



Full wwPDB EM Validation Report ⓘ

Mar 19, 2026 – 07:56 PM UTC

PDB ID : 8X9Y / pdb_00008x9y
EMDB ID : EMD-38188
Title : E-hexon capsomer of the VZV C-Capsid
Authors : Nan, W.; Lei, C.; Xiangxi, W.
Deposited on : 2023-12-01
Resolution : 3.70 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 : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

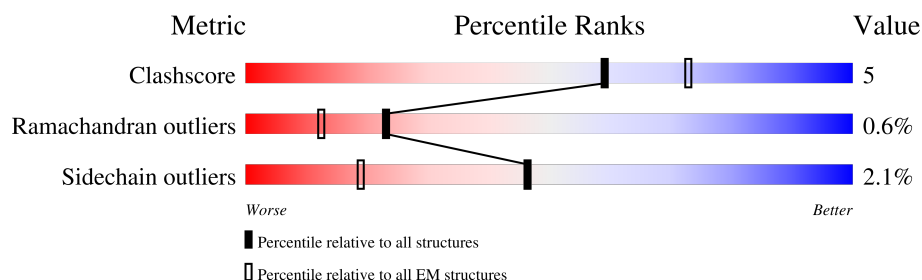
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	E	392	85% 15%
1	Z	392	83% 17%
2	A	94	69% 23% 7%
2	G	94	78% 17% . .
2	M	94	68% 28% .
2	S	94	73% 22% .
2	Y	94	71% 22% . .
2	k	94	74% 22% .
3	B	1369	85% 12% .

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Mol	Chain	Length	Quality of chain
3	C	1369	 86% 11% .
3	H	1369	 84% 13% .
3	I	1369	 83% 13% . .
3	J	1369	 84% 13% .
3	K	1369	 84% 12% . .
4	L	256	 91% 9%
4	R	256	 90% 9% .
5	O	263	 84% 16%
5	V	263	 87% 12% .

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 79700 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 Tri1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Z	392	Total	C	N	O	S	0	0
			2951	1854	552	529	16		
1	E	392	Total	C	N	O	S	0	0
			2951	1854	552	529	16		

- Molecule 2 is a protein called Small capsomere-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	94	Total	C	N	O	S	0	0
			699	437	135	125	2		
2	G	94	Total	C	N	O	S	0	0
			699	437	135	125	2		
2	M	94	Total	C	N	O	S	0	0
			699	437	135	125	2		
2	S	94	Total	C	N	O	S	0	0
			699	437	135	125	2		
2	Y	94	Total	C	N	O	S	0	0
			699	437	135	125	2		
2	k	94	Total	C	N	O	S	0	0
			699	437	135	125	2		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	95	ARG	LYS	conflict	UNP U5NQG6
G	95	ARG	LYS	conflict	UNP U5NQG6
M	95	ARG	LYS	conflict	UNP U5NQG6
S	95	ARG	LYS	conflict	UNP U5NQG6
Y	95	ARG	LYS	conflict	UNP U5NQG6
k	95	ARG	LYS	conflict	UNP U5NQG6

- Molecule 3 is a protein called Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	1331	Total	C	N	O	S	0	0
			10330	6543	1811	1910	66		
3	C	1331	Total	C	N	O	S	0	0
			10325	6541	1808	1910	66		
3	H	1331	Total	C	N	O	S	0	0
			10325	6541	1808	1910	66		
3	I	1331	Total	C	N	O	S	0	0
			10325	6541	1808	1910	66		
3	J	1331	Total	C	N	O	S	0	0
			10330	6543	1811	1910	66		
3	K	1331	Total	C	N	O	S	0	0
			10325	6541	1808	1910	66		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	814	ALA	GLY	conflict	UNP P09245
C	814	ALA	GLY	conflict	UNP P09245
H	814	ALA	GLY	conflict	UNP P09245
I	814	ALA	GLY	conflict	UNP P09245
J	814	ALA	GLY	conflict	UNP P09245
K	814	ALA	GLY	conflict	UNP P09245

- Molecule 4 is a protein called Tri2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	256	Total	C	N	O	S	0	0
			1847	1191	315	333	8		
4	R	256	Total	C	N	O	S	0	0
			1847	1191	315	333	8		

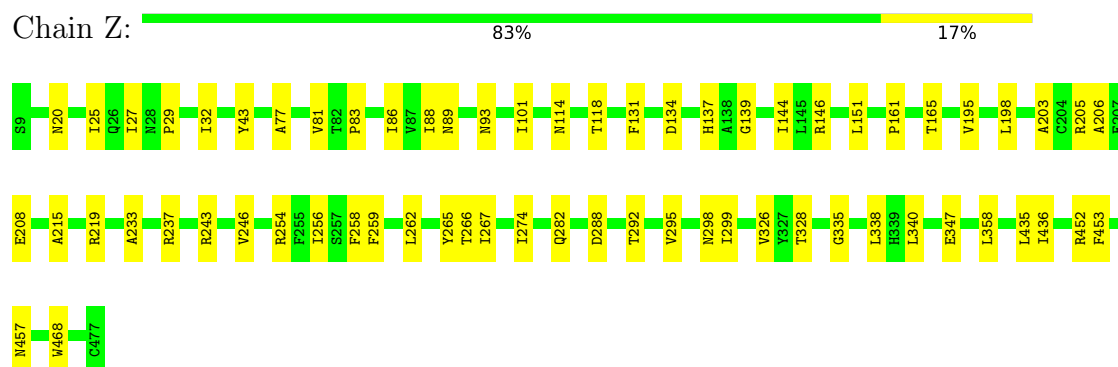
- Molecule 5 is a protein called Tri2B.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	O	263	Total	C	N	O	S	0	0
			1975	1269	339	358	9		
5	V	263	Total	C	N	O	S	0	0
			1975	1269	339	358	9		

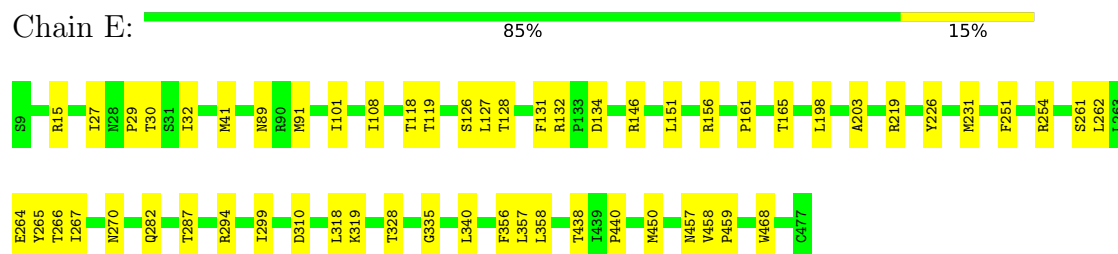
3 Residue-property plots

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. 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. 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.

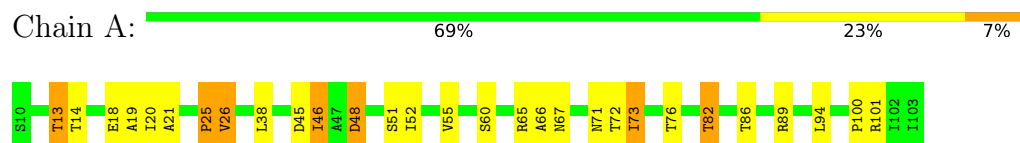
- Molecule 1: Tri1



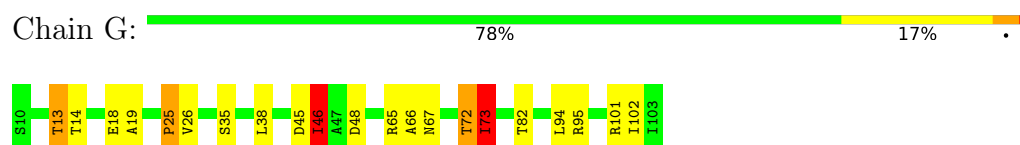
- Molecule 1: Tri1



- Molecule 2: Small capsomere-interacting protein



- Molecule 2: Small capsomere-interacting protein



- Molecule 2: Small capsomere-interacting protein

Chain M:  68% 28%



- Molecule 2: Small capsomere-interacting protein

Chain S:  73% 22%



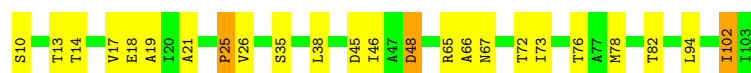
- Molecule 2: Small capsomere-interacting protein

Chain Y:  71% 22%



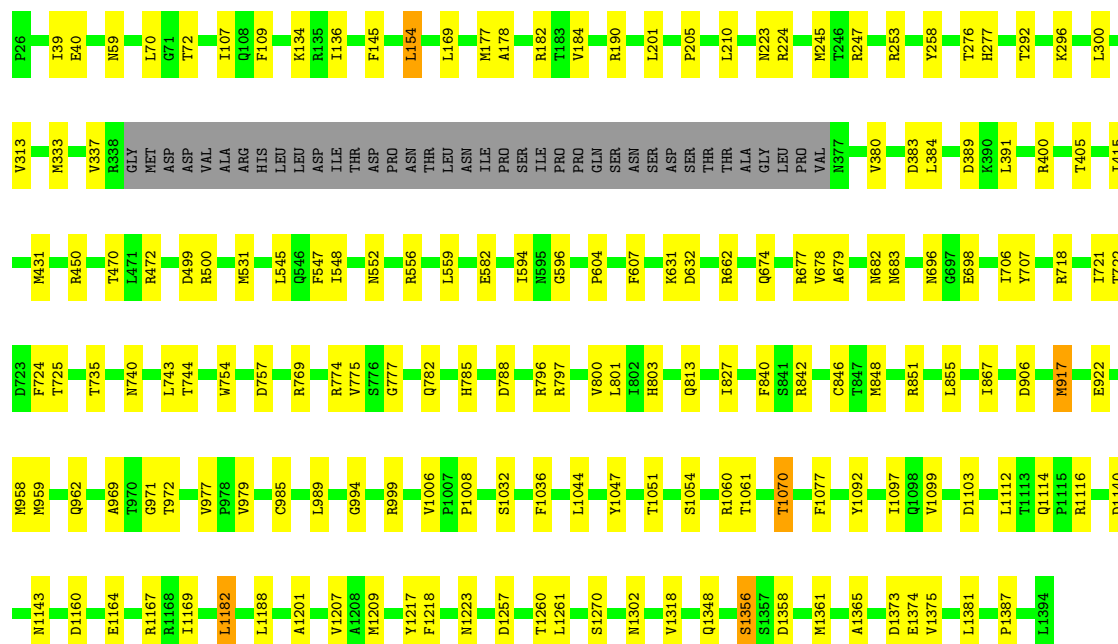
- Molecule 2: Small capsomere-interacting protein

