0
2	L	901	0	886	54	0
3	A	42	39	39	4	0
3	B	42	39	39	5	0
3	D	42	39	39	3	0
3	F	42	39	39	4	0
3	I	42	39	39	5	0
3	K	42	39	39	4	0
All	All	15042	234	14472	1104	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 37.

All (1104) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:58:ASN:HB3	1:F:101:THR:HG23	1.39	1.02
1:I:58:ASN:HB3	1:I:101:THR:HG23	1.44	0.99
1:B:58:ASN:HB3	1:B:101:THR:HG23	1.47	0.94
1:A:58:ASN:HB3	1:A:101:THR:HG23	1.56	0.87
1:K:8:GLN:HG2	1:K:9:ASP:H	1.43	0.83
1:B:109:CYS:O	1:D:2:THR:N	2.12	0.82
2:H:7:PHE:HB2	2:H:108:LEU:HD23	1.61	0.81
1:D:8:GLN:HG2	1:D:9:ASP:H	1.43	0.81
1:I:109:CYS:O	1:K:2:THR:N	2.14	0.80
1:I:8:GLN:HG2	1:I:9:ASP:H	1.45	0.80
2:L:7:PHE:HB2	2:L:108:LEU:HD23	1.63	0.80
1:F:169:MET:HE2	1:F:169:MET:HA	1.64	0.80
1:F:19:LEU:HD21	1:F:83:VAL:HB	1.63	0.79
1:K:5:PRO:HB2	1:K:67:ARG:HH12	1.45	0.79
1:K:132:ILE:HG21	1:K:137:VAL:HG21	1.63	0.79
1:I:19:LEU:HD21	1:I:83:VAL:HB	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:8:GLN:HG2	1:F:9:ASP:H	1.48	0.79
1:A:132:ILE:HG21	1:A:137:VAL:HG21	1.64	0.78
1:D:5:PRO:HB2	1:D:67:ARG:HH12	1.47	0.78
1:A:19:LEU:HD21	1:A:83:VAL:HB	1.64	0.78
1:B:8:GLN:HG2	1:B:9:ASP:H	1.49	0.78
1:A:8:GLN:HG2	1:A:9:ASP:H	1.47	0.77
2:H:29:VAL:HG22	2:H:88:HIS:HB2	1.66	0.77
1:A:2:THR:N	1:K:109:CYS:O	2.17	0.77
1:F:122:ILE:H	1:F:122:ILE:HD12	1.50	0.77
1:A:58:ASN:HB3	1:A:101:THR:CG2	2.13	0.76
1:F:58:ASN:HB3	1:F:101:THR:CG2	2.14	0.76
1:D:132:ILE:HG21	1:D:137:VAL:HG21	1.67	0.76
1:B:140:VAL:HB	1:B:175:VAL:HG12	1.68	0.76
1:B:178:MET:SD	1:B:179:ASP:N	2.53	0.76
2:C:53:VAL:HB	2:C:58:MET:HE1	1.67	0.75
1:D:109:CYS:O	1:F:2:THR:N	2.20	0.75
1:A:169:MET:HE2	1:A:169:MET:HA	1.68	0.75
2:H:9:GLU:HG3	2:H:10:THR:H	1.51	0.75
2:E:53:VAL:HB	2:E:58:MET:HE1	1.68	0.75
1:F:120:GLU:HG2	1:F:122:ILE:HD13	1.67	0.75
1:I:132:ILE:HG21	1:I:137:VAL:HG21	1.67	0.75
2:J:3:ILE:HD11	2:J:105:LEU:HB3	1.68	0.75
1:B:132:ILE:HG21	1:B:137:VAL:HG21	1.68	0.74
1:F:11:ARG:HE	1:F:69:VAL:HG13	1.52	0.74
2:C:30:VAL:HG12	2:C:43:VAL:HB	1.68	0.74
1:F:132:ILE:HG21	1:F:137:VAL:HG21	1.67	0.74
2:E:3:ILE:HD11	2:E:105:LEU:HB3	1.70	0.74
1:I:80:LYS:NZ	1:I:184:CYS:O	2.20	0.74
1:B:19:LEU:HD21	1:B:83:VAL:HB	1.69	0.73
2:G:53:VAL:HB	2:G:58:MET:HE1	1.68	0.73
1:K:169:MET:HE2	1:K:169:MET:HA	1.69	0.73
1:D:19:LEU:HD21	1:D:83:VAL:HB	1.69	0.73
1:B:100:VAL:CG1	1:B:130:ILE:HG12	2.18	0.73
2:J:30:VAL:HG12	2:J:43:VAL:HB	1.71	0.73
1:D:122:ILE:HD12	1:D:122:ILE:H	1.54	0.73
1:D:56:GLU:HG3	1:D:103:THR:HB	1.69	0.72
1:A:11:ARG:HE	1:A:69:VAL:HG13	1.54	0.72
1:F:25:TYR:OH	1:F:54:GLY:HA3	1.90	0.72
1:K:100:VAL:CG1	1:K:130:ILE:HG12	2.20	0.72
1:K:178:MET:SD	1:K:179:ASP:N	2.55	0.72
1:B:5:PRO:HB2	1:B:67:ARG:HH12	1.55	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:80:LYS:HA	2:C:105:LEU:HD12	1.72	0.72
2:L:53:VAL:HB	2:L:58:MET:HE1	1.70	0.72
2:G:3:ILE:HD11	2:G:105:LEU:HB3	1.71	0.72
1:I:122:ILE:HD12	1:I:122:ILE:H	1.55	0.71
1:K:19:LEU:HD21	1:K:83:VAL:HB	1.72	0.71
2:E:107:VAL:HG12	2:E:108:LEU:H	1.56	0.71
1:A:80:LYS:NZ	1:A:184:CYS:O	2.23	0.71
1:D:100:VAL:CG1	1:D:130:ILE:HG12	2.20	0.71
2:G:107:VAL:HG12	2:G:108:LEU:H	1.56	0.71
1:I:120:GLU:HG2	1:I:122:ILE:HD13	1.71	0.71
1:A:109:CYS:HB3	1:B:4:CYS:O	1.90	0.71
1:F:109:CYS:HB3	1:I:4:CYS:O	1.91	0.71
1:I:25:TYR:OH	1:I:54:GLY:HA3	1.91	0.71
2:L:3:ILE:HD11	2:L:105:LEU:HB3	1.72	0.71
1:B:58:ASN:HB3	1:B:101:THR:CG2	2.20	0.71
1:I:100:VAL:CG1	1:I:130:ILE:HG12	2.21	0.70
2:J:7:PHE:HB2	2:J:108:LEU:HD23	1.72	0.70
2:J:39:VAL:HG13	2:J:53:VAL:HA	1.73	0.70
1:K:122:ILE:HD12	1:K:122:ILE:H	1.57	0.70
2:C:107:VAL:HG12	2:C:108:LEU:H	1.57	0.70
1:D:25:TYR:OH	1:D:54:GLY:HA3	1.91	0.70
2:C:15:CYS:HB2	2:C:101:MET:HB3	1.72	0.70
1:F:80:LYS:NZ	1:F:184:CYS:O	2.24	0.70
1:A:25:TYR:OH	1:A:54:GLY:HA3	1.91	0.70
1:A:56:GLU:HG3	1:A:103:THR:HB	1.73	0.70
1:A:122:ILE:H	1:A:122:ILE:HD12	1.55	0.70
2:G:7:PHE:HB2	2:G:108:LEU:HD23	1.74	0.70
2:E:9:GLU:HG3	2:E:10:THR:H	1.57	0.70
1:F:56:GLU:HG3	1:F:103:THR:HB	1.72	0.70
1:B:122:ILE:HD12	1:B:122:ILE:H	1.57	0.70
2:H:9:GLU:O	2:H:75:LEU:HD13	1.92	0.69
2:J:107:VAL:HG12	2:J:108:LEU:H	1.57	0.69
1:B:109:CYS:HB3	1:D:4:CYS:O	1.91	0.69
1:K:5:PRO:HB2	1:K:67:ARG:NH1	2.07	0.69
2:H:107:VAL:HG12	2:H:108:LEU:H	1.58	0.69
1:I:56:GLU:HG3	1:I:103:THR:HB	1.74	0.69
2:L:107:VAL:HG12	2:L:108:LEU:H	1.57	0.69
1:K:56:GLU:HG3	1:K:103:THR:HB	1.74	0.69
2:C:9:GLU:O	2:C:75:LEU:HD13	1.92	0.69
1:I:12:TYR:HB2	1:I:13:TRP:CZ3	2.26	0.69
1:A:11:ARG:HB2	1:A:69:VAL:HG11	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:29:VAL:HG22	2:E:88:HIS:HB2	1.75	0.69
1:F:11:ARG:HB2	1:F:69:VAL:HG11	1.74	0.69
1:K:25:TYR:OH	1:K:54:GLY:HA3	1.93	0.69
1:D:109:CYS:HB3	1:F:4:CYS:O	1.93	0.68
2:G:30:VAL:HG12	2:G:43:VAL:HB	1.73	0.68
1:I:178:MET:SD	1:I:179:ASP:N	2.56	0.68
1:F:109:CYS:O	1:I:2:THR:N	2.26	0.68
1:K:92:ASP:OD1	1:K:93:LYS:N	2.26	0.68
1:D:5:PRO:HB2	1:D:67:ARG:NH1	2.06	0.68
1:D:92:ASP:OD1	1:D:93:LYS:N	2.26	0.68
1:I:183:GLN:HG3	2:J:37:ASN:HD21	1.58	0.68
2:E:9:GLU:O	2:E:75:LEU:HD13	1.93	0.68
1:I:92:ASP:OD1	1:I:93:LYS:N	2.26	0.68
1:B:80:LYS:NZ	1:B:184:CYS:O	2.25	0.68
2:H:30:VAL:HG12	2:H:43:VAL:HB	1.74	0.68
1:K:58:ASN:HB3	1:K:101:THR:OG1	1.93	0.68
2:H:29:VAL:CG2	2:H:88:HIS:HB2	2.23	0.68
1:D:12:TYR:HB2	1:D:13:TRP:CZ3	2.29	0.68
1:I:5:PRO:HB2	1:I:67:ARG:HH12	1.58	0.68
1:A:186:LEU:HD11	1:A:189:LYS:HG3	1.76	0.67
1:D:58:ASN:HB3	1:D:101:THR:OG1	1.93	0.67
1:B:12:TYR:HB2	1:B:13:TRP:CZ3	2.30	0.67
2:C:3:ILE:HD11	2:C:105:LEU:HB3	1.74	0.67
2:C:9:GLU:HG3	2:C:10:THR:H	1.58	0.67
1:K:12:TYR:HB2	1:K:13:TRP:CZ3	2.30	0.67
1:A:55:LEU:HD11	1:A:81:LEU:HD23	1.77	0.67
1:B:190:GLU:OE1	1:B:190:GLU:N	2.23	0.67
1:D:97:ASN:ND2	3:D:202:NAG:O5	2.27	0.67
2:J:9:GLU:HG3	2:J:10:THR:H	1.59	0.67
1:F:178:MET:SD	1:F:179:ASP:N	2.57	0.67
1:F:12:TYR:HB2	1:F:13:TRP:CE3	2.29	0.67
1:A:178:MET:SD	1:A:179:ASP:N	2.56	0.67
1:A:12:TYR:HB2	1:A:13:TRP:CE3	2.30	0.67
1:I:73:GLU:N	1:I:73:GLU:OE1	2.27	0.67
1:A:151:PRO:HB2	1:A:154:LEU:HB3	1.77	0.67
2:C:21:GLN:OE1	2:C:21:GLN:N	2.27	0.67
1:D:20:THR:HG22	1:D:141:ASN:HB3	1.77	0.67
1:D:169:MET:HE2	1:D:169:MET:HA	1.77	0.67
1:I:24:ASN:OD1	1:I:25:TYR:N	2.28	0.67
1:I:58:ASN:HB3	1:I:101:THR:CG2	2.21	0.67
1:K:50:LEU:HD11	1:K:83:VAL:HG11	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:43:ASP:O	1:I:44:ARG:HB3	1.95	0.67
1:D:140:VAL:HB	1:D:175:VAL:HG12	1.76	0.66
2:J:9:GLU:O	2:J:75:LEU:HD13	1.95	0.66
1:K:154:LEU:HB2	1:K:155:HIS:CE1	2.30	0.66
1:F:92:ASP:OD1	1:F:93:LYS:N	2.27	0.66
1:F:154:LEU:HB2	1:F:155:HIS:CE1	2.31	0.66
1:I:140:VAL:HB	1:I:175:VAL:HG12	1.77	0.66
2:L:29:VAL:HG22	2:L:88:HIS:HB2	1.77	0.66
2:C:29:VAL:HG22	2:C:88:HIS:HB2	1.77	0.66
1:I:109:CYS:HB3	1:K:4:CYS:O	1.95	0.66
2:L:15:CYS:HB2	2:L:101:MET:HB3	1.78	0.66
1:A:12:TYR:HB2	1:A:13:TRP:CZ3	2.30	0.66
1:B:120:GLU:HG2	1:B:122:ILE:HD13	1.76	0.66
1:K:43:ASP:O	1:K:44:ARG:HB3	1.96	0.66
2:L:21:GLN:N	2:L:21:GLN:OE1	2.27	0.66
1:D:11:ARG:HB2	1:D:69:VAL:HG11	1.78	0.66
2:G:21:GLN:N	2:G:21:GLN:OE1	2.29	0.66
2:J:47:LYS:HZ1	2:J:49:LYS:HD3	1.61	0.66
1:B:19:LEU:HB3	1:B:142:LEU:HD12	1.77	0.66
1:D:178:MET:SD	1:D:179:ASP:N	2.58	0.66
1:D:190:GLU:OE1	1:D:190:GLU:N	2.25	0.66
1:F:12:TYR:HB2	1:F:13:TRP:CZ3	2.31	0.66
1:A:4:CYS:O	1:K:109:CYS:HB3	1.94	0.66
1:K:140:VAL:HB	1:K:175:VAL:CG1	2.26	0.66
1:A:19:LEU:CD2	1:A:83:VAL:HB	2.26	0.65
2:E:7:PHE:HB2	2:E:108:LEU:HD23	1.78	0.65
1:F:19:LEU:CD2	1:F:83:VAL:HB	2.25	0.65
1:A:154:LEU:HB2	1:A:155:HIS:CE1	2.31	0.65
1:B:92:ASP:OD1	1:B:93:LYS:N	2.28	0.65
2:E:7:PHE:HB2	2:E:108:LEU:CD2	2.27	0.65
2:E:62:SER:O	2:E:70:LEU:HD12	1.96	0.65
1:I:154:LEU:HB2	1:I:155:HIS:CE1	2.31	0.65
1:K:179:ASP:O	1:K:180:GLU:HG3	1.97	0.65
1:A:92:ASP:OD1	1:A:93:LYS:N	2.29	0.65
1:B:20:THR:HG22	1:B:141:ASN:HB3	1.76	0.65
2:L:7:PHE:HB2	2:L:108:LEU:CD2	2.25	0.65
2:E:21:GLN:OE1	2:E:21:GLN:N	2.29	0.65
1:I:108:ASN:HB2	1:I:136:CYS:HB3	1.78	0.65
2:J:29:VAL:CG2	2:J:88:HIS:HB2	2.26	0.65
1:I:20:THR:HG22	1:I:141:ASN:HB3	1.79	0.65
2:J:105:LEU:HD12	2:J:105:LEU:O	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:12:TYR:HB2	1:B:13:TRP:CE3	2.32	0.65
1:D:12:TYR:HB2	1:D:13:TRP:CE3	2.31	0.65
1:D:19:LEU:HD23	1:D:83:VAL:O	1.96	0.65
1:I:12:TYR:HB2	1:I:13:TRP:CE3	2.32	0.65
2:J:80:LYS:HA	2:J:105:LEU:HD12	1.79	0.65
1:B:25:TYR:OH	1:B:54:GLY:HA3	1.97	0.65
1:F:50:LEU:HD11	1:F:83:VAL:HG11	1.79	0.65
1:K:11:ARG:HB2	1:K:69:VAL:HG11	1.78	0.65
1:K:12:TYR:HB2	1:K:13:TRP:CE3	2.32	0.65
1:K:190:GLU:OE1	1:K:190:GLU:N	2.26	0.65
2:H:21:GLN:OE1	2:H:21:GLN:N	2.30	0.64
1:D:154:LEU:HB2	1:D:155:HIS:CE1	2.33	0.64
1:B:55:LEU:HD11	1:B:81:LEU:HD23	1.78	0.64
1:B:43:ASP:O	1:B:44:ARG:HB3	1.97	0.64
1:D:50:LEU:HD11	1:D:83:VAL:HG11	1.79	0.64
1:F:100:VAL:CG1	1:F:130:ILE:HG12	2.26	0.64
2:J:21:GLN:OE1	2:J:21:GLN:N	2.31	0.64
2:L:29:VAL:CG2	2:L:88:HIS:HB2	2.27	0.64
2:H:3:ILE:HD11	2:H:105:LEU:HB3	1.79	0.64
1:D:120:GLU:HG2	1:D:122:ILE:HD13	1.80	0.64
1:K:80:LYS:NZ	1:K:184:CYS:O	2.29	0.64
2:H:53:VAL:HB	2:H:58:MET:HE1	1.78	0.64
2:E:26:SER:O	2:E:45:LEU:HD22	1.98	0.64
2:L:5:ALA:HB1	2:L:9:GLU:HB3	1.79	0.64
1:A:73:GLU:N	1:A:73:GLU:OE1	2.31	0.64
1:B:73:GLU:N	1:B:73:GLU:OE1	2.30	0.64
2:C:29:VAL:CG2	2:C:88:HIS:HB2	2.27	0.64
1:I:19:LEU:HD23	1:I:83:VAL:O	1.98	0.64
1:K:19:LEU:HD23	1:K:83:VAL:O	1.96	0.64
2:G:29:VAL:HG22	2:G:88:HIS:HB2	1.80	0.64
1:A:186:LEU:CD1	1:A:189:LYS:HG3	2.28	0.64
1:B:154:LEU:HB2	1:B:155:HIS:CE1	2.33	0.64
2:E:11:ALA:HB2	2:E:75:LEU:HD21	1.80	0.64
2:L:62:SER:O	2:L:70:LEU:HD12	1.97	0.64
1:B:11:ARG:HB2	1:B:69:VAL:CG1	2.28	0.63
1:F:5:PRO:HB2	1:F:67:ARG:NH1	2.13	0.63
1:F:73:GLU:N	1:F:73:GLU:OE1	2.31	0.63
1:K:50:LEU:HD23	1:K:50:LEU:H	1.64	0.63
1:B:19:LEU:HD23	1:B:83:VAL:O	1.97	0.63
1:D:8:GLN:HG2	1:D:9:ASP:N	2.13	0.63
1:D:37:MET:HE2	1:D:48:ILE:HD11	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:29:VAL:CG2	2:E:88:HIS:HB2	2.28	0.63
1:I:190:GLU:OE1	1:I:190:GLU:N	2.25	0.63
2:C:7:PHE:HB2	2:C:108:LEU:HD23	1.80	0.63
1:D:50:LEU:HD23	1:D:50:LEU:H	1.63	0.63
1:A:120:GLU:HB2	1:A:173:TYR:CD2	2.33	0.63
1:B:24:ASN:OD1	1:B:25:TYR:N	2.31	0.63
1:I:179:ASP:O	1:I:180:GLU:HG3	1.98	0.63
1:A:43:ASP:O	1:A:44:ARG:HB3	1.98	0.63
1:D:43:ASP:O	1:D:44:ARG:HB3	1.97	0.63
1:F:179:ASP:O	1:F:180:GLU:HG3	1.98	0.63
1:A:50:LEU:HD11	1:A:83:VAL:HG11	1.80	0.63
1:B:17:ALA:O	1:B:85:LEU:HD12	1.98	0.63
1:F:20:THR:CG2	1:F:141:ASN:HB3	2.29	0.63
1:F:43:ASP:O	1:F:44:ARG:HB3	1.97	0.63
1:A:11:ARG:HB2	1:A:69:VAL:CG1	2.28	0.62
2:C:105:LEU:HD12	2:C:105:LEU:O	1.98	0.62
1:D:183:GLN:NE2	1:D:185:PHE:O	2.30	0.62
2:C:62:SER:O	2:C:70:LEU:HD12	1.99	0.62
1:K:8:GLN:HG2	1:K:9:ASP:N	2.13	0.62
2:G:26:SER:O	2:G:45:LEU:HD22	2.00	0.62
1:B:183:GLN:HG3	2:C:37:ASN:HD21	1.64	0.62
2:G:44:TYR:CD1	2:G:45:LEU:HG	2.34	0.62
1:I:19:LEU:CD2	1:I:83:VAL:HB	2.28	0.62
1:B:23:VAL:HG23	1:B:136:CYS:O	2.00	0.62
1:B:46:ALA:HB2	1:B:64:THR:HG21	1.80	0.62
1:D:80:LYS:NZ	1:D:184:CYS:O	2.32	0.62
2:C:7:PHE:HB2	2:C:108:LEU:CD2	2.30	0.62
1:D:196:CYS:O	1:D:197:TYR:HB2	1.98	0.62
2:E:44:TYR:CD1	2:E:45:LEU:HG	2.35	0.62
1:F:105:MET:O	1:I:6:PRO:HB3	2.00	0.62
2:G:62:SER:O	2:G:70:LEU:HD12	2.00	0.62
1:K:20:THR:HG22	1:K:141:ASN:HB3	1.82	0.62
2:J:15:CYS:HB2	2:J:101:MET:HB3	1.82	0.61
2:H:24:SER:OG	2:H:27:GLU:OE1	2.18	0.61
2:C:53:VAL:HB	2:C:58:MET:CE	2.31	0.61
1:D:24:ASN:OD1	1:D:25:TYR:N	2.33	0.61
1:F:151:PRO:HB2	1:F:154:LEU:HB3	1.81	0.61
2:J:29:VAL:HG22	2:J:88:HIS:HB2	1.82	0.61
1:B:56:GLU:HG3	1:B:103:THR:HB	1.82	0.61
1:K:73:GLU:N	1:K:73:GLU:OE1	2.33	0.61
2:H:61:THR:HB	2:H:70:LEU:HD11	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:5:PRO:HB2	1:B:67:ARG:NH1	2.16	0.61
1:B:140:VAL:HB	1:B:175:VAL:CG1	2.30	0.61
1:D:19:LEU:CD2	1:D:83:VAL:HB	2.30	0.61
1:K:121:SER:HB3	2:L:98:ILE:O	2.00	0.61
1:A:109:CYS:O	1:B:2:THR:N	2.34	0.61
1:D:179:ASP:O	1:D:180:GLU:HG3	2.00	0.61
1:I:151:PRO:HB2	1:I:154:LEU:HB3	1.81	0.61
1:K:24:ASN:OD1	1:K:25:TYR:N	2.33	0.61
2:L:44:TYR:CD1	2:L:45:LEU:HG	2.34	0.61
1:A:183:GLN:HG3	2:H:37:ASN:HD21	1.65	0.61
1:A:179:ASP:O	1:A:180:GLU:HG3	2.00	0.61
1:D:11:ARG:HB2	1:D:69:VAL:CG1	2.30	0.61
2:G:71:ARG:HG2	2:G:73:HIS:NE2	2.15	0.61
2:J:61:THR:HB	2:J:70:LEU:HD11	1.81	0.61
2:L:26:SER:O	2:L:45:LEU:HD22	2.00	0.61
1:A:196:CYS:O	1:A:197:TYR:HB2	1.99	0.61
1:F:24:ASN:OD1	1:F:25:TYR:N	2.34	0.61