Chain k:  74% 22%



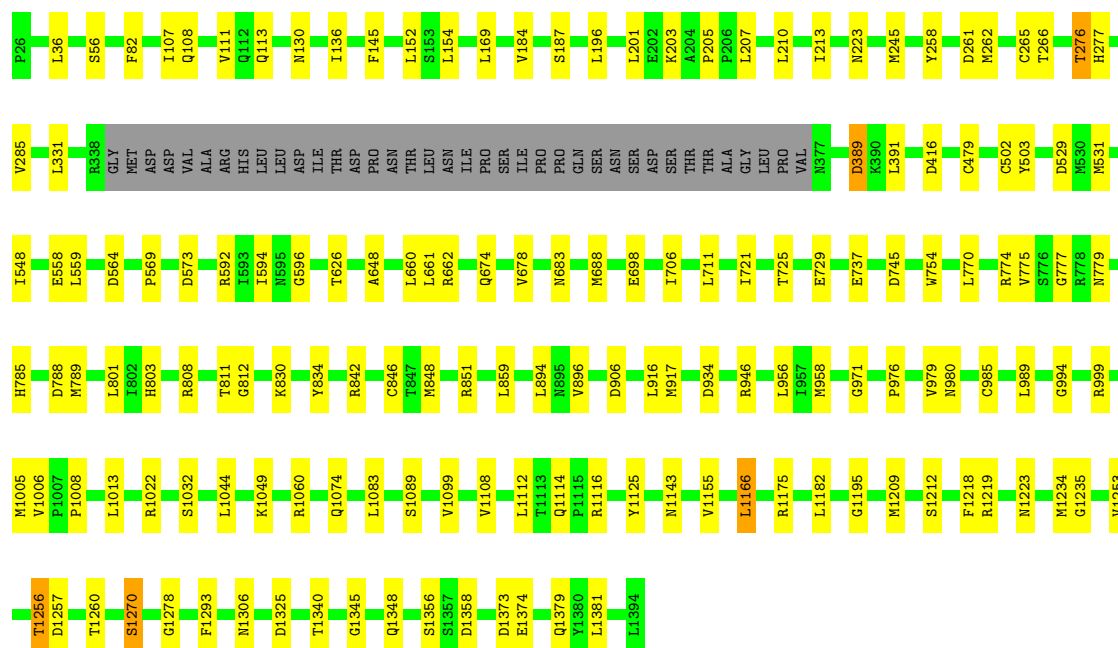
- Molecule 3: Major capsid protein

Chain B:  85% 12%



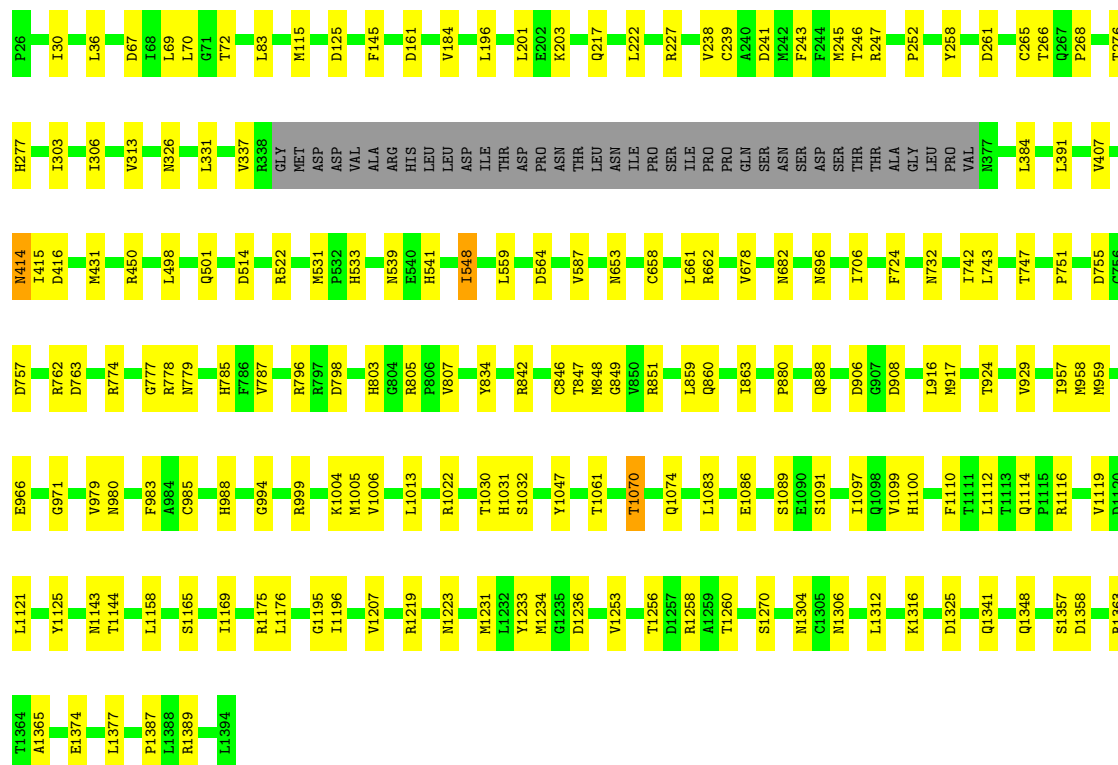
- Molecule 3: Major capsid protein

Chain C:  86% 11% .



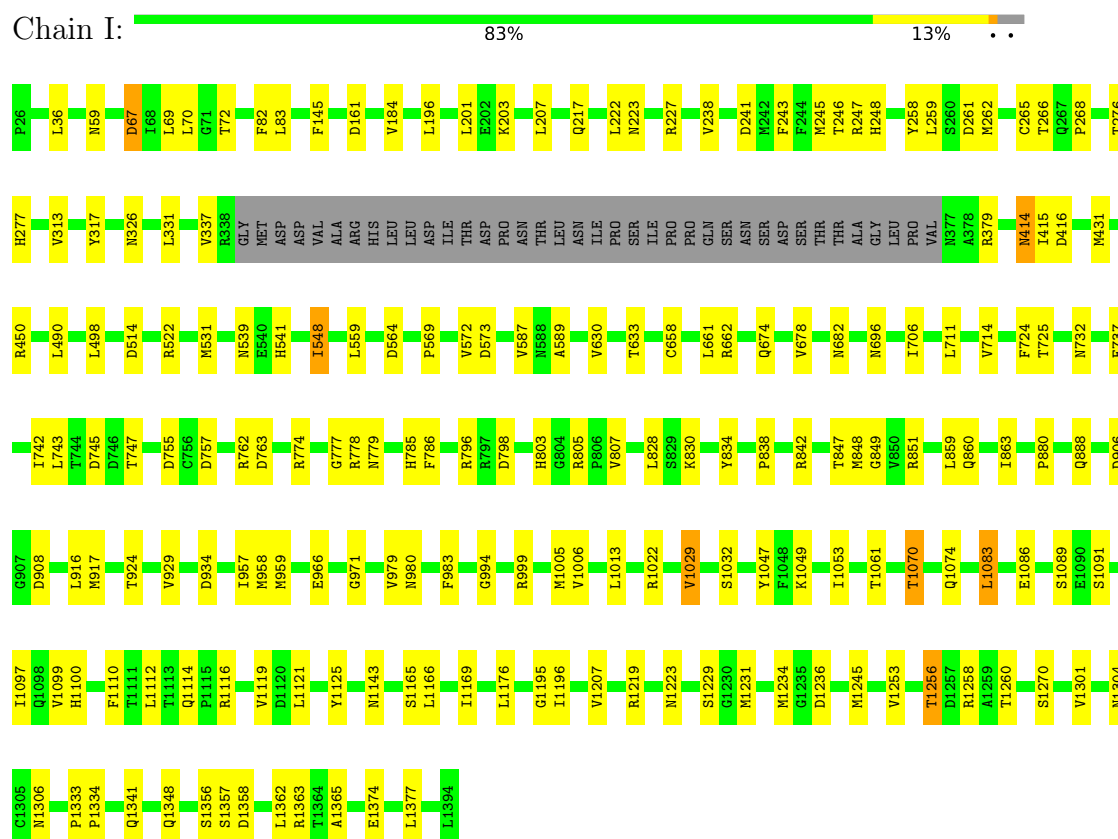
• Molecule 3: Major capsid protein

Chain H:  84% 13% .



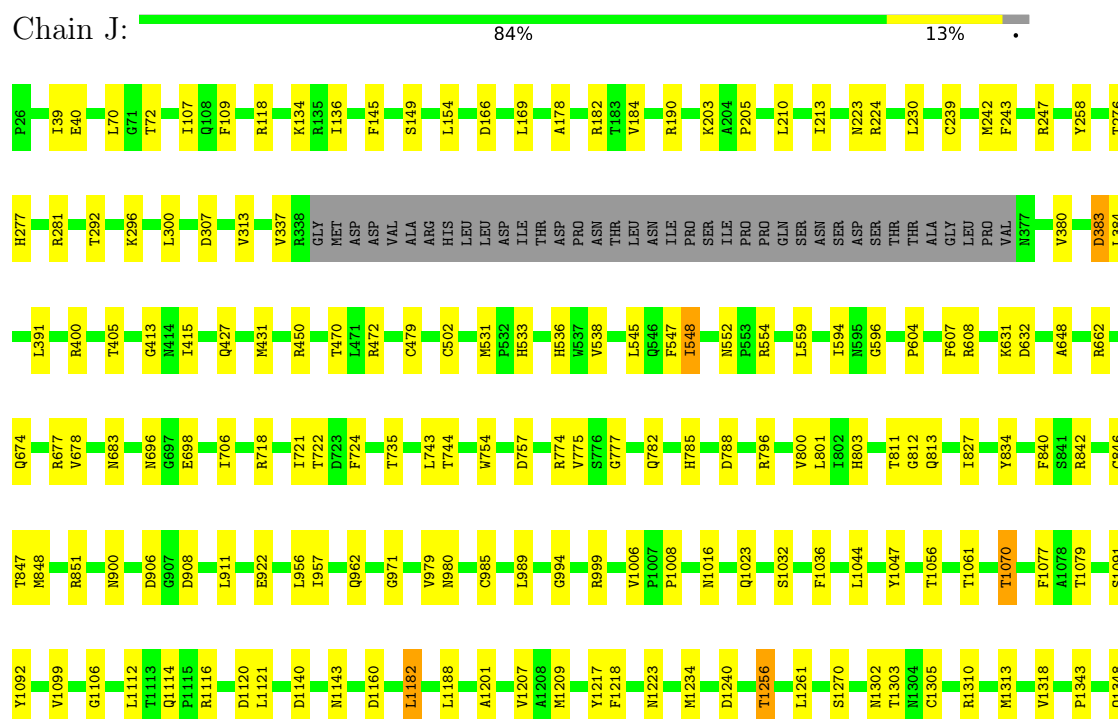
• Molecule 3: Major capsid protein

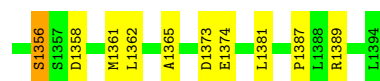
Chain I:



• Molecule 3: Major capsid protein

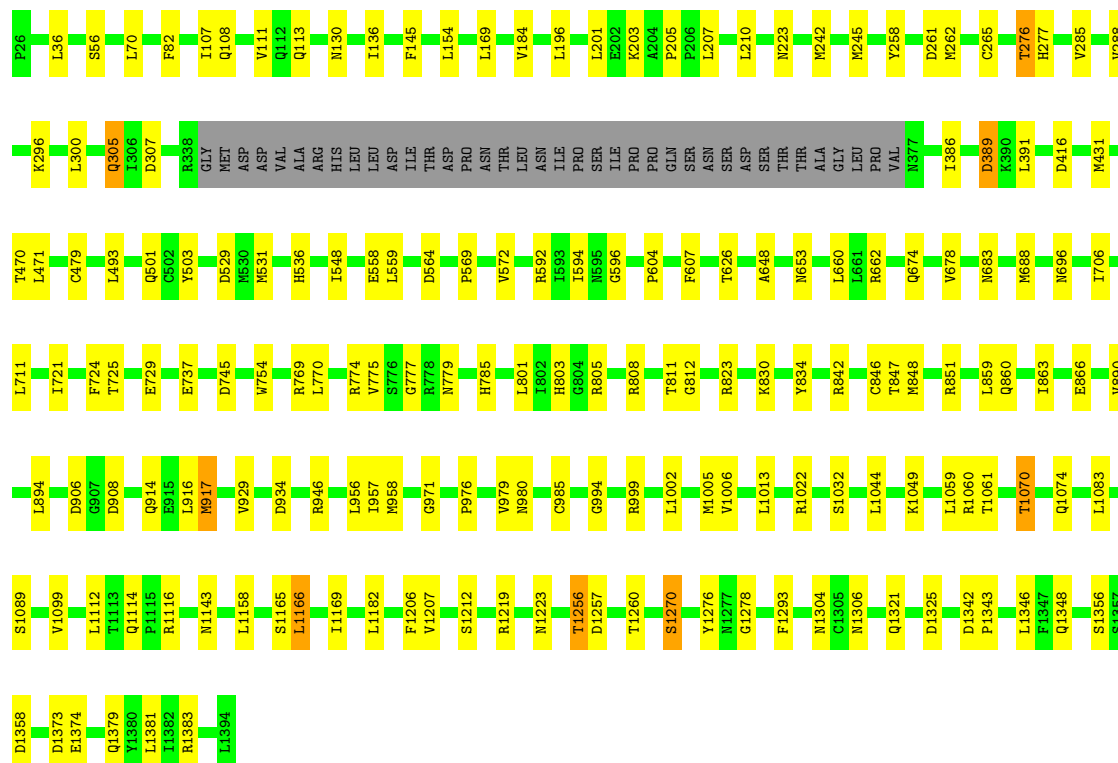
Chain J:





• Molecule 3: Major capsid protein

Chain K: 84% 12% . .



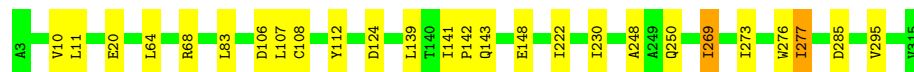
• Molecule 4: Tri2A

Chain L: 91% 9%



• Molecule 4: Tri2A

Chain R: 90% 9% .



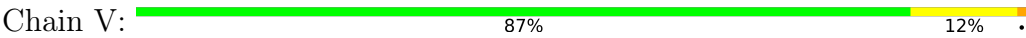
• Molecule 5: Tri2B

Chain O: 84% 16%





● Molecule 5: Tri2B



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1796810	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 BASE (4k x 4k)	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	E	0.24	0/3007	0.63	2/4094 (0.0%)
1	Z	0.25	0/3007	0.60	2/4094 (0.0%)
2	A	0.42	0/714	1.22	16/978 (1.6%)
2	G	0.43	0/714	1.24	17/978 (1.7%)
2	M	0.42	0/714	1.21	13/978 (1.3%)
2	S	0.41	0/714	1.20	16/978 (1.6%)
2	Y	0.44	0/714	1.25	17/978 (1.7%)
2	k	0.42	0/714	1.23	16/978 (1.6%)
3	B	0.22	0/10580	0.48	3/14421 (0.0%)
3	C	0.22	0/10575	0.48	2/14415 (0.0%)
3	H	0.22	0/10575	0.46	0/14415
3	I	0.21	0/10575	0.47	0/14415
3	J	0.22	0/10580	0.48	2/14421 (0.0%)
3	K	0.22	0/10575	0.47	1/14415 (0.0%)
4	L	0.20	0/1878	0.49	0/2568
4	R	0.21	0/1878	0.51	0/2568
5	O	0.20	0/2010	0.48	0/2743
5	V	0.20	0/2010	0.51	0/2743
All	All	0.23	0/81534	0.55	107/111180 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	Z	0	2
2	A	0	1
2	G	0	1
2	M	0	1
2	S	0	1
2	Y	0	1
3	J	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	8

There are no bond length outliers.