2:H:105:LEU:HD12	2:H:105:LEU:O	2.01	0.61
1:B:196:CYS:O	1:B:197:TYR:HB2	2.01	0.61
1:F:5:PRO:HB2	1:F:67:ARG:HH12	1.64	0.61
1:F:50:LEU:HD23	1:F:50:LEU:H	1.66	0.61
1:K:196:CYS:O	1:K:197:TYR:HB2	2.01	0.61
1:A:8:GLN:HG2	1:A:9:ASP:N	2.15	0.61
2:G:5:ALA:HB1	2:G:9:GLU:HB3	1.82	0.61
2:H:7:PHE:HB2	2:H:108:LEU:CD2	2.28	0.60
1:F:121:SER:HB3	2:G:98:ILE:O	2.01	0.60
1:I:196:CYS:O	1:I:197:TYR:HB2	2.00	0.60
2:J:26:SER:O	2:J:45:LEU:HD22	2.01	0.60
1:F:196:CYS:O	1:F:197:TYR:HB2	2.00	0.60
1:A:50:LEU:HD23	1:A:50:LEU:H	1.67	0.60
2:C:61:THR:HB	2:C:70:LEU:HD11	1.82	0.60
1:D:150:ASN:N	1:D:151:PRO:HD2	2.16	0.60
1:K:46:ALA:HB2	1:K:64:THR:HG21	1.83	0.60
1:A:100:VAL:CG1	1:A:130:ILE:HG12	2.30	0.60
1:B:169:MET:HA	1:B:169:MET:HE2	1.84	0.60
1:I:8:GLN:HG2	1:I:9:ASP:N	2.16	0.60
1:K:120:GLU:HB2	1:K:173:TYR:CD2	2.37	0.60
1:K:140:VAL:HB	1:K:175:VAL:HG12	1.83	0.60
1:A:19:LEU:HD23	1:A:83:VAL:O	2.01	0.60
2:L:9:GLU:O	2:L:75:LEU:HD13	2.01	0.60
1:D:73:GLU:N	1:D:73:GLU:OE1	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:82:SER:HB3	1:F:185:PHE:CE1	2.37	0.60
2:G:105:LEU:HD12	2:G:105:LEU:O	2.00	0.60
2:L:56:LYS:HG2	2:L:60:ARG:NH2	2.16	0.60
2:C:56:LYS:HG2	2:C:60:ARG:NH2	2.17	0.60
1:D:46:ALA:HB2	1:D:64:THR:HG21	1.84	0.60
2:L:47:LYS:HZ1	2:L:49:LYS:HD3	1.66	0.60
2:H:62:SER:O	2:H:70:LEU:HD12	2.02	0.60
1:F:8:GLN:HG2	1:F:9:ASP:N	2.17	0.60
2:J:53:VAL:HB	2:J:58:MET:CE	2.32	0.60
1:B:179:ASP:O	1:B:180:GLU:HG3	2.02	0.59
1:B:97:ASN:ND2	3:B:202:NAG:O5	2.35	0.59
1:A:5:PRO:HB2	1:A:67:ARG:NH1	2.17	0.59
1:B:50:LEU:HD23	1:B:50:LEU:H	1.68	0.59
2:C:26:SER:O	2:C:45:LEU:HD22	2.02	0.59
1:F:186:LEU:CD1	1:F:189:LYS:HG3	2.32	0.59
2:G:7:PHE:HB2	2:G:108:LEU:CD2	2.31	0.59
1:I:19:LEU:HB3	1:I:142:LEU:HD12	1.84	0.59
1:I:55:LEU:HD11	1:I:81:LEU:HD23	1.83	0.59
1:A:24:ASN:OD1	1:A:25:TYR:N	2.36	0.59
2:C:44:TYR:CD1	2:C:45:LEU:HG	2.38	0.59
1:D:186:LEU:CD1	1:D:189:LYS:HG3	2.33	0.59
2:G:29:VAL:CG2	2:G:88:HIS:HB2	2.33	0.59
2:G:30:VAL:CG1	2:G:43:VAL:HB	2.32	0.59
1:K:23:VAL:HG21	1:K:25:TYR:CE2	2.37	0.59
2:H:39:VAL:HG13	2:H:53:VAL:HA	1.84	0.59
1:D:151:PRO:HB2	1:D:154:LEU:HB3	1.84	0.59
1:I:169:MET:HE2	1:I:169:MET:HA	1.83	0.59
1:I:183:GLN:NE2	1:I:185:PHE:O	2.24	0.59
1:B:183:GLN:NE2	1:B:185:PHE:O	2.24	0.59
1:I:150:ASN:N	1:I:151:PRO:HD2	2.18	0.59
1:B:23:VAL:HG21	1:B:25:TYR:CE2	2.38	0.59
2:G:9:GLU:O	2:G:75:LEU:HD13	2.03	0.59
2:L:20:SER:OG	2:L:21:GLN:OE1	2.16	0.59
1:A:120:GLU:HG2	1:A:122:ILE:HD13	1.82	0.59
2:H:30:VAL:CG1	2:H:43:VAL:HB	2.32	0.59
1:D:11:ARG:HE	1:D:69:VAL:HG13	1.67	0.59
1:D:23:VAL:HG21	1:D:25:TYR:CE2	2.37	0.59
1:A:19:LEU:HB3	1:A:142:LEU:HD12	1.82	0.59
1:I:120:GLU:HB2	1:I:173:TYR:CD2	2.38	0.59
1:I:121:SER:HB3	2:J:98:ILE:O	2.02	0.59
1:K:23:VAL:HG23	1:K:136:CYS:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:PRO:HG3	1:A:163:ARG:HH22	1.68	0.58
1:A:190:GLU:OE1	1:A:190:GLU:N	2.27	0.58
1:B:8:GLN:HG2	1:B:9:ASP:N	2.18	0.58
1:F:190:GLU:OE1	1:F:190:GLU:N	2.26	0.58
2:J:44:TYR:CD1	2:J:45:LEU:HG	2.38	0.58
1:K:120:GLU:HG2	1:K:122:ILE:HD13	1.84	0.58
1:A:82:SER:HB3	1:A:185:PHE:CE1	2.38	0.58
1:A:114:TYR:CE1	1:A:116:SER:HB2	2.38	0.58
1:B:19:LEU:CD2	1:B:83:VAL:HB	2.32	0.58
2:E:64:ASP:OD1	2:E:65:SER:N	2.35	0.58
1:K:151:PRO:HB2	1:K:154:LEU:HB3	1.83	0.58
2:H:26:SER:O	2:H:45:LEU:HD22	2.04	0.58
1:B:150:ASN:N	1:B:151:PRO:HD2	2.18	0.58
1:B:11:ARG:HB2	1:B:69:VAL:HG11	1.84	0.58
2:C:24:SER:OG	2:C:27:GLU:OE1	2.20	0.58
1:D:20:THR:CG2	1:D:141:ASN:HB3	2.34	0.58
1:D:122:ILE:HD12	1:D:122:ILE:N	2.18	0.58
1:I:50:LEU:HD23	1:I:50:LEU:H	1.68	0.58
2:L:9:GLU:HG3	2:L:10:THR:H	1.69	0.58
1:F:122:ILE:HD12	1:F:122:ILE:N	2.19	0.58
1:F:140:VAL:HB	1:F:175:VAL:CG1	2.33	0.58
1:F:150:ASN:N	1:F:151:PRO:HD2	2.17	0.58
1:F:183:GLN:HG3	2:G:37:ASN:ND2	2.19	0.58
1:D:23:VAL:HG23	1:D:136:CYS:O	2.03	0.58
1:K:11:ARG:HB2	1:K:69:VAL:CG1	2.33	0.58
1:K:122:ILE:HG13	2:L:100:GLN:HB3	1.86	0.58
1:A:5:PRO:HB2	1:A:67:ARG:HH12	1.67	0.58
1:A:50:LEU:HD23	1:A:57:ILE:O	2.04	0.58
2:C:64:ASP:OD1	2:C:65:SER:N	2.37	0.58
1:I:82:SER:HB3	1:I:185:PHE:CZ	2.38	0.58
1:I:105:MET:O	1:K:6:PRO:HB3	2.04	0.58
1:D:140:VAL:HB	1:D:175:VAL:CG1	2.33	0.58
1:D:151:PRO:HG3	1:D:163:ARG:NH2	2.19	0.58
2:E:53:VAL:HB	2:E:58:MET:CE	2.34	0.58
1:F:97:ASN:ND2	3:F:202:NAG:O5	2.34	0.58
2:J:62:SER:O	2:J:70:LEU:HD12	2.04	0.58
1:K:30:THR:HG21	1:K:192:SER:HB2	1.84	0.58
1:B:108:ASN:HB2	1:B:136:CYS:HB3	1.86	0.58
1:B:120:GLU:HB2	1:B:173:TYR:CD2	2.39	0.58
1:I:17:ALA:O	1:I:85:LEU:HD12	2.03	0.58
1:I:59:MET:HE3	1:I:85:LEU:HD22	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:39:GLU:HG3	1:K:68:PHE:O	2.04	0.58
1:A:20:THR:CG2	1:A:141:ASN:HB3	2.34	0.57
1:D:121:SER:HB3	2:E:98:ILE:O	2.04	0.57
1:K:19:LEU:CD2	1:K:83:VAL:HB	2.34	0.57
2:L:30:VAL:HG12	2:L:43:VAL:HB	1.86	0.57
1:A:105:MET:O	1:B:6:PRO:HB3	2.03	0.57
1:I:5:PRO:HB2	1:I:67:ARG:NH1	2.19	0.57
1:K:186:LEU:CD1	1:K:189:LYS:HG3	2.33	0.57
2:E:56:LYS:HG2	2:E:60:ARG:NH2	2.19	0.57
1:A:56:GLU:CG	1:A:103:THR:HB	2.34	0.57
1:D:120:GLU:HB2	1:D:173:TYR:CD2	2.39	0.57
1:F:46:ALA:HB2	1:F:64:THR:HG21	1.86	0.57
1:I:46:ALA:HB2	1:I:64:THR:HG21	1.87	0.57
1:A:140:VAL:HB	1:A:175:VAL:CG1	2.35	0.57
1:F:151:PRO:HG3	1:F:163:ARG:NH2	2.20	0.57
1:K:122:ILE:HD12	1:K:122:ILE:N	2.20	0.57
1:K:150:ASN:N	1:K:151:PRO:HD2	2.19	0.57
2:H:44:TYR:CD1	2:H:45:LEU:HG	2.39	0.57
1:F:120:GLU:HB2	1:F:173:TYR:CD2	2.40	0.57
1:B:2:THR:OG1	1:B:3:ILE:HD12	2.04	0.57
1:B:186:LEU:CD1	1:B:189:LYS:HG3	2.35	0.57
1:D:183:GLN:HG3	2:E:37:ASN:HD21	1.68	0.57
1:I:118:LEU:HD13	1:I:130:ILE:HG13	1.87	0.57
1:I:183:GLN:HG3	2:J:37:ASN:ND2	2.20	0.57
2:J:32:TRP:HA	2:J:84:GLN:O	2.05	0.57
1:A:7:ARG:HD3	1:A:67:ARG:NH2	2.20	0.57
2:E:20:SER:OG	2:E:21:GLN:OE1	2.16	0.57
1:F:77:LYS:HG2	1:F:190:GLU:OE2	2.05	0.57
1:I:140:VAL:HB	1:I:175:VAL:CG1	2.34	0.57
2:L:11:ALA:HB2	2:L:75:LEU:HD21	1.87	0.56
1:A:122:ILE:HD12	1:A:122:ILE:N	2.20	0.56
1:A:183:GLN:HG3	2:H:37:ASN:ND2	2.20	0.56
1:B:105:MET:O	1:D:6:PRO:HB3	2.05	0.56
1:D:2:THR:OG1	1:D:3:ILE:HD12	2.04	0.56
1:F:140:VAL:HB	1:F:175:VAL:HG12	1.86	0.56
1:I:46:ALA:HB2	1:I:66:GLN:O	2.04	0.56
1:A:46:ALA:HB2	1:A:64:THR:HG21	1.87	0.56
1:B:121:SER:HB3	2:C:98:ILE:O	2.04	0.56
1:B:189:LYS:HB3	1:B:190:GLU:OE1	2.05	0.56
3:B:201:NAG:C8	1:D:158:ASP:HA	2.35	0.56
1:I:71:ALA:O	1:I:196:CYS:HB3	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:SER:HB3	2:H:98:ILE:O	2.05	0.56
1:A:23:VAL:HG23	1:A:136:CYS:O	2.06	0.56
1:A:150:ASN:N	1:A:151:PRO:HD2	2.21	0.56
1:B:19:LEU:HB3	1:B:142:LEU:CD1	2.35	0.56
1:F:2:THR:OG1	1:F:3:ILE:HD12	2.06	0.56
1:K:108:ASN:HB2	1:K:136:CYS:HB3	1.87	0.56
1:B:82:SER:HB3	1:B:185:PHE:CZ	2.40	0.56
1:I:122:ILE:HD12	1:I:122:ILE:N	2.20	0.56
1:K:11:ARG:HE	1:K:69:VAL:HG13	1.71	0.56
1:K:39:GLU:OE2	1:K:67:ARG:HB2	2.06	0.56
2:C:30:VAL:CG1	2:C:43:VAL:HB	2.36	0.56
1:F:183:GLN:HG3	2:G:37:ASN:HD21	1.70	0.56
1:B:71:ALA:O	1:B:196:CYS:HB3	2.06	0.55
1:F:19:LEU:HD23	1:F:83:VAL:O	2.06	0.55
1:F:56:GLU:CG	1:F:103:THR:HB	2.36	0.55
1:B:22:GLY:O	1:B:138:THR:N	2.33	0.55
2:C:71:ARG:HG2	2:C:73:HIS:NE2	2.21	0.55
1:B:44:ARG:NH1	1:B:63:ASP:HA	2.21	0.55
1:B:122:ILE:HD12	1:B:122:ILE:N	2.21	0.55
2:C:20:SER:OG	2:C:21:GLN:OE1	2.16	0.55
1:D:19:LEU:HB3	1:D:142:LEU:HD12	1.87	0.55
1:F:100:VAL:HG12	1:F:130:ILE:HG12	1.88	0.55
1:I:50:LEU:HD23	1:I:57:ILE:O	2.07	0.55
1:A:183:GLN:NE2	1:A:185:PHE:O	2.28	0.55
1:K:2:THR:OG1	1:K:3:ILE:HD12	2.07	0.55
1:A:6:PRO:HB3	1:K:105:MET:O	2.07	0.55
1:F:7:ARG:HD3	1:F:67:ARG:NH2	2.21	0.55
3:F:201:NAG:C8	1:I:158:ASP:HA	2.37	0.55
1:K:66:GLN:HB3	1:K:87:THR:OG1	2.07	0.55
2:L:105:LEU:HD12	2:L:105:LEU:O	2.06	0.55
2:J:30:VAL:CG1	2:J:43:VAL:HB	2.35	0.55
2:L:53:VAL:HB	2:L:58:MET:CE	2.37	0.55
3:A:201:NAG:C8	1:B:158:ASP:HA	2.37	0.55
1:B:118:LEU:HD13	1:B:130:ILE:HG13	1.89	0.55
1:D:151:PRO:HB3	1:D:155:HIS:CD2	2.42	0.55
2:E:105:LEU:HD12	2:E:105:LEU:O	2.07	0.55
1:F:11:ARG:HB2	1:F:69:VAL:CG1	2.36	0.55
2:G:15:CYS:HB2	2:G:101:MET:HB3	1.88	0.55
1:I:2:THR:OG1	1:I:3:ILE:HD12	2.07	0.55
1:I:186:LEU:CD1	1:I:189:LYS:HG3	2.35	0.55
1:D:108:ASN:HB2	1:D:136:CYS:HB3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:23:VAL:HG21	1:I:25:TYR:CE2	2.42	0.55
1:A:20:THR:HG22	1:A:141:ASN:HB3	1.89	0.54
1:I:11:ARG:HB2	1:I:69:VAL:HG11	1.89	0.54
1:I:151:PRO:HG3	1:I:163:ARG:NH2	2.23	0.54
2:J:3:ILE:CD1	2:J:105:LEU:HB3	2.37	0.54
2:J:17:PHE:CD2	2:J:19:ASN:HB2	2.42	0.54
1:K:20:THR:CG2	1:K:141:ASN:HB3	2.36	0.54
2:C:17:PHE:CD2	2:C:19:ASN:HB2	2.41	0.54
2:G:39:VAL:HG13	2:G:53:VAL:HA	1.89	0.54
1:K:35:CYS:SG	1:K:36:HIS:N	2.80	0.54
1:K:189:LYS:HB3	1:K:190:GLU:OE1	2.08	0.54
1:A:2:THR:OG1	1:A:3:ILE:HD12	2.06	0.54
1:F:55:LEU:HD11	1:F:81:LEU:HD23	1.88	0.54
1:B:151:PRO:HB2	1:B:154:LEU:HB3	1.88	0.54
1:F:151:PRO:HG3	1:F:163:ARG:HH22	1.71	0.54
2:H:32:TRP:HA	2:H:84:GLN:O	2.08	0.54
1:D:50:LEU:HD23	1:D:57:ILE:O	2.08	0.54
1:I:23:VAL:HG23	1:I:136:CYS:O	2.08	0.54
1:B:55:LEU:HD11	1:B:81:LEU:CD2	2.37	0.54
1:B:122:ILE:HG13	2:C:100:GLN:HB3	1.90	0.54
1:F:19:LEU:HB3	1:F:142:LEU:HD12	1.88	0.54
2:L:36:GLU:HB2	2:L:38:LEU:HD23	1.90	0.54
2:H:71:ARG:HG2	2:H:73:HIS:NE2	2.22	0.54
2:J:71:ARG:HG2	2:J:73:HIS:NE2	2.23	0.54
1:I:11:ARG:HB2	1:I:69:VAL:CG1	2.38	0.54
1:D:35:CYS:SG	1:D:36:HIS:N	2.80	0.53
1:D:56:GLU:CG	1:D:103:THR:HB	2.36	0.53
1:F:35:CYS:SG	1:F:36:HIS:N	2.81	0.53
1:B:56:GLU:CG	1:B:103:THR:HB	2.39	0.53
2:C:39:VAL:HG13	2:C:53:VAL:HA	1.90	0.53
1:D:151:PRO:HG3	1:D:163:ARG:HH22	1.73	0.53
1:D:189:LYS:HB3	1:D:190:GLU:OE1	2.07	0.53
1:K:50:LEU:HD23	1:K:57:ILE:O	2.08	0.53
1:B:151:PRO:HB3	1:B:155:HIS:CD2	2.44	0.53
2:G:62:SER:OG	2:G:71:ARG:HB3	2.07	0.53
2:J:56:LYS:HG2	2:J:60:ARG:NH2	2.24	0.53
2:E:5:ALA:HB1	2:E:9:GLU:HB3	1.90	0.53
1:I:50:LEU:HD11	1:I:83:VAL:HG11	1.90	0.53
1:B:93:LYS:HB3	1:B:169:MET:SD	2.47	0.53
1:B:145:ASP:HB3	1:B:164:ASN:HD22	1.74	0.53
1:A:23:VAL:HG21	1:A:25:TYR:CE2	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:ALA:O	1:A:196:CYS:HB3	2.08	0.53
1:A:158:ASP:HA	3:K:201:NAG:C8	2.38	0.53
2:H:13:LEU:HD11	2:H:105:LEU:HD23	1.89	0.53
1:B:151:PRO:HG3	1:B:163:ARG:NH2	2.24	0.53
2:C:11:ALA:HB2	2:C:75:LEU:HD21	1.91	0.53
2:C:32:TRP:HA	2:C:84:GLN:O	2.09	0.53
1:D:105:MET:O	1:F:6:PRO:HB3	2.09	0.53
1:D:122:ILE:H	1:D:122:ILE:CD1	2.21	0.53
1:I:20:THR:CG2	1:I:141:ASN:HB3	2.38	0.53
2:L:64:ASP:OD1	2:L:65:SER:N	2.42	0.53
1:A:13:TRP:HD1	1:A:162:TYR:HE1	1.57	0.53
2:H:17:PHE:CD2	2:H:19:ASN:HB2	2.44	0.53
1:B:114:TYR:CE1	1:B:116:SER:HB2	2.44	0.53
1:D:39:GLU:OE2	1:D:67:ARG:HB2	2.09	0.53
1:D:122:ILE:HG13	2:E:100:GLN:HB3	1.91	0.53
1:I:39:GLU:OE2	1:I:67:ARG:HB2	2.09	0.53
1:K:19:LEU:HB3	1:K:142:LEU:HD12	1.91	0.53
2:G:64:ASP:OD1	2:G:65:SER:N	2.41	0.53
2:J:53:VAL:O	2:J:58:MET:HE2	2.08	0.53
1:F:183:GLN:NE2	1:F:185:PHE:O	2.28	0.53
1:I:7:ARG:HD3	1:I:67:ARG:NH2	2.24	0.53
1:K:186:LEU:HD11	1:K:189:LYS:HG3	1.90	0.53
1:A:22:GLY:O	1:A:138:THR:N	2.35	0.52
1:B:50:LEU:HD11	1:B:83:VAL:HG11	1.91	0.52
1:D:13:TRP:HD1	1:D:162:TYR:HE1	1.56	0.52
1:F:23:VAL:HG23	1:F:136:CYS:O	2.09	0.52
1:F:186:LEU:HD11	1:F:189:LYS:HG3	1.91	0.52
2:G:17:PHE:CD2	2:G:19:ASN:HB2	2.44	0.52
1:B:183:GLN:HG3	2:C:37:ASN:ND2	2.23	0.52
1:D:142:LEU:HD23	1:D:173:TYR:CD1	2.45	0.52
1:D:186:LEU:HD11	1:D:189:LYS:HG3	1.92	0.52
1:F:50:LEU:HD23	1:F:57:ILE:O	2.10	0.52
1:F:97:ASN:HD21	3:F:202:NAG:C5	2.22	0.52
2:G:53:VAL:HB	2:G:58:MET:CE	2.37	0.52
1:A:39:GLU:OE2	1:A:67:ARG:HB2	2.09	0.52
1:A:97:ASN:HD21	3:A:202:NAG:C5	2.23	0.52
1:A:183:GLN:HE22	1:A:185:PHE:C	2.12	0.52
1:B:39:GLU:OE2	1:B:67:ARG:HB2	2.09	0.52
1:F:22:GLY:O	1:F:138:THR:N	2.35	0.52
1:F:22:GLY:O	1:F:138:THR:OG1	2.19	0.52
1:F:23:VAL:HG21	1:F:25:TYR:CE2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:56:GLU:CG	1:I:103:THR:HB	2.37	0.52
1:I:73:GLU:OE1	1:I:196:CYS:HB2	2.10	0.52
1:K:151:PRO:HG3	1:K:163:ARG:HH22	1.72	0.52
2:E:39:VAL:HG11	2:E:52:SER:OG	2.09	0.52
1:F:183:GLN:HE22	1:F:185:PHE:C	2.12	0.52
1:D:169:MET:HA	1:D:169:MET:CE	2.39	0.52
1:K:82:SER:HB3	1:K:185:PHE:CE1	2.45	0.52
1:A:82:SER:HB3	1:A:185:PHE:CZ	2.45	0.52
2:G:39:VAL:HG11	2:G:52:SER:OG	2.10	0.52
1:I:151:PRO:HG3	1:I:163:ARG:HH22	1.74	0.52
1:K:101:THR:HG22	1:K:131:THR:OG1	2.09	0.52
1:A:35:CYS:SG	1:A:36:HIS:N	2.81	0.52
1:A:100:VAL:HG12	1:A:130:ILE:HG12	1.91	0.52
1:I:44:ARG:NH1	1:I:63:ASP:HA	2.24	0.52
1:I:175:VAL:HG23	2:J:96:ILE:HG22	1.91	0.52