All (107) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	72	THR	CA-C-N	8.89	137.70	121.70
2	M	72	THR	C-N-CA	8.89	137.70	121.70
2	k	72	THR	CA-C-N	8.87	137.66	121.70
2	k	72	THR	C-N-CA	8.87	137.66	121.70
2	Y	72	THR	CA-C-N	8.47	136.95	121.70
2	Y	72	THR	C-N-CA	8.47	136.95	121.70
2	G	72	THR	CA-C-N	8.39	136.81	121.70
2	G	72	THR	C-N-CA	8.39	136.81	121.70
2	S	72	THR	CA-C-N	8.36	136.75	121.70
2	S	72	THR	C-N-CA	8.36	136.75	121.70
2	A	72	THR	CA-C-N	8.29	136.62	121.70
2	A	72	THR	C-N-CA	8.29	136.62	121.70
2	G	18	GLU	CA-C-N	7.88	135.89	121.70
2	G	18	GLU	C-N-CA	7.88	135.89	121.70
2	Y	48	ASP	CA-C-N	7.49	135.18	121.70
2	Y	48	ASP	C-N-CA	7.49	135.18	121.70
2	M	48	ASP	CA-C-N	7.48	135.17	121.70
2	M	48	ASP	C-N-CA	7.48	135.17	121.70
2	G	48	ASP	CA-C-N	7.47	135.15	121.70
2	G	48	ASP	C-N-CA	7.47	135.15	121.70
2	S	18	GLU	CA-C-N	7.45	135.11	121.70
2	S	18	GLU	C-N-CA	7.45	135.11	121.70
2	k	48	ASP	CA-C-N	7.41	135.04	121.70
2	k	48	ASP	C-N-CA	7.41	135.04	121.70
2	A	48	ASP	CA-C-N	7.36	134.94	121.70
2	A	48	ASP	C-N-CA	7.36	134.94	121.70
2	S	48	ASP	CA-C-N	7.34	134.92	121.70
2	S	48	ASP	C-N-CA	7.34	134.92	121.70
2	A	18	GLU	CA-C-N	7.22	134.70	121.70
2	A	18	GLU	C-N-CA	7.22	134.70	121.70
2	Y	18	GLU	CA-C-N	7.13	134.53	121.70
2	Y	18	GLU	C-N-CA	7.13	134.53	121.70
2	k	18	GLU	CA-C-N	7.09	134.47	121.70
2	k	18	GLU	C-N-CA	7.09	134.47	121.70
2	M	18	GLU	CA-C-N	7.06	134.41	121.70
2	M	18	GLU	C-N-CA	7.06	134.41	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	k	82	THR	CA-C-N	6.79	133.91	121.70
2	k	82	THR	C-N-CA	6.79	133.91	121.70
2	M	82	THR	CA-C-N	6.70	133.76	121.70
2	M	82	THR	C-N-CA	6.70	133.76	121.70
2	M	25	PRO	CA-C-N	6.64	133.65	121.70
2	M	25	PRO	C-N-CA	6.64	133.65	121.70
2	A	25	PRO	CA-C-N	6.62	133.62	121.70
2	A	25	PRO	C-N-CA	6.62	133.62	121.70
2	Y	82	THR	CA-C-N	6.62	133.61	121.70
2	Y	82	THR	C-N-CA	6.62	133.61	121.70
2	A	82	THR	CA-C-N	6.60	133.59	121.70
2	A	82	THR	C-N-CA	6.60	133.59	121.70
2	G	82	THR	CA-C-N	6.57	133.53	121.70
2	G	82	THR	C-N-CA	6.57	133.53	121.70
2	S	82	THR	CA-C-N	6.57	133.52	121.70
2	S	82	THR	C-N-CA	6.57	133.52	121.70
2	S	25	PRO	CA-C-N	6.47	133.34	121.70
2	S	25	PRO	C-N-CA	6.47	133.34	121.70
2	Y	25	PRO	CA-C-N	6.33	133.10	121.70
2	Y	25	PRO	C-N-CA	6.33	133.10	121.70
2	G	25	PRO	CA-C-N	6.33	133.09	121.70
2	G	25	PRO	C-N-CA	6.33	133.09	121.70
3	C	1257	ASP	N-CA-C	-6.29	104.81	113.18
2	k	25	PRO	CA-C-N	6.26	132.96	121.70
2	k	25	PRO	C-N-CA	6.26	132.96	121.70
2	Y	13	THR	CA-C-N	6.24	132.93	121.70
2	Y	13	THR	C-N-CA	6.24	132.93	121.70
2	G	13	THR	CA-C-N	6.16	132.78	121.70
2	G	13	THR	C-N-CA	6.16	132.78	121.70
2	S	13	THR	CA-C-N	6.05	132.58	121.70
2	S	13	THR	C-N-CA	6.05	132.58	121.70
2	A	13	THR	CA-C-N	6.00	132.50	121.70
2	A	13	THR	C-N-CA	6.00	132.50	121.70
2	M	20	ILE	N-CA-C	-5.95	106.96	112.43
2	S	45	ASP	CA-C-N	5.84	132.49	121.97
2	S	45	ASP	C-N-CA	5.84	132.49	121.97
2	A	45	ASP	CA-C-N	5.70	132.24	121.97
2	A	45	ASP	C-N-CA	5.70	132.24	121.97
2	Y	101	ARG	CA-C-N	5.68	132.19	121.97
2	Y	101	ARG	C-N-CA	5.68	132.19	121.97
1	Z	266	THR	CA-C-N	5.67	132.17	121.97
1	Z	266	THR	C-N-CA	5.67	132.17	121.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	101	ARG	CA-C-N	5.56	131.99	121.97
2	G	101	ARG	C-N-CA	5.56	131.99	121.97
2	M	45	ASP	CA-C-N	5.56	131.97	121.97
2	M	45	ASP	C-N-CA	5.56	131.97	121.97
3	K	1257	ASP	N-CA-C	-5.55	105.80	113.18
2	k	45	ASP	CA-C-N	5.53	131.93	121.97
2	k	45	ASP	C-N-CA	5.53	131.93	121.97
3	J	813	GLN	CB-CG-CD	5.41	121.79	112.60
3	B	813	GLN	CB-CG-CD	5.34	121.68	112.60
2	k	38	LEU	CA-C-N	5.32	131.28	121.70
2	k	38	LEU	C-N-CA	5.32	131.28	121.70
1	E	266	THR	CA-C-N	5.26	131.44	121.97
1	E	266	THR	C-N-CA	5.26	131.44	121.97
2	Y	21	ALA	CA-C-N	5.20	131.06	121.70
2	Y	21	ALA	C-N-CA	5.20	131.06	121.70
3	B	1257	ASP	N-CA-C	-5.17	107.63	114.04
2	k	21	ALA	CA-C-N	5.16	130.99	121.70
2	k	21	ALA	C-N-CA	5.16	130.99	121.70
3	B	813	GLN	CA-CB-CG	5.11	124.32	114.10
3	C	917	MET	CA-CB-CG	5.07	124.25	114.10
3	J	813	GLN	CA-CB-CG	5.07	124.23	114.10
2	G	38	LEU	CA-C-N	5.03	130.76	121.70
2	G	38	LEU	C-N-CA	5.03	130.76	121.70
2	S	38	LEU	CA-C-N	5.03	130.75	121.70
2	S	38	LEU	C-N-CA	5.03	130.75	121.70
2	G	73	ILE	CA-CB-CG2	5.02	119.04	110.50
2	Y	73	ILE	CA-CB-CG2	5.01	119.01	110.50
2	A	38	LEU	CA-C-N	5.00	130.71	121.70
2	A	38	LEU	C-N-CA	5.00	130.71	121.70

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	21	ALA	Peptide
2	G	46	ILE	Peptide
3	J	243	PHE	Peptide
2	M	21	ALA	Peptide
2	S	21	ALA	Peptide
2	Y	46	ILE	Peptide
1	Z	114	ASN	Peptide
1	Z	254	ARG	Peptide

5.2 Too-close contacts ⓘ

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	E	2951	0	2927	31	0
1	Z	2951	0	2927	31	0
2	A	699	0	696	14	0
2	G	699	0	696	8	0
2	M	699	0	696	9	0
2	S	699	0	696	10	0
2	Y	699	0	696	11	0
2	k	699	0	696	6	0
3	B	10330	0	10113	94	0
3	C	10325	0	10104	88	0
3	H	10325	0	10104	102	0
3	I	10325	0	10104	105	0
3	J	10330	0	10113	102	0
3	K	10325	0	10104	97	0
4	L	1847	0	1851	10	0
4	R	1847	0	1851	13	0
5	O	1975	0	2031	22	0
5	V	1975	0	2031	16	0
All	All	79700	0	78436	719	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 5.

All (719) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:O:215:THR:O	5:O:219:LEU:HB2	1.90	0.72
2:k:76:THR:HG23	2:k:78:MET:H	1.53	0.72
1:E:146:ARG:HE	4:L:108:CYS:HB2	1.57	0.70
3:I:261:ASP:O	3:I:265:CYS:HB2	1.95	0.67
1:E:231:MET:SD	1:E:231:MET:N	2.68	0.67
3:B:145:PHE:HB2	3:B:184:VAL:HG21	1.77	0.67
5:V:215:THR:O	5:V:219:LEU:HB2	1.95	0.66
2:k:76:THR:HG21	2:k:94:LEU:HB2	1.77	0.66
5:V:108:CYS:SG	5:V:109:ASN:N	2.69	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:146:ARG:HE	4:R:108:CYS:HB2	1.62	0.65
3:J:145:PHE:HB2	3:J:184:VAL:HG21	1.78	0.64
3:B:594:ILE:HG22	3:B:596:GLY:H	1.63	0.64
3:H:201:LEU:HD22	3:H:1083:LEU:HD13	1.80	0.64
2:Y:13:THR:H	2:Y:14:THR:HA	1.63	0.63
3:I:201:LEU:HD22	3:I:1083:LEU:HD13	1.80	0.63
3:J:594:ILE:HG22	3:J:596:GLY:H	1.63	0.63
3:H:261:ASP:O	3:H:265:CYS:HB2	1.99	0.63
3:I:1091:SER:HB3	3:I:1119:VAL:HB	1.81	0.63
2:G:13:THR:H	2:G:14:THR:HA	1.62	0.63
3:H:1091:SER:HB3	3:H:1119:VAL:HB	1.81	0.62
3:H:277:HIS:HD2	3:H:313:VAL:HG12	1.64	0.62
2:A:76:THR:HG21	2:A:94:LEU:HB2	1.82	0.62
3:I:277:HIS:HD2	3:I:313:VAL:HG12	1.64	0.61
3:I:145:PHE:HB2	3:I:184:VAL:HG21	1.83	0.61
2:A:13:THR:H	2:A:14:THR:HA	1.66	0.61
3:I:1356:SER:HB3	3:I:1362:LEU:HD12	1.83	0.61
3:J:70:LEU:HB2	3:K:107:ILE:HG22	1.83	0.61
3:K:860:GLN:NE2	3:K:917:MET:SD	2.74	0.61
4:R:222:ILE:HG21	4:R:276:TRP:HB2	1.82	0.60
3:H:678:VAL:HG21	3:H:706:ILE:HG21	1.84	0.60
5:O:107:LEU:HD23	5:O:142:PRO:HG3	1.83	0.60
3:K:145:PHE:HB2	3:K:184:VAL:HG21	1.82	0.60
3:C:594:ILE:HG22	3:C:596:GLY:H	1.67	0.60
1:Z:233:ALA:HB1	1:Z:237:ARG:HH12	1.67	0.60
3:K:242:MET:HE1	3:K:1343:PRO:HG3	1.84	0.59
3:B:848:MET:HE1	3:B:958:MET:HE2	1.84	0.59
3:K:201:LEU:HD22	3:K:1083:LEU:HD13	1.84	0.59
2:S:13:THR:H	2:S:14:THR:HA	1.66	0.59
3:C:201:LEU:HD22	3:C:1083:LEU:HD13	1.85	0.59
3:H:70:LEU:HD11	3:J:136:ILE:HD11	1.84	0.59
3:B:1217:TYR:HD1	3:B:1261:LEU:HD22	1.68	0.59
3:C:626:THR:HG22	3:C:706:ILE:HG12	1.85	0.59
3:I:1223:ASN:ND2	3:I:1348:GLN:O	2.36	0.59
1:E:282:GLN:OE1	1:E:468:TRP:NE1	2.36	0.58
3:I:678:VAL:HG21	3:I:706:ILE:HG21	1.83	0.58
3:J:1160:ASP:N	3:J:1160:ASP:OD2	2.35	0.58
3:H:145:PHE:HB2	3:H:184:VAL:HG21	1.84	0.58
3:H:1223:ASN:ND2	3:H:1348:GLN:O	2.36	0.58
3:K:934:ASP:OD1	3:K:1049:LYS:NZ	2.31	0.58
5:V:27:CYS:SG	5:V:30:LYS:NZ	2.76	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:261:ASP:O	3:C:265:CYS:HB2	2.04	0.58
3:H:203:LYS:NZ	3:H:1089:SER:OG	2.36	0.58
1:Z:77:ALA:HB1	1:Z:88:ILE:HB	1.86	0.58
3:C:145:PHE:HB2	3:C:184:VAL:HG21	1.85	0.58
3:B:785:HIS:HB3	3:B:803:HIS:HB3	1.84	0.57
1:Z:134:ASP:OD1	1:Z:134:ASP:N	2.36	0.57
3:B:224:ARG:HH12	3:I:1195:GLY:HA2	1.69	0.57
2:S:76:THR:HG21	2:S:94:LEU:HB2	1.85	0.57
5:O:108:CYS:SG	5:O:109:ASN:N	2.77	0.57
3:H:1175:ARG:NH1	3:J:1256:THR:OG1	2.37	0.57
3:H:1195:GLY:HA2	3:J:224:ARG:HH12	1.67	0.57
3:H:1114:GLN:OE1	3:H:1116:ARG:NH2	2.38	0.57
3:B:851:ARG:NH1	3:B:971:GLY:O	2.38	0.57
3:C:389:ASP:OD1	3:C:389:ASP:N	2.37	0.57
3:K:626:THR:HG22	3:K:706:ILE:HG12	1.85	0.57
4:R:10:VAL:HB	4:R:83:LEU:HB3	1.87	0.57
3:B:631:LYS:NZ	3:B:840:PHE:O	2.38	0.57
3:I:559:LEU:HB3	3:I:1270:SER:HA	1.87	0.57
3:I:1114:GLN:OE1	3:I:1116:ARG:NH2	2.38	0.57
3:J:851:ARG:NH1	3:J:971:GLY:O	2.38	0.57
3:K:848:MET:HB3	3:K:976:PRO:HA	1.87	0.57
3:K:1114:GLN:OE1	3:K:1116:ARG:NH2	2.38	0.57
4:L:10:VAL:HB	4:L:83:LEU:HB3	1.86	0.57
3:B:1160:ASP:OD2	3:B:1160:ASP:N	2.35	0.57
3:C:851:ARG:NH1	3:C:971:GLY:O	2.38	0.57
3:C:1114:GLN:OE1	3:C:1116:ARG:NH2	2.38	0.56
3:J:1114:GLN:OE1	3:J:1116:ARG:NH2	2.38	0.56
3:K:389:ASP:N	3:K:389:ASP:OD1	2.37	0.56
1:E:299:ILE:HD13	1:E:340:LEU:HD22	1.87	0.56
3:J:70:LEU:HD11	3:K:136:ILE:HD11	1.85	0.56
3:B:70:LEU:HD11	3:C:136:ILE:HD11	1.86	0.56
3:C:934:ASP:OD2	3:C:1049:LYS:NZ	2.32	0.56
3:C:808:ARG:NH2	3:H:966:GLU:O	2.38	0.56
1:Z:144:ILE:HG22	1:Z:195:VAL:HG12	1.87	0.56
3:B:384:LEU:HD23	3:B:391:LEU:HD21	1.88	0.56
3:I:416:ASP:OD2	3:I:1074:GLN:NE2	2.38	0.56
4:R:277:ILE:HD11	5:V:151:ALA:HA	1.87	0.56
3:B:1092:TYR:HE2	3:B:1116:ARG:HH11	1.53	0.56
3:H:539:ASN:OD1	3:H:541:HIS:NE2	2.39	0.56
3:H:908:ASP:OD1	3:H:908:ASP:N	2.39	0.56
3:K:851:ARG:NH1	3:K:971:GLY:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:203:LYS:NZ	3:I:1089:SER:OG	2.39	0.56
3:H:450:ARG:NH1	3:H:1358:ASP:OD2	2.39	0.56
3:J:384:LEU:HD23	3:J:391:LEU:HD21	1.87	0.56
3:H:774:ARG:NH2	3:H:777:GLY:O	2.39	0.56
3:I:539:ASN:OD1	3:I:541:HIS:NE2	2.38	0.55
3:K:1223:ASN:ND2	3:K:1348:GLN:O	2.38	0.55
1:Z:282:GLN:OE1	1:Z:468:TRP:NE1	2.35	0.55
3:H:416:ASP:OD2	3:H:1074:GLN:NE2	2.39	0.55
3:C:1223:ASN:ND2	3:C:1348:GLN:O	2.38	0.55
3:I:966:GLU:O	3:K:808:ARG:NH2	2.39	0.55
3:J:547:PHE:HA	3:J:552:ASN:HD22	1.71	0.55
3:K:688:MET:HE2	3:K:711:LEU:HD11	1.88	0.55
1:Z:144:ILE:HG23	1:Z:259:PHE:HB2	1.89	0.55
3:B:1223:ASN:ND2	3:B:1348:GLN:O	2.39	0.55
3:J:1092:TYR:HE1	3:J:1116:ARG:HH11	1.53	0.55
3:J:1223:ASN:ND2	3:J:1348:GLN:O	2.38	0.55
3:B:1209:MET:HE1	3:B:1218:PHE:HZ	1.72	0.55
3:I:498:LEU:HD11	3:I:587:VAL:HG23	1.89	0.55
4:L:11:LEU:HD11	4:L:40:ARG:HH22	1.71	0.55
3:I:450:ARG:NH1	3:I:1358:ASP:OD2	2.40	0.55
2:Y:83:ASP:O	2:Y:86:THR:OG1	2.24	0.55
3:B:788:ASP:N	3:B:788:ASP:OD1	2.40	0.55
3:C:698:GLU:OE2	2:S:95:ARG:NH2	2.40	0.55
3:I:774:ARG:NH2	3:I:777:GLY:O	2.39	0.55
3:K:594:ILE:HG22	3:K:596:GLY:H	1.71	0.55
3:B:109:PHE:HE2	3:B:134:LYS:HD2	1.72	0.54
3:I:658:CYS:HA	3:I:661:LEU:HG	1.87	0.54
3:I:908:ASP:N	3:I:908:ASP:OD1	2.38	0.54
5:O:115:LEU:H	5:O:289:THR:HG21	1.72	0.54
1:Z:146:ARG:HH22	1:Z:151:LEU:HD11	1.72	0.54
3:J:531:MET:HE1	3:J:1006:VAL:HG21	1.88	0.54
3:C:848:MET:HB3	3:C:976:PRO:HA	1.88	0.54
3:H:1365:ALA:HB1	3:J:1373:ASP:HA	1.90	0.54
3:H:559:LEU:HB3	3:H:1270:SER:HA	1.90	0.54
3:H:696:ASN:O	3:J:674:GLN:NE2	2.41	0.54
2:k:13:THR:H	2:k:14:THR:HA	1.73	0.54
3:B:632:ASP:HB3	3:B:677:ARG:HE	1.72	0.54
3:H:498:LEU:HD11	3:H:587:VAL:HG23	1.90	0.54
3:K:662:ARG:NH2	3:K:906:ASP:OD1	2.41	0.54
2:M:13:THR:H	2:M:14:THR:HA	1.73	0.54
3:C:416:ASP:OD1	3:C:1074:GLN:NE2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:89:ASN:ND2	1:Z:93:ASN:O	2.40	0.54
2:A:67:ASN:ND2	3:K:866:GLU:OE1	2.40	0.54
3:J:1356:SER:HB2	3:J:1381:LEU:HD12	1.89	0.54
3:C:207:LEU:HD22	3:C:262:MET:HE3	1.90	0.54
3:J:1217:TYR:HD2	3:J:1261:LEU:HD22	1.73	0.54
3:K:416:ASP:OD1	3:K:1074:GLN:NE2	2.41	0.54
3:B:1114:GLN:OE1	3:B:1116:ARG:NH2	2.40	0.53
3:J:631:LYS:NZ	3:J:840:PHE:O	2.40	0.53
3:J:696:ASN:O	3:K:674:GLN:NE2	2.41	0.53
3:B:136:ILE:HD11	3:I:70:LEU:HD11	1.91	0.53
3:B:1374:GLU:OE1	3:I:1363:ARG:NH1	2.41	0.53
3:B:1356:SER:HB2	3:B:1381:LEU:HD12	1.89	0.53
3:H:70:LEU:HB2	3:J:107:ILE:HG22	1.90	0.53
3:H:880:PRO:O	3:H:888:GLN:NE2	2.41	0.53
3:H:1236:ASP:N	3:H:1236:ASP:OD1	2.41	0.53
3:J:632:ASP:HB3	3:J:677:ARG:HE	1.73	0.53
3:K:479:CYS:HB3	3:K:1166:LEU:HD21	1.91	0.53
3:C:688:MET:HE2	3:C:711:LEU:HD11	1.89	0.53
3:J:109:PHE:HE2	3:J:134:LYS:HD2	1.72	0.53
3:B:547:PHE:HA	3:B:552:ASN:HD22	1.71	0.53
3:C:729:GLU:OE2	3:C:1060:ARG:NH2	2.41	0.53
3:B:662:ARG:NH2	3:B:906:ASP:OD2	2.42	0.53
3:B:718:ARG:NH1	3:B:722:THR:OG1	2.42	0.53
3:J:785:HIS:HB3	3:J:803:HIS:HB3	1.89	0.53
5:O:7:GLU:OE1	5:O:86:HIS:NE2	2.42	0.53
3:C:662:ARG:NH2	3:C:906:ASP:OD1	2.41	0.53
3:H:979:VAL:HB	3:H:1013:LEU:HD13	1.91	0.53
3:J:450:ARG:NH1	3:J:1358:ASP:OD2	2.41	0.53
3:B:696:ASN:O	3:C:674:GLN:NE2	2.41	0.52
3:B:725:THR:HG22	3:B:740:ASN:HD22	1.72	0.52
3:J:662:ARG:NH2	3:J:906:ASP:OD2	2.42	0.52
3:B:721:ILE:HG13	3:B:1044:LEU:HD11	1.91	0.52
3:C:1005:MET:HG3	3:C:1006:VAL:HG23	1.91	0.52
3:C:1209:MET:HE1	3:C:1218:PHE:HZ	1.73	0.52
3:H:252:PRO:HB3	3:H:303:ILE:HG12	1.91	0.52
3:B:1365:ALA:HB1	3:C:1373:ASP:HA	1.92	0.52
3:K:154:LEU:HD11	3:K:169:LEU:HB3	1.90	0.52
3:C:154:LEU:HD11	3:C:169:LEU:HB3	1.90	0.52
3:J:1209:MET:HE1	3:J:1218:PHE:HZ	1.74	0.52
1:E:27:ILE:HG22	1:E:29:PRO:HD3	1.90	0.52
3:B:389:ASP:OD1	3:B:389:ASP:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:678:VAL:HG21	3:C:706:ILE:HG21	1.91	0.52
2:Y:72:THR:HA	2:Y:73:ILE:HG22	1.92	0.52
5:O:218:ILE:HA	5:O:221:LEU:HB2	1.92	0.52
5:V:219:LEU:HA	5:V:222:ILE:HG12	1.91	0.52
2:A:48:ASP:N	2:A:48:ASP:OD1	2.42	0.52
3:C:1143:ASN:OD1	3:C:1143:ASN:N	2.42	0.52
3:H:994:GLY:O	3:H:999:ARG:NH1	2.43	0.52
3:I:994:GLY:O	3:I:999:ARG:NH1	2.43	0.52
5:O:27:CYS:SG	5:O:30:LYS:NZ	2.83	0.52
1:Z:292:THR:OG1	3:I:59:ASN:O	2.28	0.51
1:E:132:ARG:HG3	1:E:226:TYR:HE2	1.75	0.51
2:G:72:THR:HA	2:G:73:ILE:HG22	1.91	0.51
3:K:261:ASP:O	3:K:265:CYS:HB2	2.10	0.51
3:B:154:LEU:HD21	3:B:169:LEU:HB3	1.92	0.51
3:B:415:ILE:HG22	3:B:1077:PHE:HB2	1.92	0.51
3:I:979:VAL:HB	3:I:1013:LEU:HD13	1.91	0.51
3:K:1143:ASN:OD1	3:K:1143:ASN:N	2.43	0.51
3:J:1365:ALA:HB1	3:K:1373:ASP:HA	1.92	0.51
1:Z:203:ALA:O	1:Z:219:ARG:NH1	2.43	0.51
1:E:15:ARG:NE	1:E:30:THR:O	2.44	0.51
3:I:838:PRO:HB2	3:I:1029:VAL:HG21	1.91	0.51
1:Z:83:PRO:HB2	1:Z:86:ILE:HD12	1.92	0.51
3:C:479:CYS:HB3	3:C:1166:LEU:HD21	1.93	0.51
3:H:662:ARG:HH12	3:H:906:ASP:HB2	1.76	0.51
3:H:1363:ARG:NH1	3:J:1374:GLU:OE1	2.44	0.51
3:I:1236:ASP:OD1	3:I:1236:ASP:N	2.43	0.51
3:J:678:VAL:HG21	3:J:706:ILE:HG21	1.93	0.51
3:J:721:ILE:HG13	3:J:1044:LEU:HD11	1.91	0.51
3:J:1234:MET:HE1	3:J:1240:ASP:HB2	1.92	0.51
1:E:128:THR:OG1	1:E:270:ASN:OD1	2.29	0.51
3:B:674:GLN:NE2	3:I:696:ASN:O	2.44	0.51
3:B:698:GLU:OE2	2:Y:95:ARG:NH2	2.44	0.51
3:I:842:ARG:NH1	3:I:1032:SER:O	2.43	0.51
3:I:880:PRO:O	3:I:888:GLN:NE2	2.44	0.51
3:J:1358:ASP:HB3	3:J:1361:MET:HE3	1.93	0.51
5:O:207:LEU:HD22	5:O:211:ILE:HD11	1.91	0.51
3:H:1143:ASN:OD1	3:H:1143:ASN:N	2.44	0.51
3:K:113:GLN:NE2	3:K:130:ASN:OD1	2.42	0.51
3:K:564:ASP:OD2	3:K:1022:ARG:NH1	2.44	0.51
3:K:678:VAL:HG21	3:K:706:ILE:HG21	1.92	0.51
3:C:788:ASP:OD1	3:C:788:ASP:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:48:ASP:OD1	2:S:48:ASP:N	2.42	0.51
2:A:65:ARG:NH1	3:K:914:GLN:OE1	2.44	0.50
3:B:247:ARG:NH2	3:B:1387:PRO:O	2.44	0.50
3:C:564:ASP:OD2	3:C:1022:ARG:NH1	2.44	0.50
3:I:415:ILE:HG22	3:I:1341:GLN:HB3	1.94	0.50
3:K:1005:MET:HG3	3:K:1006:VAL:HG23	1.93	0.50
3:K:1206:PHE:O	3:K:1276:TYR:OH	2.25	0.50
2:M:35:SER:HB3	2:S:89:ARG:HH21	1.76	0.50
3:C:531:MET:HE1	3:C:1006:VAL:HG21	1.92	0.50
3:I:217:GLN:HB3	3:I:222:LEU:HD11	1.93	0.50
3:I:573:ASP:OD1	3:I:573:ASP:N	2.38	0.50
3:B:744:THR:HA	3:B:827:ILE:HD12	1.93	0.50
3:C:559:LEU:HB3	3:C:1270:SER:HA	1.94	0.50
3:C:994:GLY:O	3:C:999:ARG:NH1	2.44	0.50
3:J:718:ARG:NH1	3:J:722:THR:OG1	2.44	0.50
3:H:247:ARG:NH1	3:H:1387:PRO:O	2.41	0.50
3:J:811:THR:OG1	3:J:812:GLY:N	2.42	0.50
3:I:834:TYR:HE2	3:I:980:ASN:HD21	1.58	0.50
3:K:774:ARG:NH2	3:K:777:GLY:O	2.45	0.50
3:K:785:HIS:HB3	3:K:803:HIS:HB3	1.92	0.50
3:B:470:THR:HG22	3:B:472:ARG:H	1.77	0.50
3:H:842:ARG:NH1	3:H:1032:SER:O	2.44	0.50
3:K:729:GLU:OE2	3:K:1060:ARG:NH2	2.45	0.50
5:V:224:ARG:HH21	5:V:225:LEU:HG	1.75	0.50
2:A:52:ILE:HD12	2:A:52:ILE:H	1.77	0.50
3:H:834:TYR:HE2	3:H:980:ASN:HD21	1.59	0.50
3:C:770:LEU:HB2	3:C:946:ARG:HH12	1.77	0.50
3:J:415:ILE:HG22	3:J:1077:PHE:HB2	1.94	0.50
4:L:115:LEU:HD13	4:L:292:ILE:HD11	1.94	0.50
3:B:450:ARG:NH1	3:B:1358:ASP:OD2	2.45	0.49
3:B:1140:ASP:HB3	3:B:1201:ALA:HA	1.94	0.49
3:C:774:ARG:NH2	3:C:777:GLY:O	2.45	0.49
3:J:277:HIS:HD2	3:J:313:VAL:HG12	1.76	0.49