1:B:77:LYS:HG2	1:B:190:GLU:OE2	2.09	0.52
1:I:97:ASN:ND2	3:I:202:NAG:O5	2.39	0.52
2:J:5:ALA:HB1	2:J:9:GLU:HB3	1.91	0.52
1:B:186:LEU:HG	1:B:189:LYS:HD2	1.90	0.52
2:E:107:VAL:HG12	2:E:108:LEU:N	2.25	0.52
1:F:169:MET:HA	1:F:169:MET:CE	2.38	0.52
2:J:24:SER:OG	2:J:27:GLU:OE1	2.25	0.52
1:K:151:PRO:HB3	1:K:155:HIS:CD2	2.44	0.52
1:D:37:MET:CE	1:D:48:ILE:HD11	2.41	0.51
2:E:32:TRP:HA	2:E:84:GLN:O	2.10	0.51
1:A:106:GLU:OE2	1:B:11:ARG:HG3	2.10	0.51
1:A:186:LEU:HG	1:A:189:LYS:HD2	1.91	0.51
1:K:43:ASP:OD2	1:K:45:ASN:HB2	2.10	0.51
1:D:71:ALA:O	1:D:196:CYS:HB3	2.10	0.51
1:I:189:LYS:HB3	1:I:190:GLU:OE1	2.10	0.51
2:L:24:SER:OG	2:L:27:GLU:OE1	2.27	0.51
1:A:55:LEU:HD11	1:A:81:LEU:CD2	2.40	0.51
3:D:201:NAG:C8	1:F:158:ASP:HA	2.40	0.51
1:I:19:LEU:HB3	1:I:142:LEU:CD1	2.41	0.51
1:K:118:LEU:HD13	1:K:130:ILE:HG13	1.92	0.51
1:A:189:LYS:HB3	1:A:190:GLU:OE1	2.10	0.51
2:C:107:VAL:HG12	2:C:108:LEU:N	2.23	0.51
1:D:22:GLY:O	1:D:138:THR:N	2.38	0.51
1:I:97:ASN:HD21	3:I:202:NAG:C5	2.23	0.51
1:B:82:SER:HB3	1:B:185:PHE:CE1	2.46	0.51
1:B:169:MET:HA	1:B:169:MET:CE	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:39:VAL:HG11	2:L:52:SER:OG	2.10	0.51
2:L:61:THR:HB	2:L:70:LEU:HD11	1.93	0.51
1:A:66:GLN:HB3	1:A:87:THR:OG1	2.10	0.51
1:A:140:VAL:HB	1:A:175:VAL:HG12	1.92	0.51
1:F:39:GLU:HG3	1:F:68:PHE:O	2.11	0.51
2:J:40:LEU:HD13	2:J:57:TYR:CG	2.46	0.51
1:I:122:ILE:HG13	2:J:100:GLN:HB3	1.92	0.50
2:L:71:ARG:HG2	2:L:73:HIS:NE2	2.26	0.50
2:H:107:VAL:HG12	2:H:108:LEU:N	2.23	0.50
1:B:46:ALA:HB2	1:B:66:GLN:O	2.11	0.50
1:D:46:ALA:HB2	1:D:66:GLN:O	2.11	0.50
1:D:82:SER:HB3	1:D:185:PHE:CE1	2.47	0.50
1:F:189:LYS:HB3	1:F:190:GLU:OE1	2.10	0.50
2:J:36:GLU:HB2	2:J:38:LEU:HD23	1.94	0.50
2:L:17:PHE:CD2	2:L:19:ASN:HB2	2.47	0.50
2:C:5:ALA:HB1	2:C:9:GLU:HB3	1.92	0.50
2:E:24:SER:OG	2:E:27:GLU:OE1	2.26	0.50
1:F:39:GLU:OE2	1:F:67:ARG:HB2	2.11	0.50
1:K:46:ALA:HB2	1:K:66:GLN:O	2.10	0.50
1:K:114:TYR:CE1	1:K:116:SER:HB2	2.46	0.50
1:K:151:PRO:HG3	1:K:163:ARG:NH2	2.26	0.50
2:L:32:TRP:HA	2:L:84:GLN:O	2.11	0.50
2:L:30:VAL:CG1	2:L:43:VAL:HB	2.41	0.50
1:A:151:PRO:HB3	1:A:155:HIS:CD2	2.46	0.50
1:B:28:ASN:HD22	3:B:201:NAG:C7	2.24	0.50
1:B:167:TYR:O	1:B:170:ARG:HG2	2.12	0.50
2:E:36:GLU:HB2	2:E:38:LEU:HD23	1.93	0.50
1:I:151:PRO:HB3	1:I:155:HIS:CD2	2.46	0.50
1:D:118:LEU:N	1:D:118:LEU:HD12	2.27	0.50
2:E:23:GLN:OE1	2:E:28:LEU:HD21	2.12	0.50
1:I:64:THR:HG23	1:I:66:GLN:H	1.77	0.50
1:I:77:LYS:HG2	1:I:190:GLU:OE2	2.12	0.50
1:D:39:GLU:HG3	1:D:68:PHE:O	2.11	0.50
2:J:9:GLU:HG3	2:J:10:THR:N	2.26	0.50
1:A:77:LYS:HG2	1:A:190:GLU:OE2	2.11	0.50
1:F:71:ALA:O	1:F:196:CYS:HB3	2.12	0.50
2:G:36:GLU:HB2	2:G:38:LEU:HD23	1.93	0.50
1:B:46:ALA:CB	1:B:64:THR:HG21	2.42	0.49
3:I:201:NAG:C8	1:K:158:ASP:HA	2.42	0.49
1:D:183:GLN:HG3	2:E:37:ASN:ND2	2.27	0.49
1:I:99:SER:HA	1:I:129:ASP:OD1	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:62:SER:OG	2:J:71:ARG:HB3	2.11	0.49
2:H:5:ALA:HB1	2:H:9:GLU:HB3	1.94	0.49
2:G:32:TRP:HA	2:G:84:GLN:O	2.11	0.49
1:K:118:LEU:N	1:K:118:LEU:HD12	2.27	0.49
1:I:22:GLY:O	1:I:138:THR:N	2.33	0.49
2:L:107:VAL:HG12	2:L:108:LEU:N	2.25	0.49
1:F:20:THR:HG22	1:F:141:ASN:HB3	1.94	0.49
1:I:82:SER:HB3	1:I:185:PHE:CE1	2.48	0.49
2:J:107:VAL:HG12	2:J:108:LEU:N	2.24	0.49
1:K:37:MET:HE2	1:K:48:ILE:HD11	1.93	0.49
1:B:50:LEU:HD23	1:B:57:ILE:O	2.11	0.49
1:B:73:GLU:OE1	1:B:196:CYS:HB2	2.12	0.49
2:G:9:GLU:HG3	2:G:10:THR:H	1.76	0.49
1:K:93:LYS:N	1:K:93:LYS:HD2	2.27	0.49
1:A:151:PRO:HG3	1:A:163:ARG:NH2	2.27	0.49
1:D:31:ILE:HG22	1:D:31:ILE:O	2.12	0.49
2:E:85:CYS:O	2:E:100:GLN:HA	2.11	0.49
1:K:122:ILE:H	1:K:122:ILE:CD1	2.24	0.49
1:B:35:CYS:SG	1:B:36:HIS:N	2.84	0.49
1:D:19:LEU:HB3	1:D:142:LEU:CD1	2.43	0.49
2:E:71:ARG:HG2	2:E:73:HIS:NE2	2.28	0.49
1:A:73:GLU:OE1	1:A:196:CYS:HB2	2.13	0.49
1:D:73:GLU:OE1	1:D:196:CYS:HB2	2.13	0.49
1:F:82:SER:HB3	1:F:185:PHE:CZ	2.48	0.49
1:K:155:HIS:HB3	1:K:156:PRO:HD2	1.93	0.49
1:A:97:ASN:ND2	3:A:202:NAG:O5	2.42	0.48
1:A:98:ILE:O	1:A:128:CYS:HA	2.12	0.48
1:D:28:ASN:HD22	3:D:201:NAG:C7	2.26	0.48
1:F:155:HIS:HB3	1:F:156:PRO:HD2	1.95	0.48
2:G:107:VAL:HG12	2:G:108:LEU:N	2.24	0.48
2:E:61:THR:HB	2:E:70:LEU:HD11	1.94	0.48
1:F:19:LEU:HB3	1:F:142:LEU:CD1	2.42	0.48
1:F:106:GLU:OE2	1:I:11:ARG:HG3	2.13	0.48
2:G:80:LYS:HA	2:G:105:LEU:HD12	1.95	0.48
1:K:142:LEU:HD23	1:K:173:TYR:CD1	2.48	0.48
1:A:169:MET:HA	1:A:169:MET:CE	2.39	0.48
1:D:43:ASP:OD2	1:D:45:ASN:HB2	2.13	0.48
2:E:9:GLU:HG3	2:E:10:THR:N	2.24	0.48
1:I:122:ILE:H	1:I:122:ILE:CD1	2.23	0.48
1:A:22:GLY:O	1:A:138:THR:OG1	2.24	0.48
1:A:118:LEU:HD13	1:A:130:ILE:HG13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:64:ASP:OD1	2:H:65:SER:N	2.46	0.48
1:B:59:MET:HE3	1:B:85:LEU:HD22	1.94	0.48
1:F:31:ILE:O	1:F:31:ILE:HG22	2.14	0.48
1:B:100:VAL:HG12	1:B:130:ILE:HG12	1.95	0.48
2:C:9:GLU:HG3	2:C:10:THR:N	2.27	0.48
2:C:85:CYS:O	2:C:100:GLN:HA	2.13	0.48
1:K:19:LEU:HB3	1:K:142:LEU:CD1	2.44	0.48
1:K:109:CYS:SG	1:K:110:GLY:N	2.86	0.48
2:H:39:VAL:HG11	2:H:52:SER:OG	2.12	0.48
2:E:15:CYS:HB2	2:E:101:MET:HB3	1.95	0.48
1:F:122:ILE:H	1:F:122:ILE:CD1	2.21	0.48
1:K:71:ALA:O	1:K:196:CYS:HB3	2.14	0.48
1:A:19:LEU:HB3	1:A:142:LEU:CD1	2.43	0.48
2:H:36:GLU:HB2	2:H:38:LEU:HD23	1.94	0.48
1:D:101:THR:HG22	1:D:131:THR:OG1	2.13	0.48
1:F:108:ASN:HB2	1:F:136:CYS:HB3	1.94	0.48
2:G:24:SER:OG	2:G:27:GLU:OE1	2.30	0.48
2:G:85:CYS:O	2:G:100:GLN:HA	2.14	0.48
1:I:35:CYS:SG	1:I:36:HIS:N	2.85	0.48
1:A:31:ILE:O	1:A:31:ILE:HG22	2.14	0.48
1:D:155:HIS:HB3	1:D:156:PRO:HD2	1.95	0.48
1:F:186:LEU:HG	1:F:189:LYS:HD2	1.96	0.48
1:K:37:MET:HG2	1:K:196:CYS:O	2.13	0.48
2:H:62:SER:OG	2:H:71:ARG:HB3	2.14	0.48
1:B:186:LEU:HD11	1:B:189:LYS:HG3	1.96	0.48
1:K:31:ILE:O	1:K:31:ILE:HG22	2.14	0.48
1:A:46:ALA:HB2	1:A:66:GLN:O	2.14	0.48
1:A:155:HIS:HB3	1:A:156:PRO:HD2	1.95	0.48
2:H:80:LYS:HA	2:H:105:LEU:HD12	1.95	0.48
1:D:3:ILE:HD12	1:D:3:ILE:N	2.29	0.48
2:E:30:VAL:HG12	2:E:43:VAL:HB	1.94	0.48
1:F:13:TRP:HD1	1:F:162:TYR:HE1	1.62	0.48
1:K:37:MET:CE	1:K:48:ILE:HD11	2.44	0.48
1:K:50:LEU:HD23	1:K:50:LEU:N	2.29	0.48
2:L:85:CYS:O	2:L:100:GLN:HA	2.14	0.48
1:B:3:ILE:HD12	1:B:3:ILE:N	2.29	0.47
2:C:80:LYS:HA	2:C:105:LEU:CD1	2.42	0.47
1:D:179:ASP:C	1:D:180:GLU:HG3	2.34	0.47
1:K:28:ASN:HD22	3:K:201:NAG:C7	2.27	0.47
1:K:186:LEU:HG	1:K:189:LYS:HD2	1.94	0.47
2:L:9:GLU:HG3	2:L:10:THR:N	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:LYS:N	1:A:93:LYS:HD2	2.29	0.47
1:D:16:ALA:HB1	1:D:150:ASN:ND2	2.28	0.47
2:E:17:PHE:CD2	2:E:19:ASN:HB2	2.49	0.47
2:J:7:PHE:HB2	2:J:108:LEU:CD2	2.40	0.47
1:A:151:PRO:HB2	1:A:154:LEU:CB	2.44	0.47
2:H:85:CYS:O	2:H:100:GLN:HA	2.14	0.47
2:E:47:LYS:HZ1	2:E:49:LYS:HD3	1.78	0.47
2:J:83:TYR:HE2	2:J:105:LEU:HD21	1.79	0.47
1:A:122:ILE:HG13	2:H:100:GLN:HB3	1.95	0.47
1:B:11:ARG:HB2	1:B:69:VAL:HG13	1.96	0.47
1:F:89:GLN:HG2	1:F:90:ARG:N	2.28	0.47
1:K:73:GLU:OE1	1:K:196:CYS:HB2	2.15	0.47
1:B:122:ILE:H	1:B:122:ILE:CD1	2.25	0.47
1:F:118:LEU:HD13	1:F:130:ILE:HG13	1.97	0.47
1:K:56:GLU:CG	1:K:103:THR:HB	2.42	0.47
2:L:80:LYS:HA	2:L:105:LEU:HD12	1.96	0.47
1:I:118:LEU:N	1:I:118:LEU:HD12	2.29	0.47
2:J:53:VAL:HB	2:J:58:MET:HE1	1.95	0.47
1:A:18:GLU:HB2	1:A:84:LEU:HD23	1.97	0.47
1:A:28:ASN:HD22	3:A:201:NAG:C7	2.28	0.47
1:B:43:ASP:OD1	1:B:43:ASP:N	2.44	0.47
1:D:55:LEU:HD11	1:D:81:LEU:HD23	1.97	0.47
1:F:74:GLY:O	1:F:81:LEU:HD12	2.15	0.47
1:F:93:LYS:N	1:F:93:LYS:HD2	2.29	0.47
1:I:31:ILE:HG22	1:I:31:ILE:O	2.15	0.47
1:K:100:VAL:HG13	1:K:130:ILE:HG12	1.96	0.47
1:K:169:MET:HA	1:K:169:MET:CE	2.40	0.47
2:L:89:HIS:O	2:L:95:MET:HA	2.13	0.47
1:D:118:LEU:HD13	1:D:130:ILE:HG13	1.96	0.47
1:F:64:THR:HG23	1:F:66:GLN:H	1.80	0.47
2:G:3:ILE:CD1	2:G:105:LEU:HB3	2.44	0.47
1:K:55:LEU:HD11	1:K:81:LEU:HD23	1.96	0.47
1:A:25:TYR:HH	1:A:54:GLY:HA3	1.77	0.47
1:A:179:ASP:C	1:A:180:GLU:HG3	2.35	0.47
2:C:62:SER:OG	2:C:71:ARG:HB3	2.14	0.47
1:D:99:SER:HA	1:D:129:ASP:OD1	2.15	0.47
1:F:67:ARG:O	1:F:88:THR:HG23	2.15	0.47
1:I:62:MET:SD	1:I:62:MET:N	2.88	0.47
1:I:179:ASP:C	1:I:180:GLU:HG3	2.35	0.47
1:K:82:SER:HB3	1:K:185:PHE:CZ	2.51	0.47
1:A:109:CYS:SG	1:A:110:GLY:N	2.88	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:20:THR:CG2	1:B:141:ASN:HB3	2.45	0.46
1:B:179:ASP:C	1:B:180:GLU:HG3	2.35	0.46
1:B:183:GLN:HE22	1:B:185:PHE:C	2.13	0.46
1:F:90:ARG:NE	1:F:92:ASP:O	2.48	0.46
1:F:132:ILE:HD13	1:F:137:VAL:HG21	1.97	0.46
2:G:83:TYR:CE2	2:G:105:LEU:HD21	2.49	0.46
1:A:89:GLN:HG2	1:A:90:ARG:N	2.30	0.46
1:B:31:ILE:HG22	1:B:31:ILE:O	2.16	0.46
1:F:46:ALA:HB2	1:F:66:GLN:O	2.15	0.46
1:K:67:ARG:HG2	1:K:88:THR:HG21	1.97	0.46
1:A:122:ILE:H	1:A:122:ILE:CD1	2.24	0.46
2:H:40:LEU:HD13	2:H:57:TYR:CG	2.51	0.46
2:E:105:LEU:HD12	2:E:105:LEU:C	2.36	0.46
1:F:16:ALA:HB1	1:F:150:ASN:ND2	2.30	0.46
1:F:179:ASP:C	1:F:180:GLU:HG3	2.36	0.46
2:G:105:LEU:HD12	2:G:105:LEU:C	2.35	0.46
1:I:28:ASN:HD22	3:I:201:NAG:C7	2.27	0.46
1:I:55:LEU:HD11	1:I:81:LEU:CD2	2.44	0.46
2:H:82:LEU:N	2:H:82:LEU:HD12	2.31	0.46
1:B:155:HIS:HB3	1:B:156:PRO:HD2	1.96	0.46
2:E:13:LEU:N	2:E:13:LEU:HD22	2.31	0.46
1:B:22:GLY:O	1:B:138:THR:OG1	2.26	0.46
2:G:47:LYS:HD2	2:G:47:LYS:O	2.16	0.46
2:G:82:LEU:HD12	2:G:82:LEU:N	2.31	0.46
1:I:16:ALA:HB1	1:I:146:PRO:HG2	1.96	0.46
1:K:19:LEU:HD22	1:K:85:LEU:HD11	1.98	0.46
2:H:13:LEU:N	2:H:13:LEU:HD22	2.31	0.46
2:C:3:ILE:CD1	2:C:105:LEU:HB3	2.44	0.46
1:F:151:PRO:HB3	1:F:155:HIS:CD2	2.49	0.46
2:G:40:LEU:HD13	2:G:57:TYR:CG	2.51	0.46
1:I:100:VAL:HG12	1:I:130:ILE:HG12	1.94	0.46
1:I:154:LEU:HA	1:I:155:HIS:HA	1.50	0.46
1:B:112:THR:HA	1:B:133:ASN:OD1	2.16	0.46
1:B:118:LEU:HD12	1:B:118:LEU:N	2.30	0.46
1:D:41:TYR:HE1	1:D:64:THR:HG23	1.81	0.46
1:D:100:VAL:HG13	1:D:130:ILE:HG12	1.97	0.46
2:G:13:LEU:N	2:G:13:LEU:HD22	2.30	0.46
1:I:169:MET:HA	1:I:169:MET:CE	2.46	0.46
1:B:7:ARG:HD3	1:B:67:ARG:NH2	2.31	0.46
1:B:99:SER:HA	1:B:129:ASP:OD1	2.16	0.46
2:E:44:TYR:CE1	2:E:45:LEU:HG	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:11:ALA:CB	2:G:75:LEU:HD11	2.46	0.46
1:I:49:VAL:HG13	1:I:49:VAL:O	2.16	0.46
2:L:53:VAL:HB	2:L:58:MET:SD	2.56	0.46
2:L:105:LEU:HD12	2:L:105:LEU:C	2.35	0.46
2:H:33:GLN:HA	2:H:40:LEU:HD23	1.98	0.46
1:D:50:LEU:HD23	1:D:50:LEU:N	2.29	0.46
1:D:109:CYS:SG	1:D:110:GLY:N	2.89	0.46
1:D:164:ASN:ND2	1:D:169:MET:HB2	2.31	0.46
1:I:186:LEU:HD11	1:I:189:LYS:HG3	1.97	0.46
1:F:73:GLU:OE1	1:F:196:CYS:HB2	2.16	0.45
1:F:98:ILE:O	1:F:128:CYS:HA	2.16	0.45
2:C:105:LEU:HD12	2:C:105:LEU:C	2.36	0.45
1:I:183:GLN:HE22	1:I:185:PHE:C	2.14	0.45
1:A:118:LEU:N	1:A:118:LEU:HD12	2.30	0.45
1:D:187:ASP:O	1:D:191:VAL:HG21	2.17	0.45
1:A:17:ALA:HA	1:A:146:PRO:HD3	1.97	0.45
1:A:151:PRO:HB3	1:A:155:HIS:NE2	2.32	0.45
1:I:16:ALA:HB1	1:I:146:PRO:CG	2.46	0.45
1:K:43:ASP:O	1:K:44:ARG:CB	2.64	0.45
1:A:67:ARG:O	1:A:88:THR:HG23	2.16	0.45
1:F:50:LEU:HD23	1:F:50:LEU:N	2.29	0.45
1:F:187:ASP:O	1:F:191:VAL:HG21	2.16	0.45
1:K:3:ILE:HD12	1:K:3:ILE:N	2.32	0.45
1:K:183:GLN:NE2	1:K:185:PHE:O	2.49	0.45
1:B:93:LYS:N	1:B:93:LYS:HD2	2.31	0.45
2:C:11:ALA:CB	2:C:75:LEU:HD11	2.47	0.45
2:C:13:LEU:N	2:C:13:LEU:HD22	2.32	0.45
2:C:83:TYR:CE2	2:C:105:LEU:HD21	2.51	0.45
1:D:94:VAL:HG22	1:D:94:VAL:O	2.17	0.45
2:E:39:VAL:C	2:E:40:LEU:HD22	2.37	0.45
1:F:109:CYS:SG	1:F:110:GLY:N	2.89	0.45
2:G:20:SER:OG	2:G:21:GLN:OE1	2.23	0.45
1:I:43:ASP:O	1:I:44:ARG:CB	2.65	0.45
2:J:13:LEU:N	2:J:13:LEU:HD22	2.31	0.45
1:K:22:GLY:O	1:K:138:THR:N	2.40	0.45
1:A:90:ARG:NE	1:A:92:ASP:O	2.48	0.45
2:H:15:CYS:HB2	2:H:101:MET:HB3	1.99	0.45
1:B:109:CYS:SG	1:B:110:GLY:N	2.90	0.45
1:F:93:LYS:HB3	1:F:169:MET:SD	2.57	0.45
2:G:9:GLU:HG3	2:G:10:THR:N	2.30	0.45
1:I:93:LYS:N	1:I:93:LYS:HD2	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:179:ASP:C	1:K:180:GLU:HG3	2.36	0.45
1:A:62:MET:SD	1:A:62:MET:N	2.90	0.45
1:A:185:PHE:HE2	1:A:191:VAL:HG11	1.82	0.45
2:H:47:LYS:HD2	2:H:47:LYS:O	2.17	0.45
2:C:82:LEU:N	2:C:82:LEU:HD12	2.32	0.45
1:D:30:THR:HG21	1:D:192:SER:HB2	1.99	0.45
1:F:25:TYR:HH	1:F:54:GLY:HA3	1.78	0.45
1:I:48:ILE:HD13	1:I:85:LEU:HD23	1.98	0.45
1:I:186:LEU:HG	1:I:189:LYS:HD2	1.98	0.45
2:J:20:SER:OG	2:J:21:GLN:OE1	2.25	0.45
2:H:47:LYS:HZ1	2:H:49:LYS:HD3	1.81	0.45
2:H:83:TYR:CE2	2:H:105:LEU:HD21	2.52	0.45
1:B:49:VAL:HG13	1:B:49:VAL:O	2.16	0.45