1:Z:299:ILE:HD13	1:Z:340:LEU:HD22	1.94	0.49
1:E:310:ASP:HB3	1:E:357:LEU:HD11	1.94	0.49
3:B:277:HIS:HD2	3:B:313:VAL:HG12	1.77	0.49
3:C:1212:SER:O	3:C:1212:SER:OG	2.29	0.49
3:H:217:GLN:HB3	3:H:222:LEU:HD11	1.93	0.49
3:H:851:ARG:NH1	3:H:971:GLY:O	2.45	0.49
3:H:1325:ASP:OD2	3:H:1325:ASP:N	2.45	0.49
5:O:222:ILE:HA	5:O:225:LEU:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:227:ARG:NH2	3:H:1234:MET:O	2.45	0.49
3:J:479:CYS:SG	3:J:1056:THR:OG1	2.71	0.49
3:J:842:ARG:NH1	3:J:1032:SER:O	2.45	0.49
3:K:558:GLU:OE1	3:K:592:ARG:NH2	2.44	0.49
3:K:994:GLY:O	3:K:999:ARG:NH1	2.45	0.49
3:I:227:ARG:NH2	3:I:1234:MET:O	2.46	0.49
3:J:559:LEU:HB3	3:J:1270:SER:HA	1.93	0.49
3:B:678:VAL:HG21	3:B:706:ILE:HG21	1.93	0.49
3:C:558:GLU:OE1	3:C:592:ARG:NH2	2.46	0.49
3:H:69:LEU:HB3	3:J:337:VAL:HG12	1.95	0.49
3:I:268:PRO:HA	3:I:1086:GLU:HG2	1.93	0.49
2:A:71:ASN:ND2	2:A:101:ARG:O	2.45	0.49
3:B:796:ARG:NE	3:B:922:GLU:OE2	2.45	0.49
3:B:989:LEU:HD11	3:B:1008:PRO:HG3	1.94	0.49
3:C:1358:ASP:HB2	3:C:1379:GLN:HG2	1.93	0.49
3:J:1303:THR:HA	3:J:1310:ARG:HH22	1.78	0.49
4:L:68:ARG:NH1	4:L:285:ASP:O	2.46	0.49
5:V:212:ASN:OD1	5:V:212:ASN:N	2.46	0.49
3:B:842:ARG:NH1	3:B:1032:SER:O	2.45	0.49
3:J:744:THR:HA	3:J:827:ILE:HD12	1.94	0.49
5:V:207:LEU:HD22	5:V:211:ILE:HD11	1.95	0.49
3:H:268:PRO:HA	3:H:1086:GLU:HG2	1.94	0.49
3:H:415:ILE:HG22	3:H:1341:GLN:HB3	1.94	0.49
3:I:1091:SER:HB2	3:I:1121:LEU:HD22	1.95	0.49
1:Z:20:ASN:H	1:Z:25:ILE:HG22	1.77	0.49
3:I:851:ARG:NH1	3:I:971:GLY:O	2.45	0.49
3:K:770:LEU:HB2	3:K:946:ARG:HH12	1.77	0.49
3:K:842:ARG:NH1	3:K:1032:SER:O	2.46	0.49
3:K:531:MET:HE1	3:K:1006:VAL:HG21	1.94	0.48
3:I:774:ARG:NH1	3:I:779:ASN:OD1	2.46	0.48
3:I:1005:MET:HG3	3:I:1006:VAL:HG23	1.94	0.48
3:J:247:ARG:NH2	3:J:1387:PRO:O	2.46	0.48
3:K:305:GLN:HE22	3:K:386:ILE:HB	1.79	0.48
3:K:559:LEU:HB3	3:K:1270:SER:HA	1.94	0.48
3:H:774:ARG:NH1	3:H:779:ASN:OD1	2.46	0.48
3:H:785:HIS:HB3	3:H:803:HIS:HB3	1.95	0.48
3:I:564:ASP:OD2	3:I:1022:ARG:NH1	2.46	0.48
3:K:1358:ASP:HB2	3:K:1379:GLN:HG2	1.95	0.48
3:B:70:LEU:HB2	3:C:107:ILE:HG22	1.95	0.48
3:B:559:LEU:HB3	3:B:1270:SER:HA	1.95	0.48
3:H:1097:ILE:HD11	3:H:1112:LEU:HD13	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:1097:ILE:HD11	3:I:1112:LEU:HD13	1.95	0.48
3:I:1143:ASN:OD1	3:I:1143:ASN:N	2.44	0.48
3:J:1140:ASP:HB3	3:J:1201:ALA:HA	1.94	0.48
3:K:811:THR:OG1	3:K:812:GLY:N	2.46	0.48
4:R:139:LEU:HD23	4:R:141:ILE:HD11	1.95	0.48
5:V:8:ILE:HD11	5:V:37:LEU:HD23	1.95	0.48
3:I:785:HIS:HB3	3:I:803:HIS:HB3	1.94	0.48
3:J:1302:ASN:N	3:J:1302:ASN:OD1	2.46	0.48
3:K:111:VAL:HG13	3:K:130:ASN:HB2	1.95	0.48
5:V:131:VAL:HG13	5:V:133:LEU:HD12	1.95	0.48
1:E:132:ARG:NH2	1:E:134:ASP:OD2	2.46	0.48
3:J:154:LEU:HD21	3:J:169:LEU:HB3	1.94	0.48
3:C:811:THR:OG1	3:C:812:GLY:N	2.46	0.48
3:C:842:ARG:NH1	3:C:1032:SER:O	2.47	0.48
3:H:1091:SER:HB2	3:H:1121:LEU:HD22	1.94	0.48
3:I:243:PHE:HB3	3:I:246:THR:HG22	1.95	0.48
3:I:745:ASP:O	3:I:830:LYS:NZ	2.45	0.48
3:K:721:ILE:HG13	3:K:1044:LEU:HD11	1.96	0.48
5:O:8:ILE:HD11	5:O:37:LEU:HD23	1.94	0.48
5:V:107:LEU:HD23	5:V:142:PRO:HG3	1.95	0.48
1:Z:205:ARG:NE	1:Z:208:GLU:OE1	2.43	0.48
3:J:470:THR:HG22	3:J:472:ARG:H	1.77	0.48
3:K:1321:GLN:NE2	3:K:1342:ASP:OD2	2.44	0.48
5:O:33:THR:OG1	5:O:51:TYR:OH	2.28	0.48
3:B:296:LYS:O	3:B:300:LEU:HB2	2.14	0.48
3:B:500:ARG:NH1	3:B:582:GLU:OE2	2.47	0.48
3:H:1005:MET:HG3	3:H:1006:VAL:HG23	1.96	0.48
3:J:834:TYR:HE1	3:J:980:ASN:HD21	1.59	0.48
1:E:299:ILE:HG21	1:E:340:LEU:HD13	1.96	0.47
3:C:785:HIS:HB3	3:C:803:HIS:HB3	1.96	0.47
3:J:190:ARG:NH1	3:J:400:ARG:O	2.47	0.47
2:A:26:VAL:O	2:A:60:SER:OG	2.33	0.47
2:A:65:ARG:O	2:A:67:ASN:N	2.48	0.47
3:C:111:VAL:HG13	3:C:130:ASN:HB2	1.96	0.47
3:C:721:ILE:HG13	3:C:1044:LEU:HD11	1.96	0.47
3:I:755:ASP:N	3:I:755:ASP:OD1	2.47	0.47
1:E:146:ARG:HH22	1:E:151:LEU:HD11	1.80	0.47
3:C:745:ASP:O	3:C:830:LYS:NZ	2.42	0.47
3:H:755:ASP:OD1	3:H:755:ASP:N	2.47	0.47
2:k:65:ARG:O	2:k:67:ASN:N	2.47	0.47
3:C:276:THR:OG1	3:C:277:HIS:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:778:ARG:NH2	3:I:798:ASP:OD1	2.46	0.47
4:L:222:ILE:HG21	4:L:276:TRP:HB2	1.97	0.47
1:E:328:THR:OG1	1:E:335:GLY:O	2.32	0.47
3:B:190:ARG:NH1	3:B:400:ARG:O	2.47	0.47
3:B:337:VAL:HG12	3:I:69:LEU:HB3	1.96	0.47
3:K:296:LYS:O	3:K:300:LEU:HB2	2.15	0.47
3:B:245:MET:HE3	3:B:245:MET:HB2	1.74	0.47
3:H:564:ASP:OD2	3:H:1022:ARG:NH1	2.48	0.47
3:H:778:ARG:NH2	3:H:798:ASP:OD1	2.46	0.47
3:K:205:PRO:HG2	3:K:210:LEU:HD22	1.97	0.47
1:Z:161:PRO:HB2	1:Z:165:THR:HG21	1.97	0.47
2:G:65:ARG:O	2:G:67:ASN:N	2.48	0.47
2:Y:65:ARG:O	2:Y:67:ASN:N	2.48	0.47
1:E:198:LEU:HD12	1:E:198:LEU:HA	1.76	0.46
3:B:846:CYS:HB2	3:B:985:CYS:HB3	1.39	0.46
3:H:1219:ARG:NH1	3:H:1374:GLU:OE1	2.48	0.46
3:J:536:HIS:HD2	3:J:554:ARG:HD2	1.80	0.46
3:K:1165:SER:O	3:K:1169:ILE:HG13	2.14	0.46
1:Z:27:ILE:HG22	1:Z:29:PRO:HD3	1.96	0.46
1:E:161:PRO:HB2	1:E:165:THR:HG21	1.97	0.46
3:K:245:MET:HE2	3:K:245:MET:HB2	1.88	0.46
1:Z:206:ALA:HB1	1:Z:215:ALA:HB1	1.97	0.46
3:H:125:ASP:OD1	3:H:125:ASP:N	2.38	0.46
3:J:994:GLY:O	3:J:999:ARG:NH1	2.48	0.46
3:K:745:ASP:O	3:K:830:LYS:NZ	2.42	0.46
3:B:223:ASN:OD1	3:B:223:ASN:N	2.49	0.46
3:H:1144:THR:HG22	3:H:1175:ARG:HD3	1.98	0.46
3:J:683:ASN:OD1	3:J:754:TRP:NE1	2.44	0.46
3:J:796:ARG:NE	3:J:922:GLU:OE2	2.49	0.46
3:K:1099:VAL:HG12	3:K:1112:LEU:HG	1.97	0.46
3:K:1325:ASP:OD1	3:K:1325:ASP:N	2.47	0.46
3:B:1099:VAL:HG22	3:B:1112:LEU:HG	1.97	0.46
2:G:95:ARG:NH2	3:J:698:GLU:OE2	2.48	0.46
3:H:1070:THR:HG23	3:H:1207:VAL:HB	1.98	0.46
3:J:774:ARG:NH2	3:J:777:GLY:O	2.49	0.46
3:J:1143:ASN:OD1	3:J:1143:ASN:N	2.47	0.46
3:K:276:THR:OG1	3:K:277:HIS:N	2.48	0.46
2:A:89:ARG:HH21	2:k:35:SER:HB3	1.81	0.46
3:B:224:ARG:HB3	3:I:1196:ILE:HD11	1.98	0.46
3:H:1231:MET:HE3	3:H:1231:MET:HB3	1.76	0.46
3:J:413:GLY:O	3:J:1079:THR:OG1	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:161:ASP:N	3:H:161:ASP:OD1	2.49	0.46
3:H:326:ASN:ND2	3:H:337:VAL:O	2.49	0.46
3:J:296:LYS:O	3:J:300:LEU:HB2	2.16	0.46
3:J:846:CYS:HB2	3:J:985:CYS:HB3	1.37	0.46
3:J:1099:VAL:HG22	3:J:1112:LEU:HG	1.98	0.46
3:I:934:ASP:OD2	3:I:1049:LYS:NZ	2.41	0.46
3:K:1070:THR:HG23	3:K:1207:VAL:HB	1.97	0.46
3:H:1165:SER:O	3:H:1169:ILE:HG13	2.15	0.46
3:K:285:VAL:HG12	3:K:391:LEU:HD22	1.98	0.46
3:K:847:THR:HG22	3:K:957:ILE:HG12	1.98	0.46
3:B:774:ARG:NH2	3:B:777:GLY:O	2.49	0.46
3:I:980:ASN:HB3	3:I:983:PHE:H	1.81	0.46
3:I:1070:THR:HG23	3:I:1207:VAL:HB	1.98	0.46
3:J:989:LEU:HD11	3:J:1008:PRO:HG3	1.97	0.46
3:B:1097:ILE:HD11	3:B:1112:LEU:HD23	1.97	0.45
3:C:113:GLN:NE2	3:C:130:ASN:OD1	2.42	0.45
3:C:285:VAL:HG12	3:C:391:LEU:HD22	1.98	0.45
3:C:846:CYS:HB2	3:C:985:CYS:HB3	1.42	0.45
3:K:203:LYS:NZ	3:K:1089:SER:OG	2.50	0.45
3:K:471:LEU:HB3	3:K:1059:LEU:HD22	1.98	0.45
1:Z:347:GLU:HB2	1:Z:435:LEU:HD12	1.96	0.45
3:H:239:CYS:SG	3:H:1389:ARG:NH2	2.90	0.45
1:Z:198:LEU:HD11	1:Z:338:LEU:HD22	1.98	0.45
3:C:1099:VAL:HG12	3:C:1112:LEU:HG	1.97	0.45
3:H:1304:ASN:N	3:H:1304:ASN:OD1	2.48	0.45
3:I:724:PHE:HA	3:I:1061:THR:HG21	1.98	0.45
3:J:149:SER:OG	3:J:1106:GLY:O	2.31	0.45
3:B:39:ILE:HD12	3:B:40:GLU:H	1.81	0.45
3:K:859:LEU:HD12	3:K:894:LEU:HD21	1.99	0.45
1:Z:326:VAL:HG21	1:Z:358:LEU:HD11	1.99	0.45
3:C:1234:MET:SD	3:C:1235:GLY:N	2.89	0.45
3:H:860:GLN:NE2	3:H:917:MET:SD	2.90	0.45
1:E:450:MET:HE2	1:E:457:ASN:HB3	1.98	0.45
3:B:431:MET:HE3	3:B:431:MET:HB3	1.89	0.45
3:B:679:ALA:O	3:B:707:TYR:OH	2.31	0.45
3:B:1070:THR:HG23	3:B:1207:VAL:HB	1.99	0.45
3:I:490:LEU:HD11	3:I:589:ALA:HB2	1.99	0.45
3:J:1305:CYS:O	3:J:1310:ARG:NH2	2.48	0.45
1:E:318:LEU:HD12	1:E:440:PRO:HA	1.99	0.45
3:B:531:MET:HE1	3:B:1006:VAL:HG21	1.98	0.45
3:K:711:LEU:HD12	3:K:711:LEU:HA	1.86	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:725:THR:HG21	3:K:737:GLU:HG2	1.99	0.45
3:K:1219:ARG:NH1	3:K:1374:GLU:OE1	2.50	0.45
3:B:683:ASN:OD1	3:B:754:TRP:NE1	2.46	0.44
3:H:243:PHE:HB3	3:H:246:THR:HG22	1.98	0.44
3:H:724:PHE:HA	3:H:1061:THR:HG21	1.98	0.44
3:K:834:TYR:HE1	3:K:980:ASN:HD21	1.65	0.44
1:E:134:ASP:N	1:E:134:ASP:OD1	2.51	0.44
1:E:251:PHE:HD1	1:E:254:ARG:HH21	1.64	0.44
3:B:1302:ASN:N	3:B:1302:ASN:OD1	2.51	0.44
3:I:161:ASP:OD1	3:I:161:ASP:N	2.49	0.44
1:E:89:ASN:HB3	1:E:91:MET:HE3	2.00	0.44
3:B:72:THR:HG22	3:C:108:GLN:HB2	1.99	0.44
3:B:333:MET:HE2	3:B:333:MET:HB3	1.85	0.44
3:C:1256:THR:O	3:C:1256:THR:OG1	2.32	0.44
3:I:1306:ASN:OD1	3:I:1306:ASN:N	2.48	0.44
3:J:39:ILE:HD12	3:J:40:GLU:H	1.82	0.44
3:K:223:ASN:OD1	3:K:223:ASN:N	2.51	0.44
5:O:219:LEU:O	5:O:223:THR:OG1	2.32	0.44
3:B:1051:THR:O	3:B:1054:SER:OG	2.33	0.44
2:Y:35:SER:O	2:Y:35:SER:OG	2.33	0.44
3:C:775:VAL:HG11	3:C:801:LEU:HD21	1.99	0.44
3:C:1345:GLY:O	3:C:1348:GLN:NE2	2.50	0.44
3:H:1306:ASN:OD1	3:H:1306:ASN:N	2.49	0.44
3:I:1304:ASN:OD1	3:I:1304:ASN:N	2.49	0.44
2:A:73:ILE:HG21	2:A:100:PRO:HB3	2.00	0.44
3:H:277:HIS:CD2	3:H:313:VAL:HG12	2.51	0.44
3:J:724:PHE:HA	3:J:1061:THR:HG21	2.00	0.44
5:O:58:PRO:HB2	5:O:63:LEU:HG	1.99	0.44
3:B:1358:ASP:HB3	3:B:1361:MET:HE3	2.00	0.44
2:M:10:SER:O	2:M:13:THR:OG1	2.35	0.44
2:M:71:ASN:ND2	2:M:101:ARG:O	2.50	0.44
1:Z:258:PHE:CG	1:Z:436:ILE:HD11	2.52	0.44
3:C:245:MET:HE2	3:C:245:MET:HB2	1.81	0.44
3:C:594:ILE:HG22	3:C:596:GLY:N	2.31	0.44
3:C:896:VAL:HG22	2:Y:94:LEU:HD21	1.99	0.44
3:H:196:LEU:HD23	3:H:196:LEU:HA	1.87	0.44
3:H:1004:LYS:HE2	3:H:1004:LYS:HB2	1.84	0.44
3:I:830:LYS:O	3:I:834:TYR:HB2	2.18	0.44
2:k:10:SER:O	2:k:13:THR:OG1	2.34	0.44
1:E:264:GLU:HB3	1:E:287:THR:HG23	2.00	0.44
3:C:834:TYR:HE1	3:C:980:ASN:HD21	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:502:CYS:H	3:J:533:HIS:HE1	1.65	0.44
3:K:604:PRO:HD2	3:K:607:PHE:HB3	1.99	0.44
3:B:917:MET:HE2	3:B:917:MET:HB2	1.92	0.43
3:H:747:THR:HA	3:H:762:ARG:HG3	2.00	0.43
3:H:1312:LEU:O	3:H:1316:LYS:NZ	2.50	0.43
3:J:1070:THR:HG23	3:J:1207:VAL:HB	2.00	0.43
3:K:775:VAL:HG11	3:K:801:LEU:HD21	1.98	0.43
1:Z:328:THR:OG1	1:Z:335:GLY:O	2.35	0.43
3:I:223:ASN:OD1	3:I:223:ASN:N	2.50	0.43
3:I:747:THR:HA	3:I:762:ARG:HG3	1.99	0.43
3:J:775:VAL:HG11	3:J:801:LEU:HD21	1.98	0.43
2:S:65:ARG:O	2:S:67:ASN:N	2.51	0.43
4:R:269:ILE:O	4:R:273:ILE:HG22	2.18	0.43
3:C:152:LEU:HD11	3:C:1108:VAL:HG22	2.00	0.43
3:K:823:ARG:HE	3:K:823:ARG:HB2	1.60	0.43
3:K:1256:THR:O	3:K:1256:THR:OG1	2.33	0.43
5:O:116:LEU:HD22	5:O:141:ILE:HG12	2.00	0.43
5:V:101:ASN:HB3	5:V:306:PRO:HA	2.00	0.43
1:Z:436:ILE:HD12	1:Z:436:ILE:HA	1.84	0.43
1:Z:452:ARG:NH1	1:Z:457:ASN:OD1	2.50	0.43
3:B:782:GLN:HB2	3:B:800:VAL:HG12	2.00	0.43
3:C:205:PRO:HG2	3:C:210:LEU:HD22	2.00	0.43
3:C:266:THR:OG1	3:C:1125:TYR:O	2.33	0.43
3:C:1325:ASP:OD1	3:C:1325:ASP:N	2.46	0.43
3:J:205:PRO:HG2	3:J:210:LEU:HD22	1.99	0.43
3:J:239:CYS:SG	3:J:1389:ARG:NH2	2.91	0.43
5:O:212:ASN:OD1	5:O:212:ASN:N	2.51	0.43
1:E:126:SER:OG	1:E:127:LEU:N	2.49	0.43
3:C:848:MET:SD	3:C:958:MET:HE2	2.58	0.43
2:G:35:SER:O	2:G:35:SER:OG	2.33	0.43
2:S:50:ARG:HE	2:S:50:ARG:HB2	1.64	0.43
3:C:502:CYS:SG	3:C:503:TYR:N	2.91	0.43
3:H:331:LEU:HD23	3:H:331:LEU:HA	1.90	0.43
3:I:548:ILE:HG22	3:I:1258:ARG:HB2	2.00	0.43
3:J:631:LYS:HE2	3:J:1036:PHE:HZ	1.83	0.43