2:C:36:GLU:HB2	2:C:38:LEU:HD23	1.99	0.45
1:D:13:TRP:CD1	1:D:162:TYR:HE1	2.34	0.45
1:K:97:ASN:ND2	3:K:202:NAG:O5	2.49	0.45
2:L:44:TYR:HB3	2:L:47:LYS:HE3	1.98	0.45
1:A:41:TYR:HE1	1:A:64:THR:HG23	1.82	0.44
1:A:64:THR:HG23	1:A:65:ASP:N	2.32	0.44
1:B:98:ILE:O	1:B:128:CYS:HA	2.17	0.44
1:D:82:SER:HB3	1:D:185:PHE:CZ	2.51	0.44
1:D:183:GLN:HE22	1:D:185:PHE:C	2.20	0.44
1:I:109:CYS:SG	1:I:110:GLY:N	2.90	0.44
1:I:145:ASP:HB3	1:I:164:ASN:HD22	1.83	0.44
2:L:13:LEU:N	2:L:13:LEU:HD22	2.31	0.44
1:B:94:VAL:HG22	1:B:94:VAL:O	2.17	0.44
1:D:164:ASN:HD21	1:D:169:MET:HB2	1.83	0.44
1:K:99:SER:HA	1:K:129:ASP:OD1	2.17	0.44
1:F:118:LEU:N	1:F:118:LEU:HD12	2.32	0.44
1:I:43:ASP:OD2	1:I:45:ASN:HB2	2.17	0.44
2:J:82:LEU:HD12	2:J:82:LEU:N	2.31	0.44
1:K:87:THR:OG1	1:K:88:THR:N	2.51	0.44
2:L:82:LEU:HD12	2:L:82:LEU:N	2.32	0.44
1:A:191:VAL:O	1:A:191:VAL:HG23	2.17	0.44
1:D:19:LEU:HD22	1:D:85:LEU:HD11	1.99	0.44
2:G:11:ALA:HB2	2:G:75:LEU:HD11	1.98	0.44
2:G:61:THR:HB	2:G:70:LEU:HD11	1.98	0.44
1:I:155:HIS:HB3	1:I:156:PRO:HD2	1.98	0.44
1:D:67:ARG:HG2	1:D:88:THR:HG21	1.99	0.44
1:F:3:ILE:HD12	1:F:3:ILE:N	2.32	0.44
1:F:154:LEU:N	1:F:154:LEU:HD23	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:89:HIS:O	2:G:95:MET:HA	2.18	0.44
1:K:98:ILE:O	1:K:128:CYS:HA	2.18	0.44
2:C:40:LEU:HD13	2:C:57:TYR:CG	2.52	0.44
2:E:53:VAL:HB	2:E:58:MET:SD	2.58	0.44
1:I:94:VAL:HG22	1:I:94:VAL:O	2.17	0.44
1:K:144:THR:HG23	1:K:173:TYR:HE1	1.81	0.44
1:A:3:ILE:HD12	1:A:3:ILE:N	2.33	0.44
1:A:31:ILE:HB	1:A:34:GLU:HB2	1.99	0.44
1:A:87:THR:OG1	1:A:88:THR:N	2.51	0.44
1:B:154:LEU:HA	1:B:155:HIS:HA	1.52	0.44
2:C:39:VAL:HG11	2:C:52:SER:OG	2.18	0.44
1:D:43:ASP:O	1:D:44:ARG:CB	2.65	0.44
1:I:3:ILE:HD12	1:I:3:ILE:N	2.33	0.44
1:K:91:LEU:N	1:K:91:LEU:HD22	2.33	0.44
1:K:93:LYS:HB3	1:K:169:MET:SD	2.58	0.44
2:L:23:GLN:OE1	2:L:28:LEU:HD21	2.17	0.44
1:A:60:THR:HG22	1:A:62:MET:SD	2.58	0.43
1:I:16:ALA:HB1	1:I:150:ASN:ND2	2.33	0.43
2:J:47:LYS:NZ	2:J:49:LYS:HD3	2.31	0.43
1:K:187:ASP:O	1:K:191:VAL:HG21	2.18	0.43
1:F:28:ASN:HD22	3:F:201:NAG:C7	2.30	0.43
2:H:3:ILE:CD1	2:H:105:LEU:HB3	2.47	0.43
2:H:105:LEU:HD12	2:H:105:LEU:C	2.38	0.43
1:B:136:CYS:O	1:B:136:CYS:SG	2.76	0.43
1:D:191:VAL:HB	1:D:193:TYR:CE2	2.52	0.43
1:F:91:LEU:N	1:F:91:LEU:HD22	2.33	0.43
1:K:16:ALA:HB1	1:K:150:ASN:ND2	2.34	0.43
1:K:120:GLU:HB2	1:K:173:TYR:HD2	1.83	0.43
1:A:94:VAL:HG22	1:A:94:VAL:O	2.18	0.43
2:C:64:ASP:HB3	2:C:67:SER:OG	2.19	0.43
2:E:54:HIS:CE1	2:E:56:LYS:H	2.36	0.43
1:I:84:LEU:HG	1:I:193:TYR:HE1	1.83	0.43
3:I:201:NAG:H81	1:K:158:ASP:HA	1.99	0.43
2:J:15:CYS:HB2	2:J:101:MET:CB	2.49	0.43
2:J:85:CYS:O	2:J:100:GLN:HA	2.19	0.43
1:D:62:MET:N	1:D:62:MET:SD	2.92	0.43
2:E:90:LYS:HA	2:E:95:MET:HG2	2.01	0.43
1:F:99:SER:HA	1:F:129:ASP:OD1	2.18	0.43
1:F:154:LEU:HD23	1:F:154:LEU:H	1.84	0.43
1:K:89:GLN:HG2	1:K:90:ARG:N	2.33	0.43
1:D:98:ILE:O	1:D:128:CYS:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:186:LEU:HD12	1:D:189:LYS:HG3	1.99	0.43
1:D:188:ILE:HG23	1:D:188:ILE:O	2.19	0.43
2:J:105:LEU:HD12	2:J:105:LEU:C	2.38	0.43
1:A:93:LYS:HB3	1:A:169:MET:SD	2.59	0.43
1:B:151:PRO:HB3	1:B:155:HIS:NE2	2.33	0.43
1:I:136:CYS:O	1:I:136:CYS:SG	2.76	0.43
1:K:90:ARG:NE	1:K:92:ASP:O	2.48	0.43
1:K:151:PRO:HB3	1:K:155:HIS:NE2	2.34	0.43
1:A:91:LEU:N	1:A:91:LEU:HD22	2.33	0.43
1:D:48:ILE:HG23	1:D:48:ILE:O	2.18	0.43
1:D:93:LYS:N	1:D:93:LYS:HD2	2.33	0.43
1:F:64:THR:HG23	1:F:65:ASP:N	2.34	0.43
1:I:46:ALA:CB	1:I:64:THR:HG21	2.48	0.43
2:J:47:LYS:HD2	2:J:47:LYS:O	2.19	0.43
1:A:99:SER:HA	1:A:129:ASP:OD1	2.19	0.43
1:D:191:VAL:HG23	1:D:191:VAL:O	2.19	0.43
2:E:82:LEU:HD12	2:E:82:LEU:N	2.34	0.43
1:F:118:LEU:HD11	1:F:130:ILE:HD12	2.01	0.43
2:G:17:PHE:CD1	2:G:87:ILE:HD12	2.54	0.43
1:I:186:LEU:HD12	1:I:189:LYS:HG3	2.01	0.43
1:B:48:ILE:HG23	1:B:48:ILE:O	2.19	0.42
1:B:127:SER:OG	3:B:202:NAG:O7	2.25	0.42
1:D:18:GLU:HB2	1:D:84:LEU:HD23	2.01	0.42
1:F:150:ASN:N	1:F:151:PRO:CD	2.82	0.42
1:A:49:VAL:HG13	1:A:49:VAL:O	2.19	0.42
1:B:89:GLN:HG2	1:B:90:ARG:N	2.34	0.42
1:D:91:LEU:N	1:D:91:LEU:HD22	2.34	0.42
2:E:39:VAL:HG22	2:E:40:LEU:N	2.34	0.42
1:F:43:ASP:O	1:F:44:ARG:CB	2.65	0.42
1:I:98:ILE:O	1:I:128:CYS:HA	2.19	0.42
1:I:187:ASP:O	1:I:191:VAL:HG21	2.19	0.42
1:B:149:ILE:HG22	1:B:163:ARG:HH12	1.83	0.42
1:D:22:GLY:HA2	1:D:80:LYS:HD3	2.00	0.42
1:D:44:ARG:NH1	1:D:63:ASP:HA	2.34	0.42
1:F:154:LEU:HA	1:F:155:HIS:HA	1.51	0.42
1:F:185:PHE:HE2	1:F:191:VAL:HG11	1.84	0.42
2:G:71:ARG:NH1	2:G:71:ARG:HB2	2.34	0.42
1:I:188:ILE:HG23	1:I:188:ILE:O	2.20	0.42
1:K:15:PHE:HB3	1:K:87:THR:HG23	2.01	0.42
1:K:154:LEU:HG	1:K:154:LEU:O	2.19	0.42
1:B:27:ILE:HG21	1:B:75:VAL:HG11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:86:ILE:HG22	2:C:88:HIS:CD2	2.55	0.42
1:F:60:THR:HG22	1:F:62:MET:SD	2.59	0.42
1:I:50:LEU:HD23	1:I:50:LEU:N	2.35	0.42
1:K:48:ILE:HD12	1:K:68:PHE:HB3	2.02	0.42
1:K:58:ASN:HB3	1:K:101:THR:HG1	1.81	0.42
1:K:62:MET:SD	1:K:62:MET:N	2.93	0.42
1:K:64:THR:HG23	1:K:65:ASP:N	2.34	0.42
1:K:67:ARG:O	1:K:88:THR:HG23	2.19	0.42
1:K:85:LEU:HD12	1:K:85:LEU:N	2.34	0.42
1:K:164:ASN:ND2	1:K:169:MET:HB2	2.35	0.42
1:B:97:ASN:HD21	3:B:202:NAG:C5	2.31	0.42
1:F:94:VAL:HG22	1:F:94:VAL:O	2.20	0.42
1:K:7:ARG:H	1:K:67:ARG:NH1	2.18	0.42
1:K:154:LEU:N	1:K:154:LEU:HD23	2.35	0.42
1:K:188:ILE:HG23	1:K:188:ILE:O	2.19	0.42
1:B:188:ILE:HG23	1:B:188:ILE:O	2.20	0.42
1:F:101:THR:HB	1:F:131:THR:OG1	2.19	0.42
2:L:54:HIS:CE1	2:L:56:LYS:H	2.38	0.42
1:A:13:TRP:CD1	1:A:162:TYR:HE1	2.37	0.42
1:A:43:ASP:O	1:A:44:ARG:CB	2.66	0.42
1:A:64:THR:O	1:A:65:ASP:HB2	2.19	0.42
1:B:187:ASP:O	1:B:191:VAL:HG21	2.20	0.42
2:C:47:LYS:HD2	2:C:47:LYS:O	2.19	0.42
1:D:132:ILE:HD13	1:D:137:VAL:HG21	2.02	0.42
1:F:188:ILE:HG23	1:F:188:ILE:O	2.20	0.42
1:I:154:LEU:HD23	1:I:154:LEU:N	2.35	0.42
1:A:48:ILE:HG23	1:A:48:ILE:O	2.20	0.42
2:C:17:PHE:CD1	2:C:87:ILE:HD12	2.54	0.42
2:C:47:LYS:HZ1	2:C:49:LYS:HD3	1.85	0.42
1:I:48:ILE:HG23	1:I:48:ILE:O	2.19	0.42
1:I:154:LEU:O	1:I:154:LEU:HG	2.19	0.42
1:A:154:LEU:H	1:A:154:LEU:HD23	1.85	0.42
2:H:44:TYR:CE1	2:H:45:LEU:HG	2.55	0.42
1:B:90:ARG:NE	1:B:92:ASP:O	2.48	0.42
1:D:17:ALA:HA	1:D:146:PRO:HD3	2.02	0.42
1:D:18:GLU:OE1	1:D:19:LEU:N	2.53	0.42
2:E:80:LYS:HA	2:E:105:LEU:HD12	2.01	0.42
1:I:59:MET:HE3	1:I:85:LEU:CD2	2.50	0.42
1:I:60:THR:HG22	1:I:62:MET:SD	2.60	0.42
1:K:94:VAL:HG22	1:K:94:VAL:O	2.20	0.42
2:L:47:LYS:HD2	2:L:47:LYS:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:47:LYS:NZ	2:L:49:LYS:HD3	2.33	0.42
1:A:18:GLU:OE1	1:A:19:LEU:N	2.53	0.42
1:A:154:LEU:HG	1:A:154:LEU:O	2.20	0.42
1:B:64:THR:HG23	1:B:66:GLN:H	1.85	0.42
1:B:154:LEU:O	1:B:154:LEU:HG	2.20	0.42
1:F:48:ILE:O	1:F:48:ILE:HG23	2.20	0.42
1:F:64:THR:O	1:F:65:ASP:HB2	2.19	0.42
1:I:44:ARG:HG3	1:I:44:ARG:O	2.20	0.42
1:K:77:LYS:HG2	1:K:190:GLU:OE2	2.18	0.42
1:A:154:LEU:HD23	1:A:154:LEU:N	2.35	0.41
1:B:62:MET:SD	1:B:62:MET:N	2.93	0.41
1:B:111:THR:OG1	1:B:112:THR:N	2.52	0.41
2:C:54:HIS:CE1	2:C:56:LYS:H	2.38	0.41
1:D:49:VAL:HG13	1:D:49:VAL:O	2.20	0.41
1:F:154:LEU:HG	1:F:154:LEU:O	2.20	0.41
1:K:150:ASN:N	1:K:151:PRO:CD	2.83	0.41
2:H:27:GLU:HA	2:H:45:LEU:HD22	2.01	0.41
2:C:66:ASP:OD1	2:C:66:ASP:N	2.53	0.41
1:D:136:CYS:O	1:D:136:CYS:SG	2.79	0.41
2:G:33:GLN:HA	2:G:40:LEU:HD23	2.01	0.41
1:K:48:ILE:HG23	1:K:48:ILE:O	2.20	0.41
1:A:74:GLY:O	1:A:81:LEU:HD12	2.21	0.41
1:B:118:LEU:HD21	1:B:130:ILE:HD12	2.02	0.41
1:B:154:LEU:HD23	1:B:154:LEU:H	1.85	0.41
2:C:36:GLU:O	2:C:37:ASN:HB2	2.19	0.41
2:E:71:ARG:NH1	2:E:71:ARG:HB2	2.35	0.41
1:F:115:ASP:OD1	1:F:131:THR:HG22	2.21	0.41
2:G:38:LEU:N	2:G:38:LEU:HD22	2.35	0.41
1:I:150:ASN:N	1:I:151:PRO:CD	2.84	0.41
1:I:191:VAL:HB	1:I:193:TYR:CE2	2.54	0.41
2:J:108:LEU:HD12	2:J:109:ALA:H	1.86	0.41
1:K:46:ALA:CB	1:K:64:THR:HG21	2.48	0.41
1:B:13:TRP:CD1	1:B:162:TYR:HE1	2.37	0.41
1:B:50:LEU:HD23	1:B:50:LEU:N	2.35	0.41
2:C:13:LEU:HG	2:C:83:TYR:HD2	1.84	0.41
2:E:13:LEU:HD11	2:E:105:LEU:HD23	2.01	0.41
2:J:44:TYR:HB3	2:J:47:LYS:HE3	2.02	0.41
1:K:97:ASN:HD21	3:K:202:NAG:C5	2.33	0.41
2:L:90:LYS:HA	2:L:95:MET:HG2	2.01	0.41
2:H:44:TYR:HB3	2:H:47:LYS:HE3	2.01	0.41
1:B:191:VAL:HG23	1:B:191:VAL:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:186:LEU:HD12	1:D:186:LEU:C	2.41	0.41
1:F:17:ALA:HA	1:F:146:PRO:HD3	2.01	0.41
1:K:191:VAL:HB	1:K:193:TYR:CE2	2.55	0.41
2:H:20:SER:OG	2:H:21:GLN:OE1	2.21	0.41
1:D:43:ASP:OD1	1:D:43:ASP:N	2.48	0.41
1:D:64:THR:HG23	1:D:65:ASP:N	2.35	0.41
1:D:154:LEU:HD23	1:D:154:LEU:N	2.36	0.41
2:E:47:LYS:HD2	2:E:47:LYS:O	2.21	0.41
1:F:49:VAL:O	1:F:49:VAL:HG13	2.20	0.41
1:I:166:GLU:OE1	1:I:168:GLY:N	2.54	0.41
1:K:22:GLY:HA2	1:K:80:LYS:HD3	2.02	0.41
1:A:50:LEU:HD23	1:A:50:LEU:N	2.32	0.41
1:A:154:LEU:HA	1:A:155:HIS:HA	1.51	0.41
1:A:188:ILE:HG23	1:A:188:ILE:O	2.21	0.41
1:B:184:CYS:O	1:B:185:PHE:HB3	2.20	0.41
1:D:150:ASN:N	1:D:151:PRO:CD	2.83	0.41
2:L:17:PHE:CD1	2:L:87:ILE:HD12	2.56	0.41
2:L:39:VAL:HG22	2:L:40:LEU:N	2.35	0.41
2:L:39:VAL:C	2:L:40:LEU:HD22	2.40	0.41
2:H:89:HIS:O	2:H:95:MET:HA	2.20	0.41
1:B:154:LEU:HD23	1:B:154:LEU:N	2.35	0.41
1:F:43:ASP:OD1	1:F:43:ASP:N	2.47	0.41
2:G:27:GLU:O	2:G:28:LEU:HD23	2.20	0.41
1:I:89:GLN:HG2	1:I:90:ARG:N	2.35	0.41
1:K:64:THR:O	1:K:65:ASP:HB2	2.20	0.41
1:K:154:LEU:HD23	1:K:154:LEU:H	1.86	0.41
1:A:83:VAL:HG12	1:A:85:LEU:HD21	2.03	0.41
1:A:136:CYS:O	1:A:136:CYS:SG	2.79	0.41
1:B:19:LEU:HD22	1:B:85:LEU:HD11	2.03	0.41
2:C:38:LEU:N	2:C:38:LEU:HD22	2.35	0.41
1:D:21:ILE:CD1	1:D:140:VAL:HG13	2.50	0.41
1:D:48:ILE:HD12	1:D:68:PHE:HB3	2.03	0.41
2:G:11:ALA:HB2	2:G:75:LEU:HD21	2.02	0.41
1:I:191:VAL:HG23	1:I:191:VAL:O	2.20	0.41
1:K:186:LEU:HD12	1:K:186:LEU:C	2.41	0.41
2:H:53:VAL:HB	2:H:58:MET:CE	2.48	0.41
1:D:77:LYS:HG2	1:D:190:GLU:OE2	2.20	0.41
1:D:85:LEU:HD12	1:D:85:LEU:N	2.36	0.41
1:K:136:CYS:O	1:K:136:CYS:SG	2.78	0.41
2:L:27:GLU:O	2:L:28:LEU:HD23	2.21	0.41
2:L:96:ILE:O	2:L:98:ILE:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:39:GLU:HG3	1:A:68:PHE:O	2.21	0.40
1:B:191:VAL:HB	1:B:193:TYR:CE2	2.55	0.40
1:D:44:ARG:HG3	1:D:44:ARG:O	2.21	0.40
1:D:53:TYR:CD2	1:D:81:LEU:HD11	2.56	0.40
1:D:154:LEU:O	1:D:154:LEU:HG	2.20	0.40
2:E:86:ILE:HG23	2:E:97:ARG:HD3	2.03	0.40
2:J:17:PHE:CD1	2:J:87:ILE:HD12	2.55	0.40
2:J:38:LEU:HD22	2:J:38:LEU:N	2.36	0.40
2:L:13:LEU:HD11	2:L:105:LEU:HD23	2.03	0.40
1:A:16:ALA:HB1	1:A:150:ASN:ND2	2.35	0.40
1:A:23:VAL:HG23	1:A:136:CYS:C	2.40	0.40
2:H:64:ASP:HB3	2:H:67:SER:OG	2.21	0.40
1:B:94:VAL:HG12	1:B:96:HIS:CE1	2.56	0.40
1:I:13:TRP:CD1	1:I:162:TYR:HE1	2.39	0.40
2:J:56:LYS:O	2:J:60:ARG:NH2	2.55	0.40
2:E:96:ILE:O	2:E:98:ILE:HG23	2.21	0.40
1:F:62:MET:SD	1:F:62:MET:N	2.94	0.40
1:F:136:CYS:O	1:F:136:CYS:SG	2.80	0.40
1:K:132:ILE:HD13	1:K:137:VAL:HG21	2.02	0.40
1:B:84:LEU:HG	1:B:193:TYR:HE1	1.87	0.40
2:G:44:TYR:CE1	2:G:45:LEU:HG	2.57	0.40
1:F:151:PRO:HB3	1:F:155:HIS:NE2	2.37	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	194/204 (95%)	159 (82%)	35 (18%)	0	100	100
1	B	194/204 (95%)	157 (81%)	37 (19%)	0	100	100
1	D	194/204 (95%)	160 (82%)	34 (18%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	194/204 (95%)	161 (83%)	33 (17%)	0	100	100
1	I	194/204 (95%)	154 (79%)	40 (21%)	0	100	100
1	K	194/204 (95%)	159 (82%)	35 (18%)	0	100	100
2	C	108/219 (49%)	102 (94%)	6 (6%)	0	100	100
2	E	108/219 (49%)	104 (96%)	4 (4%)	0	100	100
2	G	108/219 (49%)	103 (95%)	5 (5%)	0	100	100
2	H	108/219 (49%)	103 (95%)	5 (5%)	0	100	100
2	J	108/219 (49%)	105 (97%)	3 (3%)	0	100	100
2	L	108/219 (49%)	105 (97%)	3 (3%)	0	100	100
All	All	1812/2538 (71%)	1572 (87%)	240 (13%)	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	179/186 (96%)	168 (94%)	11 (6%)	15	43
1	B	179/186 (96%)	166 (93%)	13 (7%)	11	36
1	D	179/186 (96%)	167 (93%)	12 (7%)	13	40
1	F	179/186 (96%)	167 (93%)	12 (7%)	13	40
1	I	179/186 (96%)	169 (94%)	10 (6%)	17	46
1	K	179/186 (96%)	169 (94%)	10 (6%)	17	46
2	C	102/209 (49%)	101 (99%)	1 (1%)	73	84
2	E	102/209 (49%)	101 (99%)	1 (1%)	73	84
2	G	102/209 (49%)	101 (99%)	1 (1%)	73	84
2	H	102/209 (49%)	101 (99%)	1 (1%)	73	84
2	J	102/209 (49%)	101 (99%)	1 (1%)	73	84
2	L	102/209 (49%)	101 (99%)	1 (1%)	73	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1686/2370 (71%)	1612 (96%)	74 (4%)	26 53

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	CYS
1	A	11	ARG
1	A	27	ILE
1	A	35	CYS
1	A	50	LEU
1	A	55	LEU
1	A	87	THR
1	A	139	CYS
1	A	183	GLN
1	A	185	PHE
1	A	197	TYR
2	H	47	LYS
1	B	4	CYS
1	B	11	ARG
1	B	34	GLU
1	B	35	CYS
1	B	50	LEU
1	B	55	LEU
1	B	85	LEU
1	B	87	THR
1	B	101	THR
1	B	139	CYS
1	B	183	GLN
1	B	185	PHE
1	B	197	TYR
2	C	47	LYS
1	D	4	CYS
1	D	11	ARG
1	D	34	GLU
1	D	35	CYS
1	D	37	MET
1	D	50	LEU
1	D	55	LEU
1	D	87	THR
1	D	139	CYS
1	D	143	GLU
1	D	185	PHE

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Mol	Chain	Res	Type
1	D	197	TYR
2	E	47	LYS
1	F	4	CYS
1	F	11	ARG
1	F	35	CYS
1	F	50	LEU
1	F	55	LEU
1	F	87	THR
1	F	101	THR
1	F	139	CYS
1	F	143	GLU
1	F	183	GLN
1	F	185	PHE
1	F	197	TYR
2	G	47	LYS
1	I	4	CYS
1	I	11	ARG
1	I	35	CYS
1	I	50	LEU
1	I	55	LEU
1	I	101	THR
1	I	139	CYS
1	I	183	GLN
1	I	185	PHE
1	I	197	TYR
2	J	47	LYS
1	K	4	CYS
1	K	11	ARG
1	K	35	CYS
1	K	37	MET
1	K	50	LEU
1	K	55	LEU
1	K	87	THR
1	K	139	CYS
1	K	185	PHE
1	K	197	TYR
2	L	47	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
2	H	37	ASN