2:M:65:ARG:O	2:M:67:ASN:N	2.51	0.43
5:O:160:ARG:NH1	5:O:190:LEU:O	2.52	0.43
5:V:304:VAL:HG11	5:V:310:THR:HB	2.00	0.43
3:B:1373:ASP:HA	3:I:1365:ALA:HB1	2.01	0.43
3:H:266:THR:OG1	3:H:1125:TYR:O	2.34	0.43
3:H:682:ASN:HB3	3:H:959:MET:SD	2.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:674:GLN:NE2	3:K:696:ASN:O	2.51	0.43
3:K:660:LEU:HD11	3:K:916:LEU:HB2	2.00	0.43
3:K:846:CYS:HB2	3:K:985:CYS:HB3	1.41	0.43
4:R:68:ARG:NH1	4:R:285:ASP:O	2.52	0.43
3:B:775:VAL:HG11	3:B:801:LEU:HD21	2.00	0.43
3:B:1060:ARG:HH12	3:B:1169:ILE:HD13	1.83	0.43
3:C:660:LEU:HD11	3:C:916:LEU:HB2	2.01	0.43
3:H:384:LEU:HB3	3:H:391:LEU:HD11	1.99	0.43
3:H:407:VAL:HG21	3:J:118:ARG:HD3	2.01	0.43
3:J:223:ASN:OD1	3:J:223:ASN:N	2.50	0.43
3:K:431:MET:HE2	3:K:431:MET:HB3	1.91	0.43
4:R:148:GLU:OE1	4:R:148:GLU:N	2.52	0.43
5:O:54:ASN:OD1	5:O:54:ASN:N	2.50	0.43
1:E:156:ARG:HH22	4:L:153:VAL:HG23	1.84	0.43
3:C:725:THR:HG21	3:C:737:GLU:HG2	2.01	0.43
3:C:859:LEU:HD12	3:C:894:LEU:HD21	2.00	0.43
3:C:1356:SER:HB3	3:C:1381:LEU:HD13	2.01	0.43
3:H:414:ASN:OD1	3:H:414:ASN:N	2.51	0.43
3:I:207:LEU:HD22	3:I:262:MET:HE3	1.99	0.43
3:I:247:ARG:HB3	3:I:248:HIS:HD2	1.83	0.43
4:R:112:TYR:O	4:R:143:GLN:N	2.47	0.43
1:Z:151:LEU:HD22	4:R:106:ASP:HB2	2.01	0.42
3:B:178:ALA:O	3:B:182:ARG:HB2	2.18	0.42
3:B:205:PRO:HG2	3:B:210:LEU:HD22	2.00	0.42
3:I:1219:ARG:NH1	3:I:1374:GLU:OE1	2.52	0.42
3:J:782:GLN:HB2	3:J:800:VAL:HG12	2.00	0.42
5:V:88:ILE:HA	5:V:314:GLN:HE21	1.83	0.42
1:Z:137:HIS:HE1	1:Z:453:PHE:HA	1.84	0.42
1:E:356:PHE:O	1:E:358:LEU:N	2.52	0.42
3:B:757:ASP:N	3:B:757:ASP:OD1	2.52	0.42
3:I:1357:SER:O	3:I:1357:SER:OG	2.37	0.42
3:J:962:GLN:OE1	3:J:962:GLN:N	2.48	0.42
3:K:979:VAL:HG21	3:K:1013:LEU:HB3	2.01	0.42
5:O:293:LEU:HD13	5:O:312:VAL:HG11	2.01	0.42
3:C:1306:ASN:N	3:C:1306:ASN:OD1	2.52	0.42
3:H:514:ASP:OD2	3:H:522:ARG:NH1	2.53	0.42
3:I:1165:SER:O	3:I:1169:ILE:HG13	2.19	0.42
3:K:207:LEU:HD22	3:K:262:MET:HE3	2.01	0.42
3:B:107:ILE:HG22	3:B:134:LYS:HB2	2.02	0.42
3:J:178:ALA:O	3:J:182:ARG:HB2	2.18	0.42
3:J:548:ILE:HD13	3:J:548:ILE:HA	1.86	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:788:ASP:N	3:J:788:ASP:OD1	2.50	0.42
3:K:503:TYR:HE1	3:K:569:PRO:HB3	1.84	0.42
2:A:20:ILE:HG21	2:A:46:ILE:HB	2.01	0.42
3:B:556:ARG:H	3:B:556:ARG:HG2	1.57	0.42
3:C:82:PHE:HZ	3:C:196:LEU:HD12	1.84	0.42
3:I:196:LEU:HD23	3:I:196:LEU:HA	1.86	0.42
3:I:514:ASP:OD2	3:I:522:ARG:NH1	2.52	0.42
3:I:725:THR:HG21	3:I:737:GLU:HG2	2.02	0.42
3:I:1256:THR:O	3:I:1256:THR:OG1	2.31	0.42
3:K:604:PRO:HG3	3:K:1212:SER:HB3	2.00	0.42
3:K:1356:SER:HB3	3:K:1381:LEU:HD13	2.01	0.42
2:M:76:THR:HG21	2:M:94:LEU:HD22	2.02	0.42
1:Z:139:GLY:O	1:Z:298:ASN:ND2	2.53	0.42
3:B:177:MET:HE3	3:B:177:MET:HB2	1.90	0.42
3:B:724:PHE:HA	3:B:1061:THR:HG21	2.01	0.42
2:G:45:ASP:OD1	2:G:45:ASP:N	2.53	0.42
3:H:245:MET:HE2	3:H:245:MET:HB2	1.82	0.42
3:H:849:GLY:HA3	3:H:924:THR:HG21	2.02	0.42
3:I:569:PRO:HG2	3:I:572:VAL:HG11	2.01	0.42
3:I:682:ASN:HB3	3:I:959:MET:SD	2.59	0.42
3:K:648:ALA:HB2	3:K:956:LEU:HD11	2.01	0.42
2:Y:76:THR:HG21	2:Y:94:LEU:HD12	2.00	0.42
3:C:187:SER:HB2	3:H:115:MET:HE3	2.01	0.42
3:C:683:ASN:OD1	3:C:754:TRP:NE1	2.47	0.42
3:H:548:ILE:HG22	3:H:1258:ARG:HB2	2.02	0.42
3:H:743:LEU:HD11	3:H:1047:TYR:HD2	1.85	0.42
3:I:331:LEU:HD23	3:I:331:LEU:HA	1.90	0.42
3:J:757:ASP:OD1	3:J:757:ASP:N	2.52	0.42
3:C:1195:GLY:HA3	3:H:1233:TYR:HB3	2.00	0.42
2:G:35:SER:HB3	2:M:89:ARG:NH2	2.35	0.42
3:H:653:ASN:HD21	3:H:805:ARG:H	1.66	0.42
3:J:1091:SER:HB2	3:J:1121:LEU:HD22	2.02	0.42
2:S:73:ILE:HG21	2:S:100:PRO:HB3	2.01	0.42
3:C:223:ASN:OD1	3:C:223:ASN:N	2.53	0.42
3:C:789:MET:HB3	2:S:55:VAL:HG13	2.01	0.42
3:H:145:PHE:HD2	3:H:1110:PHE:HB2	1.85	0.42
3:H:1158:LEU:HD23	3:H:1158:LEU:HA	1.89	0.42
3:I:326:ASN:ND2	3:I:337:VAL:O	2.53	0.42
3:I:414:ASN:N	3:I:414:ASN:OD1	2.51	0.42
3:I:743:LEU:HD11	3:I:1047:TYR:HD2	1.85	0.42
3:J:203:LYS:NZ	3:J:1120:ASP:OD1	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:1304:ASN:OD1	3:K:1304:ASN:N	2.53	0.42
5:O:146:MET:HE1	5:O:289:THR:H	1.84	0.42
5:V:275:SER:O	5:V:279:THR:HG23	2.19	0.42
3:C:1278:GLY:HA3	3:C:1293:PHE:HE1	1.85	0.42
3:H:751:PRO:HD3	3:H:834:TYR:CZ	2.55	0.42
3:I:1333:PRO:HA	3:I:1334:PRO:HD3	1.94	0.42
3:K:307:ASP:HB2	3:K:386:ILE:HG13	2.02	0.42
3:B:499:ASP:OD1	3:B:499:ASP:N	2.44	0.41
3:C:648:ALA:HB2	3:C:956:LEU:HD11	2.02	0.41
3:H:1196:ILE:HD11	3:J:224:ARG:HB3	2.01	0.41
3:I:83:LEU:HD21	3:I:317:TYR:HE1	1.85	0.41
3:I:266:THR:OG1	3:I:1125:TYR:O	2.35	0.41
3:J:72:THR:HG22	3:K:108:GLN:HB2	2.02	0.41
3:J:431:MET:HE3	3:J:431:MET:HB3	1.88	0.41
3:J:743:LEU:HD11	3:J:1047:TYR:HD2	1.85	0.41
3:J:1182:LEU:HD13	3:J:1188:LEU:HD21	2.01	0.41
3:K:683:ASN:OD1	3:K:754:TRP:NE1	2.49	0.41
3:K:724:PHE:HA	3:K:1061:THR:HG21	2.01	0.41
3:K:1306:ASN:OD1	3:K:1306:ASN:N	2.51	0.41
2:Y:45:ASP:OD1	2:Y:45:ASP:N	2.52	0.41
3:B:1143:ASN:OD1	3:B:1143:ASN:N	2.48	0.41
3:H:796:ARG:HG2	3:H:798:ASP:H	1.85	0.41
3:H:848:MET:SD	3:H:958:MET:HE2	2.60	0.41
3:J:277:HIS:CD2	3:J:313:VAL:HG12	2.55	0.41
3:J:847:THR:HG22	3:J:957:ILE:HG12	2.02	0.41
3:K:1002:LEU:HD23	3:K:1002:LEU:HA	1.92	0.41
2:S:76:THR:OG1	2:S:77:ALA:N	2.53	0.41
2:Y:101:ARG:C	2:Y:103:ILE:H	2.28	0.41
4:R:107:LEU:HG	4:R:142:PRO:HG3	2.02	0.41
3:I:1053:ILE:HD13	3:I:1166:LEU:HD13	2.01	0.41
3:K:569:PRO:HG2	3:K:572:VAL:HG11	2.02	0.41
1:E:261:SER:O	1:E:261:SER:OG	2.36	0.41
3:B:743:LEU:HD11	3:B:1047:TYR:HD2	1.84	0.41
3:H:115:MET:HE2	3:H:115:MET:HB3	1.93	0.41
3:H:859:LEU:HD23	3:H:917:MET:HE1	2.01	0.41
3:H:1357:SER:O	3:H:1357:SER:OG	2.37	0.41
3:I:241:ASP:OD1	3:I:241:ASP:N	2.53	0.41
3:I:757:ASP:N	3:I:757:ASP:OD1	2.52	0.41
3:K:493:LEU:HD23	3:K:493:LEU:HA	1.94	0.41
3:K:501:GLN:HE22	3:K:536:HIS:CE1	2.38	0.41
3:K:653:ASN:HD21	3:K:805:ARG:H	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Y:101:ARG:HD2	2:Y:101:ARG:HA	1.87	0.41
1:E:108:ILE:H	1:E:108:ILE:HG13	1.70	0.41
1:E:458:VAL:HA	1:E:459:PRO:HD3	1.91	0.41
2:A:51:SER:O	2:A:55:VAL:HG12	2.20	0.41
3:H:757:ASP:OD1	3:H:757:ASP:N	2.52	0.41
3:I:245:MET:HE2	3:I:245:MET:HB2	1.92	0.41
3:I:379:ARG:HA	3:I:379:ARG:HD3	1.79	0.41
3:I:662:ARG:HH12	3:I:906:ASP:HB2	1.86	0.41
3:I:786:PHE:CE1	3:I:805:ARG:HD3	2.55	0.41
3:I:860:GLN:NE2	3:I:917:MET:SD	2.93	0.41
3:I:1229:SER:HB2	3:I:1245:MET:HG3	2.02	0.41
3:J:900:ASN:O	2:M:95:ARG:NH2	2.54	0.41
3:K:769:ARG:H	3:K:769:ARG:HG2	1.50	0.41
3:K:863:ILE:HG13	3:K:890:VAL:HG12	2.02	0.41
3:K:1278:GLY:HA3	3:K:1293:PHE:HE1	1.85	0.41
1:E:319:LYS:HE3	1:E:319:LYS:HB3	1.93	0.41
3:B:631:LYS:HE2	3:B:1036:PHE:HZ	1.86	0.41
3:B:962:GLN:OE1	3:B:962:GLN:N	2.46	0.41
3:B:1182:LEU:HD13	3:B:1188:LEU:HD21	2.03	0.41
3:I:67:ASP:N	3:I:67:ASP:OD1	2.53	0.41
3:I:1231:MET:HG3	3:I:1301:VAL:HG21	2.02	0.41
4:L:79:ILE:HD11	4:L:82:LYS:HE2	2.01	0.41
1:Z:198:LEU:HD12	1:Z:198:LEU:HA	1.72	0.41
1:E:203:ALA:O	1:E:219:ARG:NH1	2.54	0.41
3:B:253:ARG:HA	3:B:253:ARG:HD2	1.96	0.41
3:H:846:CYS:HB2	3:H:985:CYS:HB3	1.39	0.41
3:J:383:ASP:OD1	3:J:383:ASP:N	2.53	0.41
4:L:112:TYR:HE2	4:L:315:VAL:HG21	1.86	0.41
3:H:985:CYS:HB2	3:H:988:HIS:HB2	2.03	0.41
3:I:145:PHE:HD2	3:I:1110:PHE:HB2	1.85	0.41
3:I:711:LEU:HD12	3:I:711:LEU:HA	1.85	0.41
3:J:1016:ASN:HD21	3:J:1023:GLN:HB2	1.86	0.41
1:Z:282:GLN:HE21	1:Z:295:VAL:HG13	1.86	0.41
1:E:294:ARG:HA	1:E:294:ARG:HD3	1.95	0.41
3:B:769:ARG:H	3:B:769:ARG:HG3	1.62	0.41
3:B:867:ILE:HD13	3:B:867:ILE:HA	1.90	0.41
3:C:989:LEU:HD11	3:C:1008:PRO:HG3	2.03	0.41
3:H:658:CYS:HA	3:H:661:LEU:HG	2.03	0.41
3:J:281:ARG:NH2	3:J:307:ASP:O	2.53	0.41
3:J:908:ASP:HA	3:J:911:LEU:HB2	2.03	0.41
2:M:23:TYR:HE2	2:M:26:VAL:H	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:O:304:VAL:HG11	5:O:310:THR:HG22	2.02	0.41
1:E:118:THR:OG1	1:E:119:THR:N	2.53	0.41
3:B:59:ASN:OD1	3:B:59:ASN:N	2.54	0.41
3:C:331:LEU:HD23	3:C:331:LEU:HA	1.96	0.41
3:H:980:ASN:HB3	3:H:983:PHE:H	1.85	0.41
3:I:762:ARG:NH1	3:I:763:ASP:OD1	2.54	0.41
3:J:604:PRO:HD2	3:J:607:PHE:HB3	2.03	0.41
3:K:594:ILE:HG22	3:K:596:GLY:N	2.33	0.41
1:Z:205:ARG:HH22	1:Z:243:ARG:HH21	1.68	0.40
3:C:1182:LEU:HD12	3:C:1182:LEU:HA	1.90	0.40
3:C:1219:ARG:NH1	3:C:1374:GLU:OE1	2.54	0.40
3:I:259:LEU:HD23	3:I:259:LEU:HA	1.94	0.40
3:K:1158:LEU:HD23	3:K:1158:LEU:HA	1.86	0.40
4:L:36:THR:OG1	4:L:38:ARG:NH1	2.54	0.40
5:O:200:ILE:O	5:O:204:VAL:HG22	2.21	0.40
3:C:661:LEU:HD23	3:C:661:LEU:HA	1.92	0.40
3:C:979:VAL:HG21	3:C:1013:LEU:HB3	2.03	0.40
3:H:1030:THR:HG23	3:H:1031:HIS:ND1	2.36	0.40
3:I:82:PHE:HZ	3:I:196:LEU:HD12	1.86	0.40
3:I:859:LEU:HD23	3:I:917:MET:HE1	2.03	0.40
3:J:1356:SER:HB3	3:J:1362:LEU:HD13	2.03	0.40
5:V:63:LEU:HD23	5:V:63:LEU:HA	1.84	0.40
3:B:682:ASN:HB3	3:B:959:MET:SD	2.62	0.40
3:C:213:ILE:HD13	3:C:213:ILE:HA	1.85	0.40
2:G:94:LEU:HD23	2:G:94:LEU:HA	1.91	0.40
3:H:501:GLN:HE21	3:H:533:HIS:CE1	2.39	0.40
3:H:847:THR:HG22	3:H:957:ILE:HG12	2.02	0.40
3:I:630:VAL:HA	3:I:633:THR:HG22	2.03	0.40
3:I:796:ARG:HG2	3:I:798:ASP:H	1.87	0.40
3:I:847:THR:HG22	3:I:957:ILE:HG12	2.04	0.40
3:I:848:MET:SD	3:I:958:MET:HE2	2.61	0.40
3:K:82:PHE:HZ	3:K:196:LEU:HD12	1.87	0.40
3:B:969:ALA:O	3:B:972:THR:OG1	2.33	0.40
3:B:1164:GLU:OE1	3:B:1167:ARG:NH1	2.55	0.40
3:C:1175:ARG:HE	3:H:1256:THR:HB	1.86	0.40
3:H:67:ASP:N	3:H:67:ASP:OD1	2.54	0.40
3:I:714:VAL:HG12	3:I:828:LEU:HD22	2.03	0.40
3:I:849:GLY:HA3	3:I:924:THR:HG21	2.03	0.40
3:J:213:ILE:HD13	3:J:230:LEU:HD21	2.02	0.40
3:J:596:GLY:O	3:J:608:ARG:NH2	2.55	0.40
3:J:648:ALA:HB2	3:J:956:LEU:HD11	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1217:TYR:CD2	3:J:1261:LEU:HD22	2.55	0.40
5:O:63:LEU:HD23	5:O:63:LEU:HA	1.87	0.40
2:A:82:THR:HG22	2:A:86:THR:HG21	2.03	0.40
3:B:604:PRO:HD2	3:B:607:PHE:HB3	2.03	0.40
3:B:994:GLY:O	3:B:999:ARG:NH1	2.55	0.40
3:C:196:LEU:HD23	3:C:196:LEU:HA	1.90	0.40
3:C:203:LYS:NZ	3:C:1089:SER:OG	2.54	0.40
3:C:503:TYR:HE1	3:C:569:PRO:HB3	1.86	0.40
3:H:762:ARG:NH1	3:H:763:ASP:OD1	2.55	0.40
3:J:242:MET:HE1	3:J:1343:PRO:HG3	2.03	0.40
3:K:1374:GLU:OE2	3:K:1383:ARG:NH2	2.55	0.40
4:R:248:ALA:O	4:R:250:GLN:N	2.54	0.40
4:R:273:ILE:HD13	4:R:273:ILE:HG21	1.92	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	E	384/392 (98%)	317 (83%)	61 (16%)	6 (2%)	7	35
1	Z	384/392 (98%)	325 (85%)	51 (13%)	8 (2%)	5	31
2	A	92/94 (98%)	62 (67%)	24 (26%)	6 (6%)	1	14
2	G	92/94 (98%)	64 (70%)	21 (23%)	7 (8%)	1	10
2	M	92/94 (98%)	65 (71%)	19 (21%)	8 (9%)	0	8
2	S	92/94 (98%)	64 (70%)	22 (24%)	6 (6%)	1	14
2	Y	92/94 (98%)	63 (68%)	22 (24%)	7 (8%)	1	10
2	k	92/94 (98%)	64 (70%)	21 (23%)	7 (8%)	1	10
3	B	1327/1369 (97%)	1235 (93%)	92 (7%)	0	100	100
3	C	1327/1369 (97%)	1238 (93%)	89 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	H	1327/1369 (97%)	1237 (93%)	90 (7%)	0	100	100
3	I	1327/1369 (97%)	1237 (93%)	90 (7%)	0	100	100
3	J	1327/1369 (97%)	1234 (93%)	93 (7%)	0	100	100
3	K	1327/1369 (97%)	1235 (93%)	92 (7%)	0	100	100
4	L	248/256 (97%)	232 (94%)	15 (6%)	1 (0%)	30	60
4	R	248/256 (97%)	233 (94%)	14 (6%)	1 (0%)	30	60
5	O	257/263 (98%)	237 (92%)	20 (8%)	0	100	100
5	V	257/263 (98%)	242 (94%)	15 (6%)	0	100	100
All	All	10292/10600 (97%)	9384 (91%)	851 (8%)	57 (1%)	23	52