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Mol	Chain	Res	Type
2	C	37	ASN
2	C	89	HIS
2	E	37	ASN
2	E	89	HIS
2	G	37	ASN
2	J	37	ASN
2	J	89	HIS
1	K	183	GLN
2	L	37	ASN
2	L	89	HIS

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](#)

18 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	$\# Z > 2$
3	NAG	D	203	1	14,14,15	0.21	0	17,19,21	0.50	0
3	NAG	I	202	-	14,14,15	0.19	0	17,19,21	0.42	0
3	NAG	B	201	1	14,14,15	0.20	0	17,19,21	0.41	0
3	NAG	B	203	1	14,14,15	0.22	0	17,19,21	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	F	202	-	14,14,15	0.17	0	17,19,21	0.45	0
3	NAG	K	202	-	14,14,15	0.20	0	17,19,21	0.44	0
3	NAG	A	202	-	14,14,15	0.19	0	17,19,21	0.45	0
3	NAG	K	201	1	14,14,15	0.20	0	17,19,21	0.42	0
3	NAG	F	203	1	14,14,15	0.25	0	17,19,21	0.47	0
3	NAG	I	201	1	14,14,15	0.21	0	17,19,21	0.44	0
3	NAG	A	203	1	14,14,15	0.25	0	17,19,21	0.44	0
3	NAG	D	202	-	14,14,15	0.22	0	17,19,21	0.44	0
3	NAG	B	202	-	14,14,15	0.21	0	17,19,21	0.43	0
3	NAG	I	203	1	14,14,15	0.27	0	17,19,21	0.50	0
3	NAG	F	201	1	14,14,15	0.20	0	17,19,21	0.45	0
3	NAG	A	201	1	14,14,15	0.21	0	17,19,21	0.46	0
3	NAG	K	203	1	14,14,15	0.21	0	17,19,21	0.50	0
3	NAG	D	201	1	14,14,15	0.21	0	17,19,21	0.43	0

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
3	NAG	D	203	1	-	2/6/23/26	0/1/1/1
3	NAG	I	202	-	-	4/6/23/26	0/1/1/1
3	NAG	B	201	1	-	2/6/23/26	0/1/1/1
3	NAG	B	203	1	-	2/6/23/26	0/1/1/1
3	NAG	F	202	-	-	4/6/23/26	0/1/1/1
3	NAG	K	202	-	-	4/6/23/26	0/1/1/1
3	NAG	A	202	-	-	4/6/23/26	0/1/1/1
3	NAG	K	201	1	-	2/6/23/26	0/1/1/1
3	NAG	F	203	1	-	2/6/23/26	0/1/1/1
3	NAG	I	201	1	-	2/6/23/26	0/1/1/1
3	NAG	A	203	1	-	2/6/23/26	0/1/1/1
3	NAG	D	202	-	-	4/6/23/26	0/1/1/1
3	NAG	B	202	-	-	4/6/23/26	0/1/1/1
3	NAG	I	203	1	-	2/6/23/26	0/1/1/1
3	NAG	F	201	1	-	2/6/23/26	0/1/1/1
3	NAG	A	201	1	-	2/6/23/26	0/1/1/1
3	NAG	K	203	1	-	2/6/23/26	0/1/1/1
3	NAG	D	201	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (48) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	I	202	NAG	C1-C2-N2-C7
3	D	201	NAG	O5-C5-C6-O6
3	F	201	NAG	O5-C5-C6-O6
3	I	202	NAG	O5-C5-C6-O6
3	F	202	NAG	O5-C5-C6-O6
3	A	201	NAG	O5-C5-C6-O6
3	B	201	NAG	O5-C5-C6-O6
3	D	203	NAG	O5-C5-C6-O6
3	I	201	NAG	O5-C5-C6-O6
3	K	201	NAG	O5-C5-C6-O6
3	K	203	NAG	O5-C5-C6-O6
3	F	201	NAG	C4-C5-C6-O6
3	B	202	NAG	O5-C5-C6-O6
3	D	201	NAG	C4-C5-C6-O6
3	K	203	NAG	C4-C5-C6-O6
3	A	201	NAG	C4-C5-C6-O6
3	B	201	NAG	C4-C5-C6-O6
3	D	203	NAG	C4-C5-C6-O6
3	K	202	NAG	O5-C5-C6-O6
3	A	202	NAG	O5-C5-C6-O6
3	I	202	NAG	C4-C5-C6-O6
3	K	201	NAG	C4-C5-C6-O6
3	I	201	NAG	C4-C5-C6-O6
3	K	202	NAG	C4-C5-C6-O6
3	B	203	NAG	O5-C5-C6-O6
3	I	203	NAG	O5-C5-C6-O6
3	A	202	NAG	C4-C5-C6-O6
3	D	202	NAG	O5-C5-C6-O6
3	F	202	NAG	C4-C5-C6-O6
3	F	203	NAG	O5-C5-C6-O6
3	B	202	NAG	C4-C5-C6-O6
3	D	202	NAG	C4-C5-C6-O6
3	A	203	NAG	O5-C5-C6-O6
3	I	203	NAG	C4-C5-C6-O6
3	B	203	NAG	C4-C5-C6-O6
3	F	203	NAG	C4-C5-C6-O6
3	A	202	NAG	C3-C2-N2-C7

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Mol	Chain	Res	Type	Atoms
3	B	202	NAG	C3-C2-N2-C7
3	D	202	NAG	C3-C2-N2-C7
3	F	202	NAG	C3-C2-N2-C7
3	I	202	NAG	C3-C2-N2-C7
3	K	202	NAG	C3-C2-N2-C7
3	A	203	NAG	C4-C5-C6-O6
3	A	202	NAG	C1-C2-N2-C7
3	B	202	NAG	C1-C2-N2-C7
3	D	202	NAG	C1-C2-N2-C7
3	F	202	NAG	C1-C2-N2-C7
3	K	202	NAG	C1-C2-N2-C7

There are no ring outliers.

12 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	202	NAG	2	0
3	B	201	NAG	2	0
3	F	202	NAG	2	0
3	K	202	NAG	2	0
3	A	202	NAG	2	0
3	K	201	NAG	2	0
3	I	201	NAG	3	0
3	D	202	NAG	1	0
3	B	202	NAG	3	0
3	F	201	NAG	2	0
3	A	201	NAG	2	0
3	D	201	NAG	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

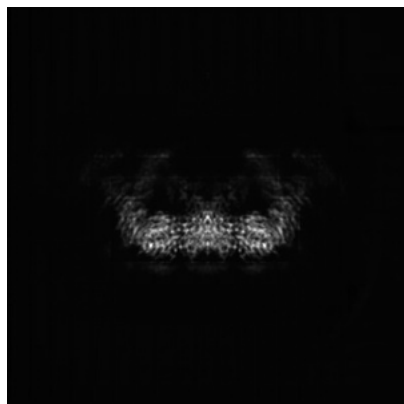
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29548. These allow visual inspection of the internal detail of the map and identification of artifacts.

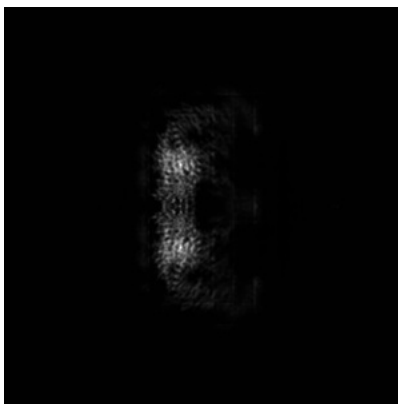
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

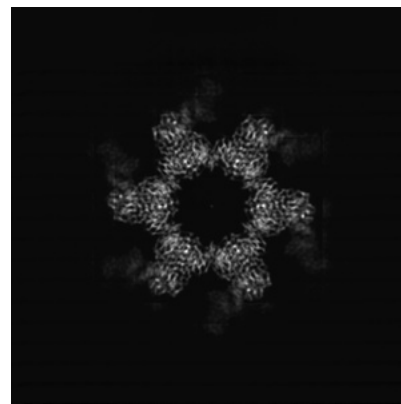
6.1.1 Primary map



X

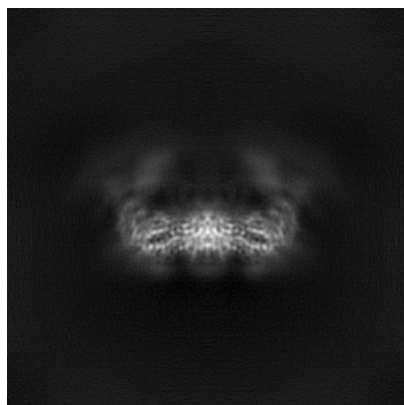


Y

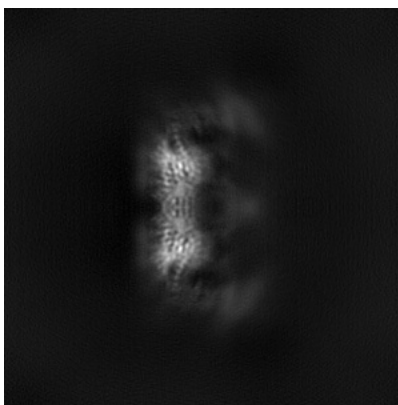


Z

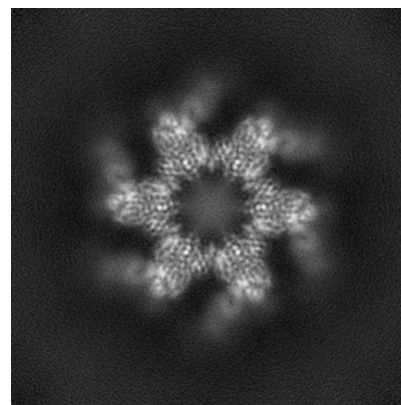
6.1.2 Raw map



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: 140

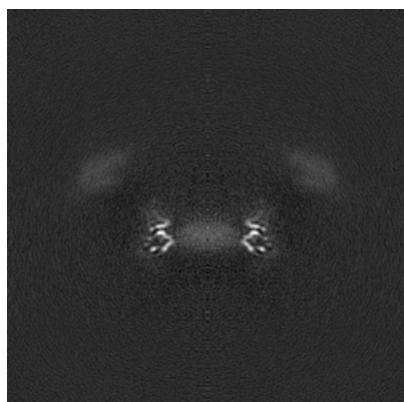


Y Index: 140

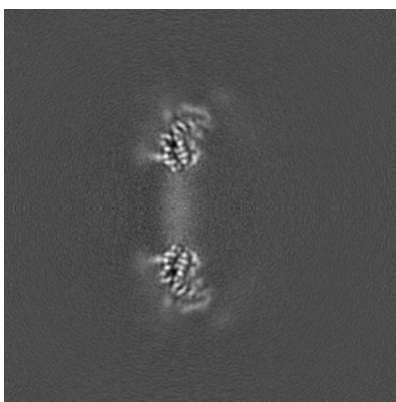


Z Index: 140

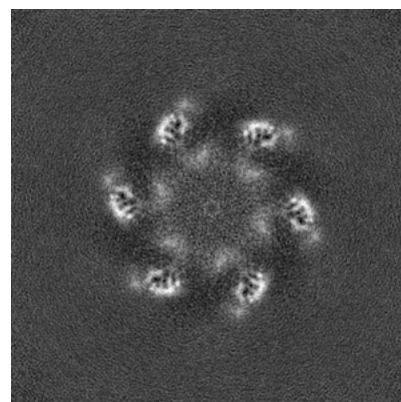
6.2.2 Raw map



X Index: 140



Y Index: 140



Z Index: 140

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

6.3 Largest variance slices [i](#)

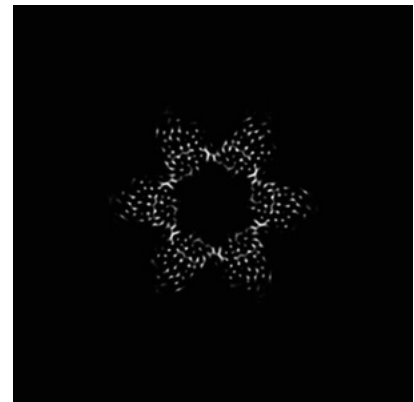
6.3.1 Primary map



X Index: 108

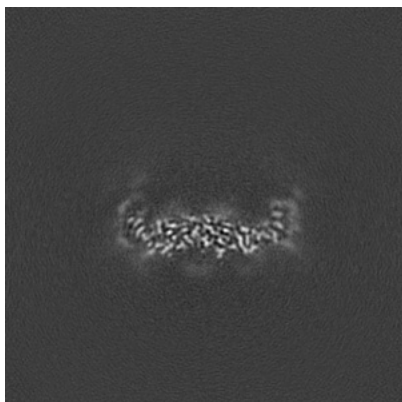


Y Index: 140

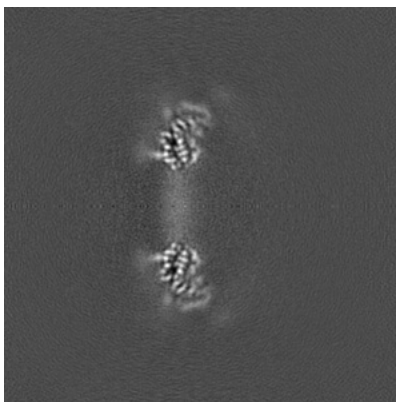


Z Index: 123

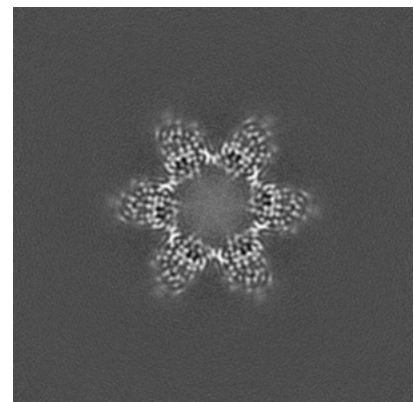
6.3.2 Raw map



X Index: 108



Y Index: 140

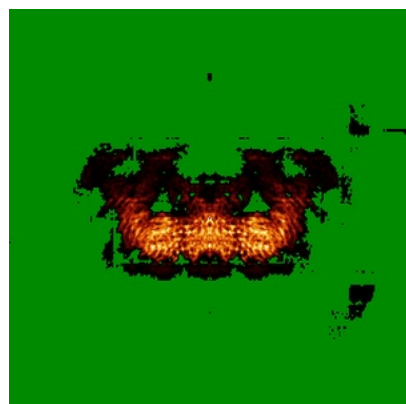


Z Index: 123

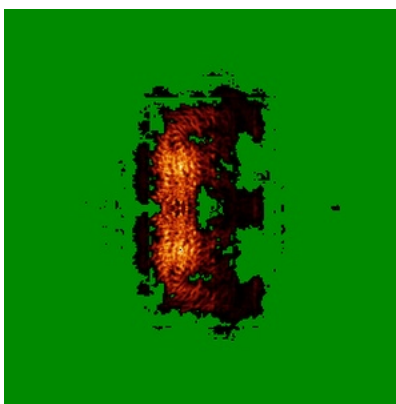
The images above show the largest variance slices of the map in three orthogonal directions.

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

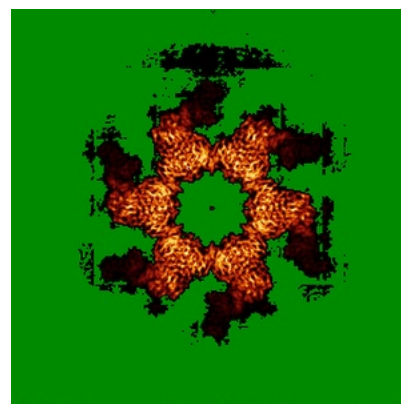
6.4.1 Primary map



X

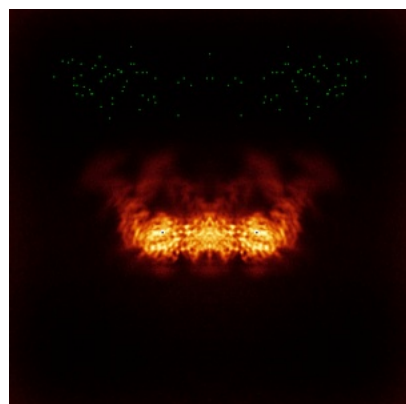


Y

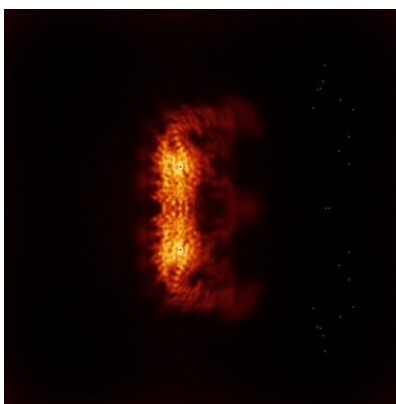


Z

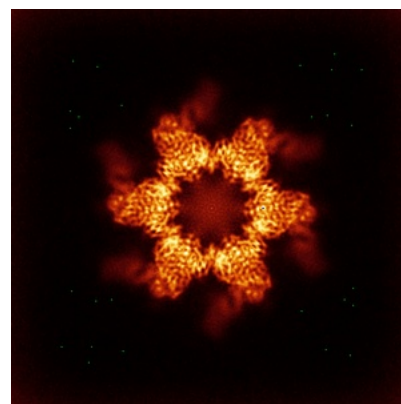
6.4.2 Raw map



X



Y

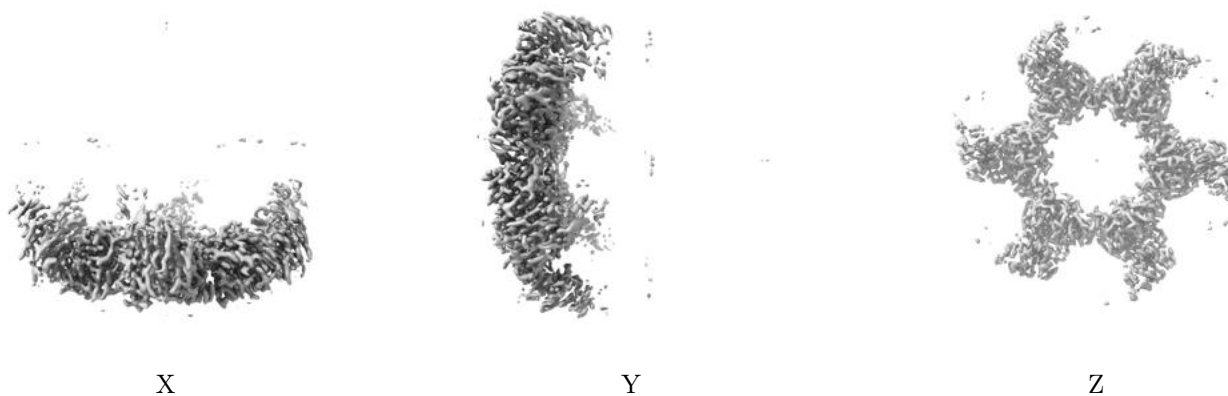


Z

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 0.25. 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.

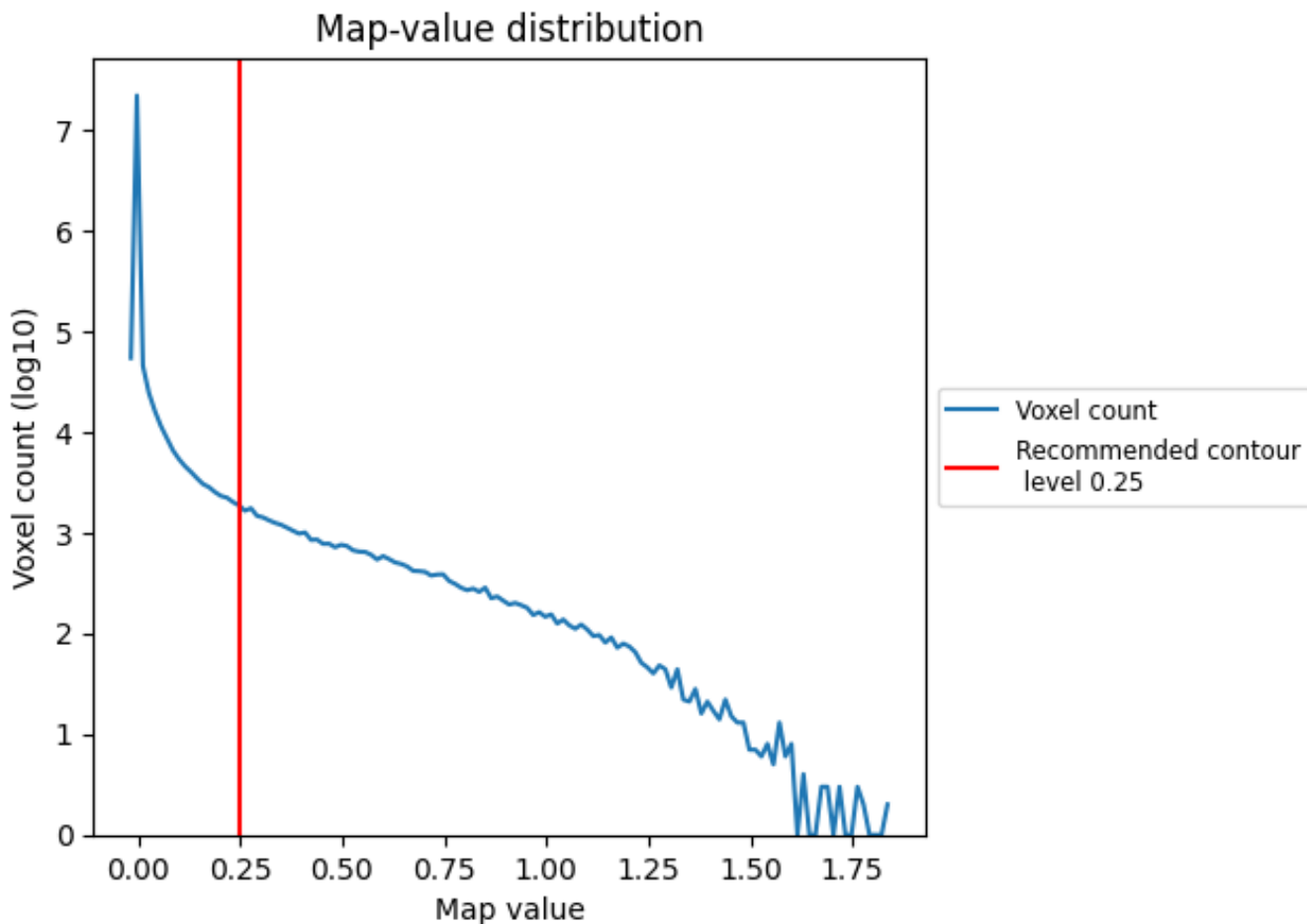
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

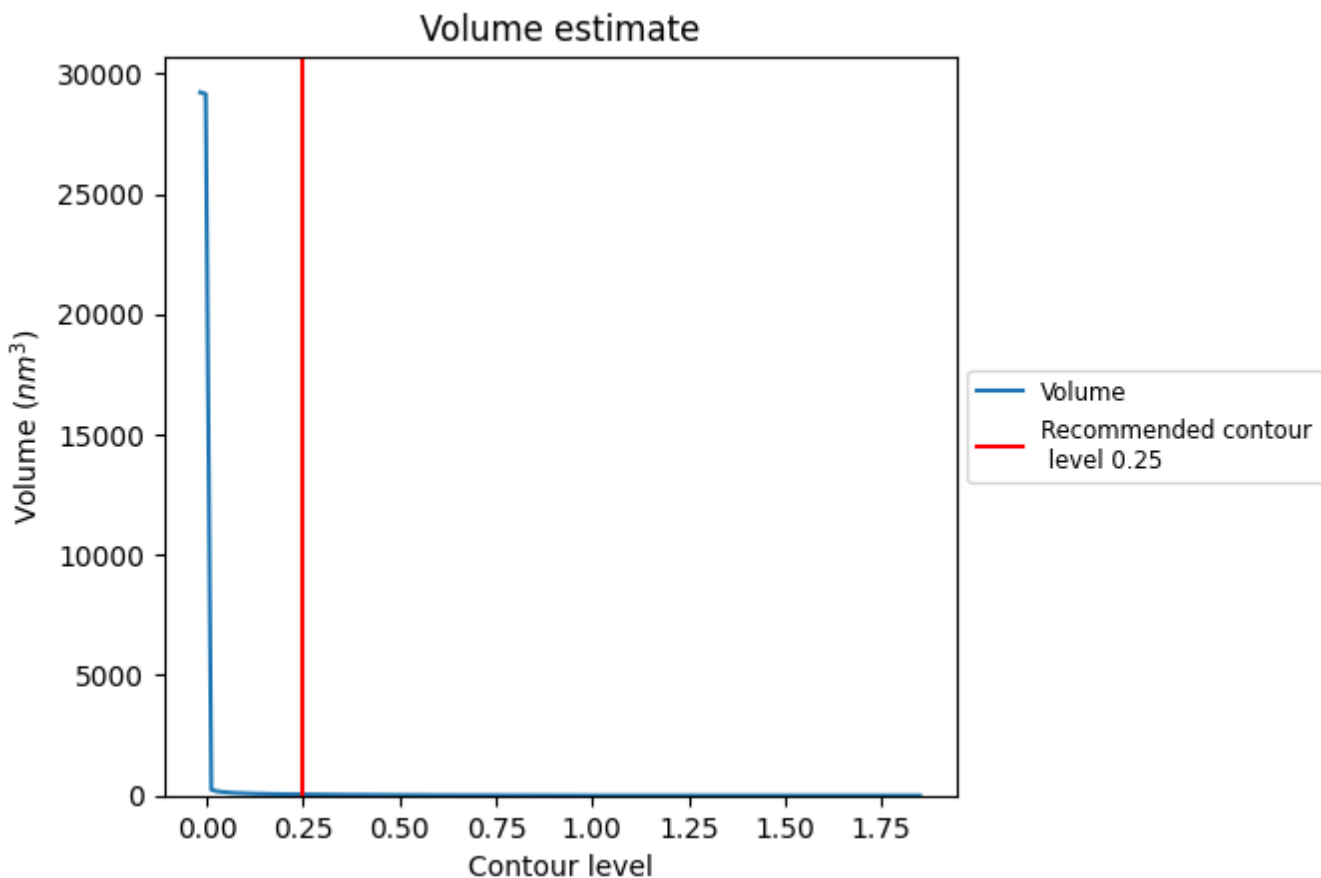
This section contains the results of statistical analysis of the map.

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.