All (57) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Z	267	ILE
1	E	267	ILE
2	A	19	ALA
2	A	46	ILE
2	A	66	ALA
2	G	19	ALA
2	G	66	ALA
2	G	102	ILE
2	M	19	ALA
2	M	46	ILE
2	M	66	ALA
2	M	102	ILE
2	S	19	ALA
2	S	66	ALA
2	Y	19	ALA
2	Y	66	ALA
2	Y	102	ILE
2	k	19	ALA
2	k	46	ILE
2	k	66	ALA
2	k	102	ILE
1	Z	118	THR
2	G	46	ILE
2	S	46	ILE
2	Y	46	ILE
4	L	230	ILE

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Mol	Chain	Res	Type
4	R	230	ILE
1	Z	265	TYR
1	Z	131	PHE
1	E	131	PHE
1	E	265	TYR
1	Z	262	LEU
1	E	262	LEU
2	A	26	VAL
2	G	26	VAL
2	M	49	ALA
2	S	26	VAL
2	Y	26	VAL
2	k	25	PRO
2	A	25	PRO
2	G	25	PRO
2	M	25	PRO
2	S	25	PRO
2	Y	25	PRO
1	Z	256	ILE
2	G	73	ILE
2	M	73	ILE
2	Y	73	ILE
2	k	26	VAL
2	k	73	ILE
1	E	101	ILE
2	A	73	ILE
2	S	73	ILE
1	Z	32	ILE
1	Z	101	ILE
1	E	32	ILE
2	M	26	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	295/309 (96%)	293 (99%)	2 (1%)	76	77
1	Z	295/309 (96%)	290 (98%)	5 (2%)	53	67
2	A	69/73 (94%)	69 (100%)	0	100	100
2	G	69/73 (94%)	68 (99%)	1 (1%)	59	70
2	M	69/73 (94%)	65 (94%)	4 (6%)	18	45
2	S	69/73 (94%)	69 (100%)	0	100	100
2	Y	69/73 (94%)	66 (96%)	3 (4%)	26	50
2	k	69/73 (94%)	66 (96%)	3 (4%)	26	50
3	B	1107/1158 (96%)	1084 (98%)	23 (2%)	47	64
3	C	1106/1158 (96%)	1090 (99%)	16 (1%)	59	70
3	H	1106/1158 (96%)	1079 (98%)	27 (2%)	43	61
3	I	1106/1158 (96%)	1080 (98%)	26 (2%)	43	61
3	J	1107/1158 (96%)	1087 (98%)	20 (2%)	51	67
3	K	1106/1158 (96%)	1083 (98%)	23 (2%)	47	64
4	L	188/218 (86%)	183 (97%)	5 (3%)	39	59
4	R	188/218 (86%)	181 (96%)	7 (4%)	30	54
5	O	214/224 (96%)	210 (98%)	4 (2%)	50	65
5	V	214/224 (96%)	207 (97%)	7 (3%)	33	55
All	All	8446/8888 (95%)	8270 (98%)	176 (2%)	46	64

All (176) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Z	43	TYR
1	Z	81	VAL
1	Z	246	VAL
1	Z	274	ILE
1	Z	288	ASP
1	E	41	MET
1	E	438	THR
3	B	154	LEU
3	B	201	LEU
3	B	258	TYR
3	B	276	THR

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Mol	Chain	Res	Type
3	B	292	THR
3	B	380	VAL
3	B	383	ASP
3	B	405	THR
3	B	545	LEU
3	B	548	ILE
3	B	735	THR
3	B	797	ARG
3	B	855	LEU
3	B	917	MET
3	B	977	VAL
3	B	979	VAL
3	B	1070	THR
3	B	1103	ASP
3	B	1182	LEU
3	B	1260	THR
3	B	1318	VAL
3	B	1356	SER
3	B	1375	VAL
3	C	36	LEU
3	C	56	SER
3	C	258	TYR
3	C	276	THR
3	C	389	ASP
3	C	529	ASP
3	C	548	ILE
3	C	573	ASP
3	C	779	ASN
3	C	1155	VAL
3	C	1166	LEU
3	C	1253	VAL
3	C	1256	THR
3	C	1260	THR
3	C	1270	SER
3	C	1340	THR
2	G	46	ILE
3	H	30	ILE
3	H	36	LEU
3	H	72	THR
3	H	83	LEU
3	H	238	VAL
3	H	241	ASP

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Mol	Chain	Res	Type
3	H	258	TYR
3	H	276	THR
3	H	306	ILE
3	H	414	ASN
3	H	431	MET
3	H	531	MET
3	H	548	ILE
3	H	732	ASN
3	H	742	ILE
3	H	787	VAL
3	H	807	VAL
3	H	863	ILE
3	H	916	LEU
3	H	929	VAL
3	H	1070	THR
3	H	1099	VAL
3	H	1100	HIS
3	H	1176	LEU
3	H	1253	VAL
3	H	1260	THR
3	H	1377	LEU
3	I	36	LEU
3	I	67	ASP
3	I	72	THR
3	I	238	VAL
3	I	258	TYR
3	I	276	THR
3	I	414	ASN
3	I	431	MET
3	I	531	MET
3	I	548	ILE
3	I	732	ASN
3	I	742	ILE
3	I	807	VAL
3	I	863	ILE
3	I	916	LEU
3	I	929	VAL
3	I	1029	VAL
3	I	1070	THR
3	I	1083	LEU
3	I	1099	VAL
3	I	1100	HIS

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Mol	Chain	Res	Type
3	I	1176	LEU
3	I	1253	VAL
3	I	1256	THR
3	I	1260	THR
3	I	1377	LEU
3	J	166	ASP
3	J	258	TYR
3	J	276	THR
3	J	292	THR
3	J	380	VAL
3	J	383	ASP
3	J	405	THR
3	J	427	GLN
3	J	538	VAL
3	J	545	LEU
3	J	548	ILE
3	J	735	THR
3	J	848	MET
3	J	979	VAL
3	J	1070	THR
3	J	1182	LEU
3	J	1256	THR
3	J	1313	MET
3	J	1318	VAL
3	J	1356	SER
3	K	36	LEU
3	K	56	SER
3	K	70	LEU
3	K	258	TYR
3	K	276	THR
3	K	288	VAL
3	K	305	GLN
3	K	389	ASP
3	K	470	THR
3	K	529	ASP
3	K	548	ILE
3	K	779	ASN
3	K	908	ASP
3	K	917	MET
3	K	929	VAL
3	K	958	MET
3	K	1070	THR

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Mol	Chain	Res	Type
3	K	1166	LEU
3	K	1182	LEU
3	K	1256	THR
3	K	1260	THR
3	K	1270	SER
3	K	1346	LEU
2	M	17	VAL
2	M	44	VAL
2	M	48	ASP
2	M	102	ILE
2	Y	15	PHE
2	Y	46	ILE
2	Y	52	ILE
2	k	17	VAL
2	k	48	ASP
2	k	102	ILE
4	L	20	GLU
4	L	64	LEU
4	L	69	MET
4	L	124	ASP
4	L	226	LEU
4	R	11	LEU
4	R	20	GLU
4	R	64	LEU
4	R	124	ASP
4	R	269	ILE
4	R	277	ILE
4	R	295	VAL
5	O	90	VAL
5	O	131	VAL
5	O	176	VAL
5	O	188	THR
5	V	10	VAL
5	V	100	GLN
5	V	188	THR
5	V	212	ASN
5	V	292	ILE
5	V	310	THR
5	V	312	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (88) such sidechains are listed below:

Mol	Chain	Res	Type
1	Z	24	ASN
1	Z	123	GLN
1	Z	137	HIS
1	Z	247	GLN
1	Z	298	ASN
1	E	24	ASN
1	E	80	GLN
1	E	249	HIS
1	E	348	GLN
1	E	472	ASN
3	B	157	ASN
3	B	546	GLN
3	B	595	ASN
3	B	674	GLN
3	B	712	GLN
3	B	782	GLN
3	B	899	HIS
3	B	1016	ASN
3	B	1037	ASN
3	B	1161	ASN
3	B	1329	GLN
3	B	1348	GLN
3	B	1376	HIS
3	C	157	ASN
3	C	175	GLN
3	C	541	HIS
3	C	595	ASN
3	C	666	GLN
3	C	674	GLN
3	C	696	ASN
3	C	713	HIS
3	C	860	GLN
3	C	1250	GLN
3	C	1329	GLN
3	C	1348	GLN
2	G	11	ASN
3	H	267	GLN
3	H	501	GLN
3	H	519	GLN
3	H	712	GLN
3	H	820	HIS
3	H	892	ASN
3	H	1037	ASN

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Mol	Chain	Res	Type
3	H	1329	GLN
3	H	1376	HIS
3	I	248	HIS
3	I	519	GLN
3	I	674	GLN
3	I	696	ASN
3	I	712	GLN
3	I	821	HIS
3	I	1329	GLN
3	I	1376	HIS
3	J	157	ASN
3	J	546	GLN
3	J	595	ASN
3	J	674	GLN
3	J	712	GLN
3	J	782	GLN
3	J	892	ASN
3	J	899	HIS
3	J	1016	ASN
3	J	1037	ASN
3	J	1161	ASN
3	J	1329	GLN
3	J	1348	GLN
3	J	1376	HIS
3	K	108	GLN
3	K	157	ASN
3	K	305	GLN
3	K	541	HIS
3	K	595	ASN
3	K	666	GLN
3	K	674	GLN
3	K	696	ASN
3	K	813	GLN
3	K	980	ASN
3	K	1250	GLN
3	K	1329	GLN
2	M	68	HIS
2	M	69	ASN
2	M	99	ASN
2	S	11	ASN
2	Y	11	ASN
4	L	314	GLN

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Mol	Chain	Res	Type
5	O	191	GLN
5	O	192	HIS
5	O	206	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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
4	L	3
4	R	3
1	E	3
1	Z	3
5	V	2
5	O	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	V	226:LEU	C	266:ARG	N	28.68
1	O	226:LEU	C	266:ARG	N	28.52
1	L	236:LEU	C	244:VAL	N	20.76
1	R	236:LEU	C	244:VAL	N	20.24
1	L	260:MET	C	267:LEU	N	18.68
1	R	260:MET	C	267:LEU	N	18.27
1	O	163:ALA	C	175:ASP	N	17.74
1	V	163:ALA	C	175:ASP	N	16.28
1	E	179:SER	C	192:ARG	N	13.77
1	E	362:ILE	C	428:CYS	N	13.56
1	Z	362:ILE	C	428:CYS	N	13.46
1	Z	179:SER	C	192:ARG	N	12.75
1	L	161:LEU	C	206:ASN	N	12.43
1	R	161:LEU	C	206:ASN	N	12.20
1	E	45:ASN	C	46:ALA	N	3.92
1	Z	45:ASN	C	46:ALA	N	3.82

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-38188. 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

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation ⓘ

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

9 Map-model fit

This section was not generated.