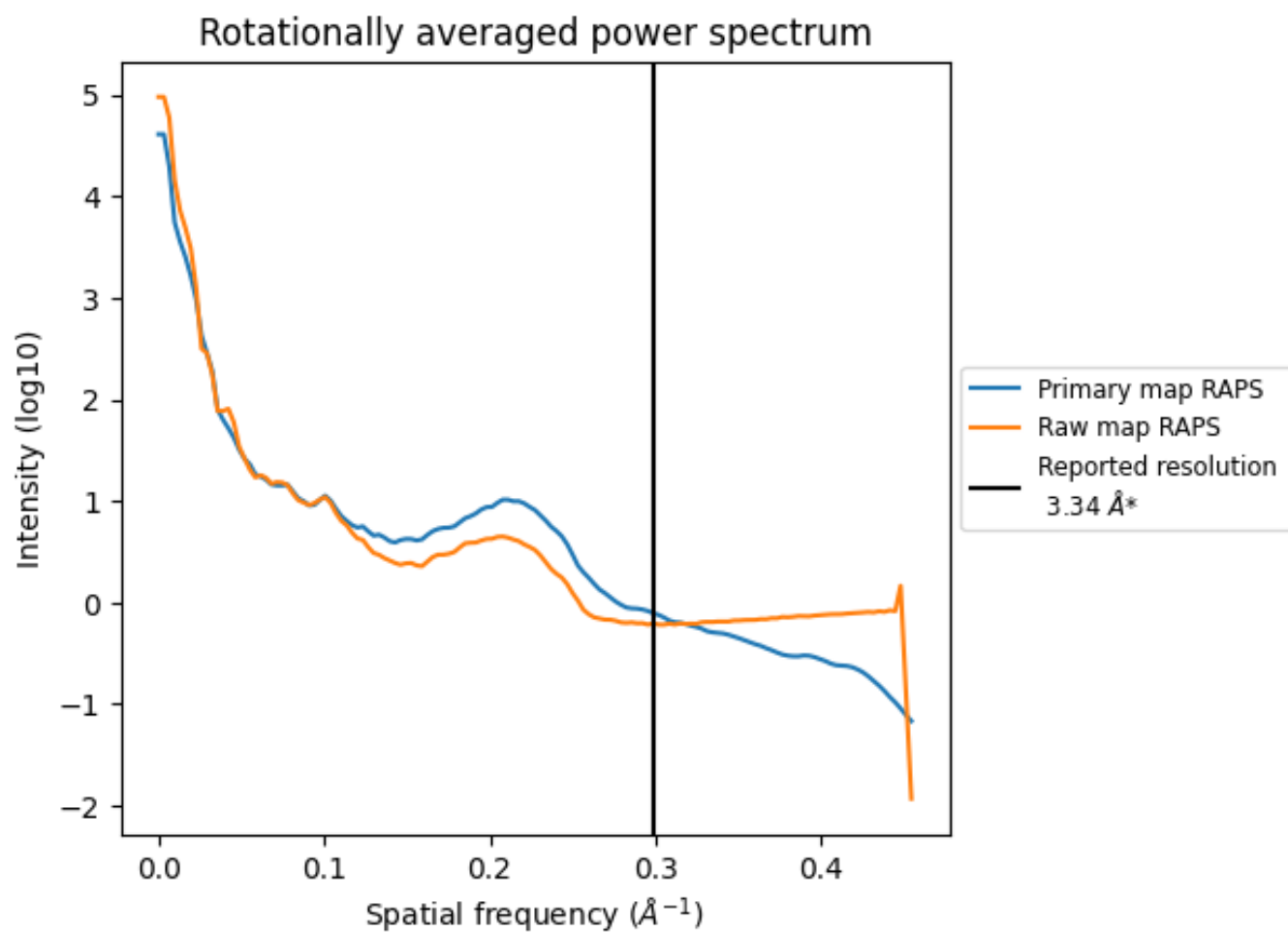
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 47 nm^3 ; this corresponds to an approximate mass of 42 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 i

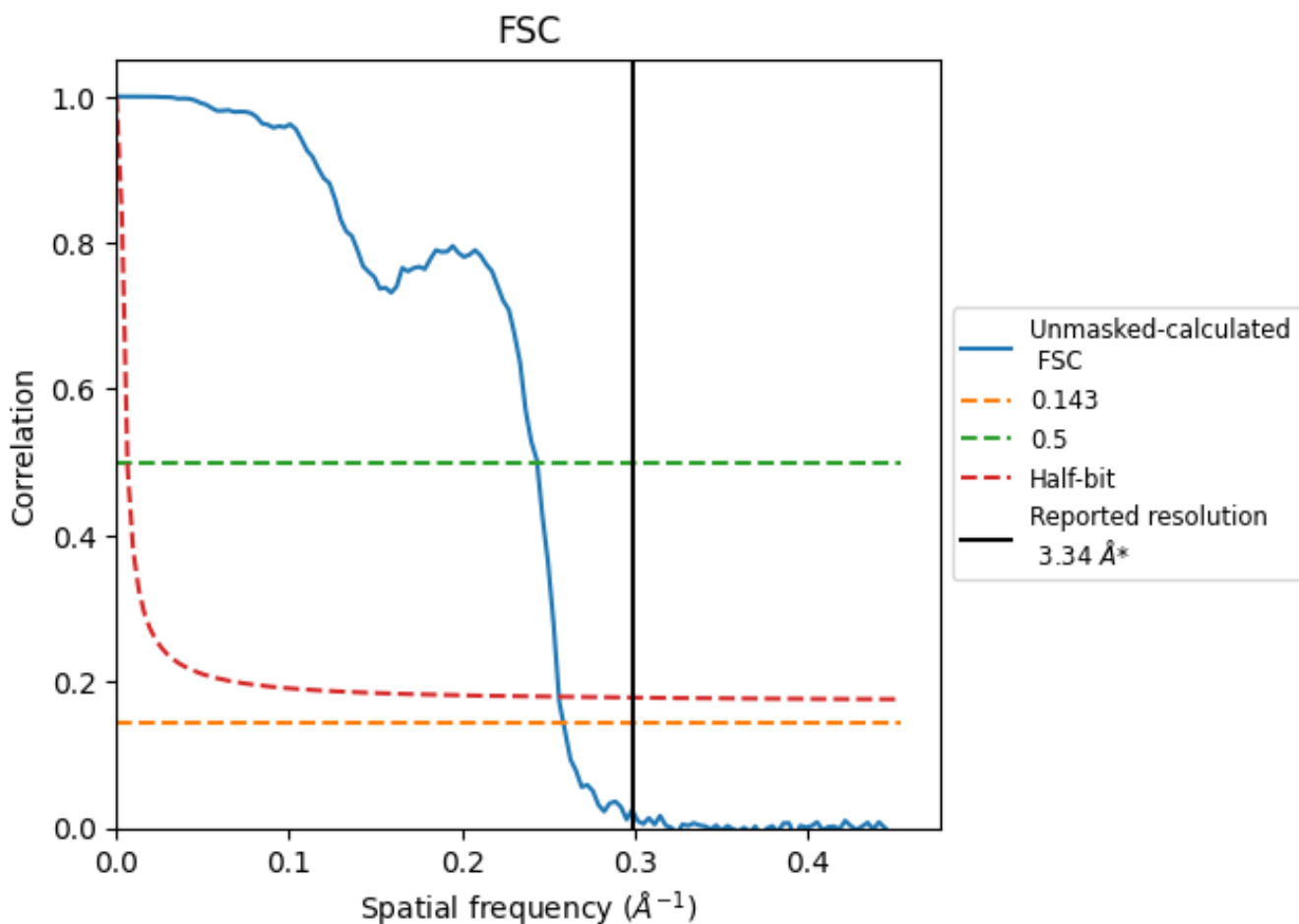


*Reported resolution corresponds to spatial frequency of 0.299 Å⁻¹

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 0.299 Å⁻¹

8.2 Resolution estimates [i](#)

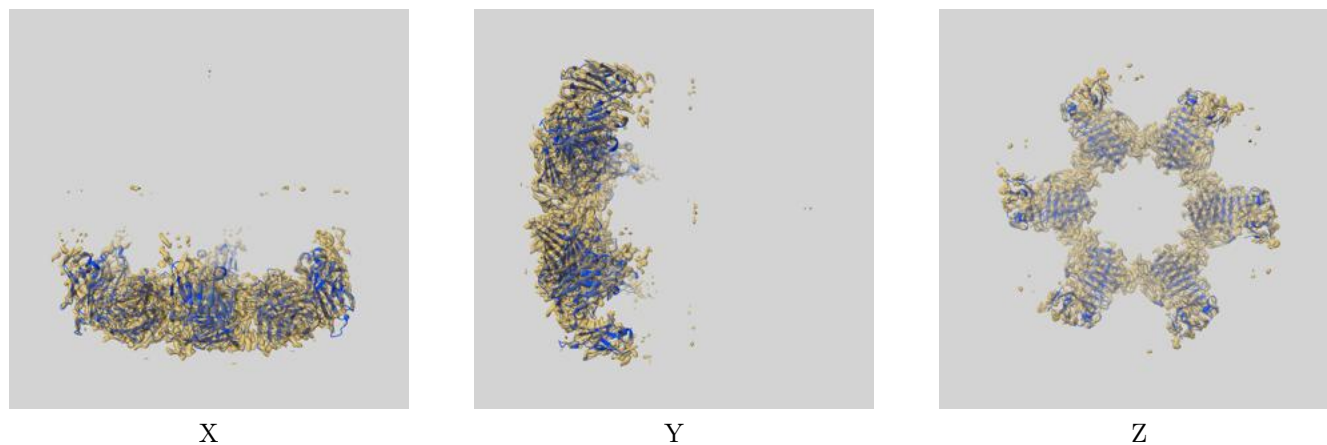
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.34	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.86	4.11	3.90

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.86 differs from the reported value 3.34 by more than 10 %

9 Map-model fit [i](#)

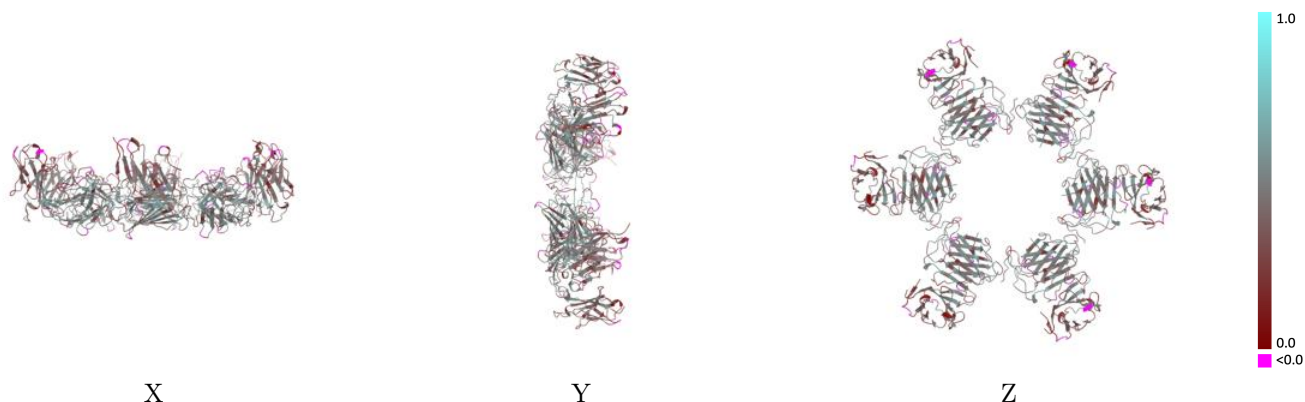
This section contains information regarding the fit between EMDB map EMD-29548 and PDB model 8FXY. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



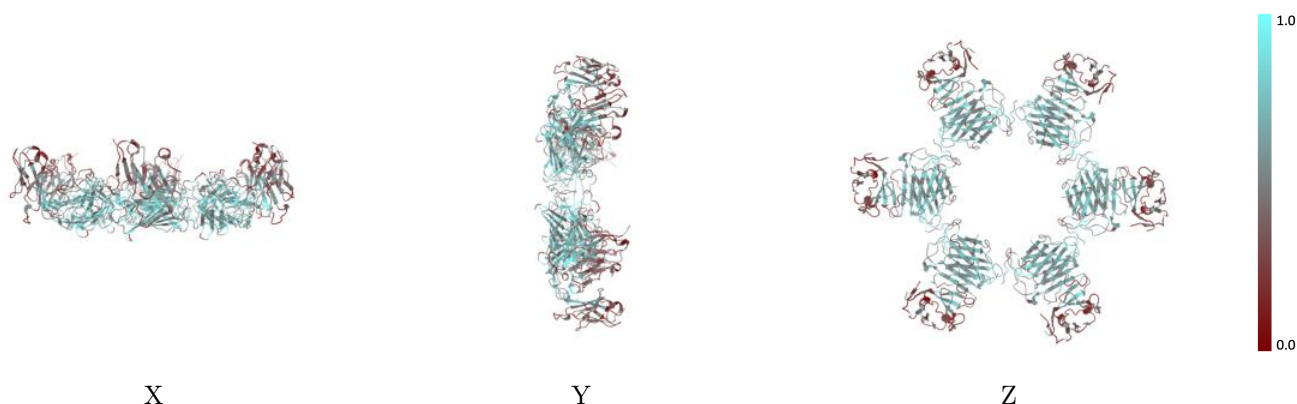
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



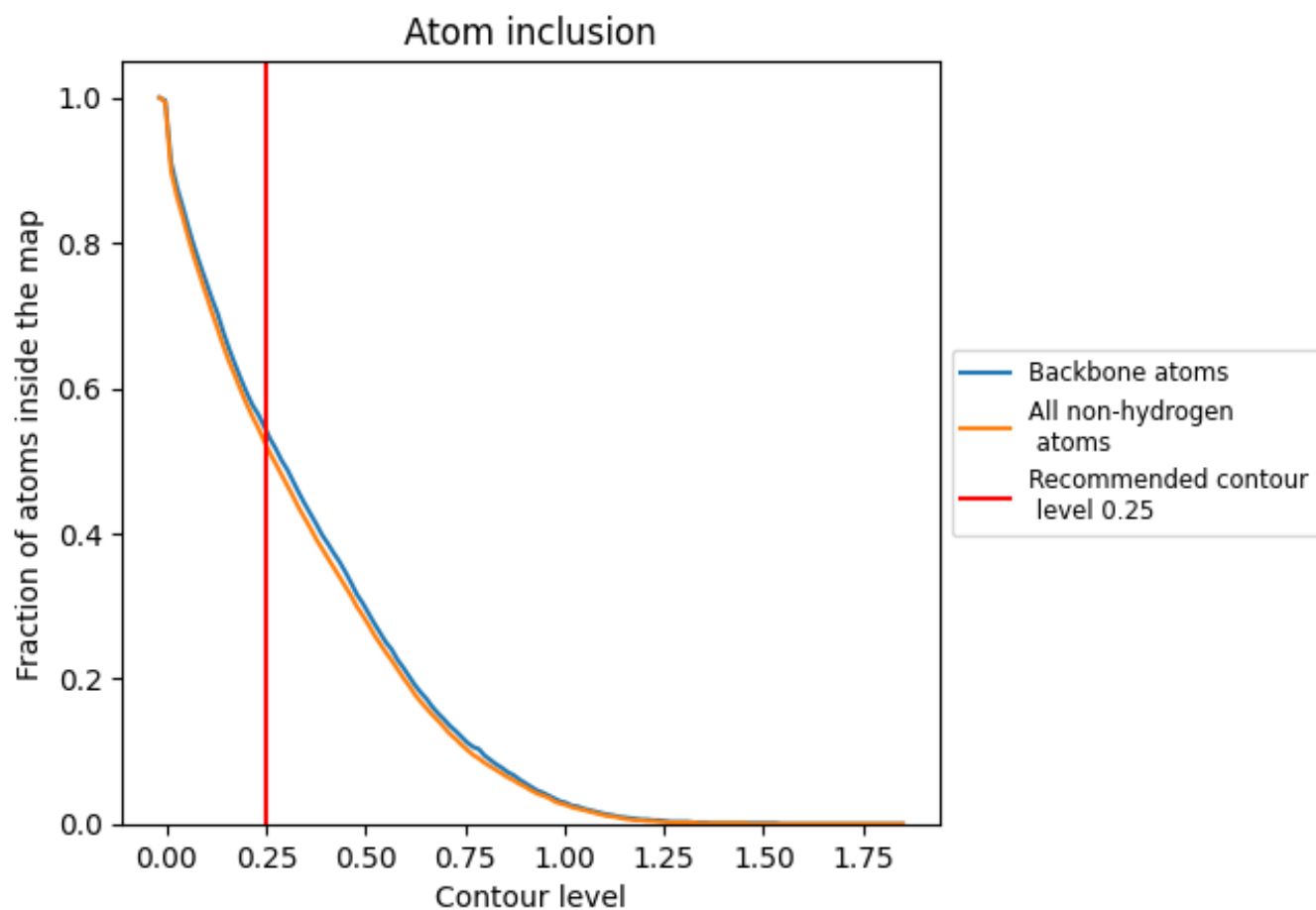
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).



























9.4 Atom inclusion [i](#)



At the recommended contour level, 54% of all backbone atoms, 52% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5220	 0.3950
A	 0.6040	 0.4220
B	 0.6040	 0.4220
C	 0.4030	 0.3490
D	 0.6010	 0.4190
E	 0.3880	 0.3520
F	 0.6040	 0.4180
G	 0.3840	 0.3460
H	 0.3950	 0.3500
I	 0.5900	 0.4210
J	 0.3770	 0.3510
K	 0.5890	 0.4220
L	 0.3930	 0.3450

