



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:30 PM GMT

PDB ID : 3ZKR
Title : X-ray structure of a pentameric ligand gated ion channel from *Erwinia chrysanthemi* (ELIC) in complex with bromoform
Authors : Spurny, R.; Billen, B.; Howard, R.J.; Brams, M.; Debaveye, S.; Price, K.L.; Weston, D.A.; Strelkov, S.V.; Tytgat, J.; Bertrand, S.; Bertrand, D.; Lummis, S.C.R.; Ulens, C.
Deposited on : 2013-01-24
Resolution : 3.65 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

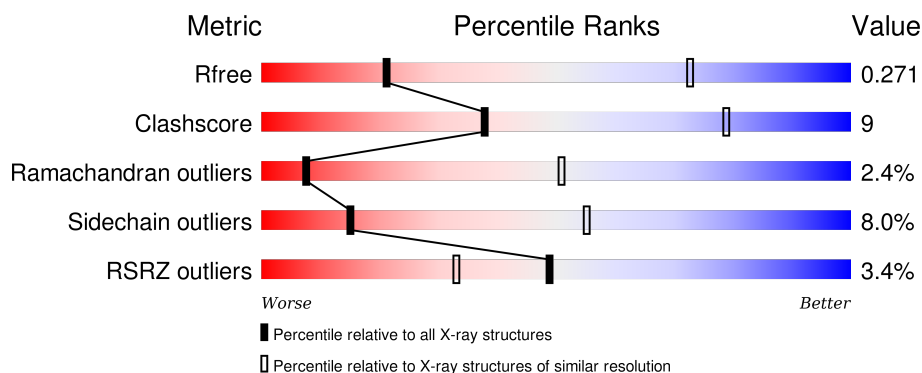
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.65 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1014 (3.80-3.48)
Clashscore	102246	1130 (3.80-3.48)
Ramachandran outliers	100387	1084 (3.80-3.48)
Sidechain outliers	100360	1083 (3.80-3.48)
RSRZ outliers	91569	1021 (3.80-3.48)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	307	<div> <div>4%</div> <div>70%</div> <div>26%</div> <div>.</div> </div>
1	B	307	<div> <div>3%</div> <div>71%</div> <div>27%</div> <div>.</div> </div>
1	C	307	<div> <div>3%</div> <div>73%</div> <div>25%</div> <div>.</div> </div>
1	D	307	<div> <div>2%</div> <div>71%</div> <div>27%</div> <div>.</div> </div>
1	E	307	<div> <div>2%</div> <div>70%</div> <div>26%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	307	
1	G	307	
1	H	307	
1	I	307	
1	J	307	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MBR	A	402	-	-	X	X
2	MBR	B	402	-	-	X	X
2	MBR	C	401	-	-	-	X
2	MBR	C	402	-	-	X	X
2	MBR	D	402	-	-	X	X
2	MBR	E	401	-	-	X	X
2	MBR	E	402	-	-	X	X
2	MBR	F	401	-	-	X	-
2	MBR	F	402	-	-	X	X
2	MBR	G	402	-	-	X	X
2	MBR	H	402	-	-	X	X
2	MBR	I	401	-	-	-	X
2	MBR	I	402	-	-	X	X
2	MBR	J	401	-	-	-	X
2	MBR	J	402	-	-	X	X

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 25042 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 CYS-LOOP LIGAND-GATED ION CHANNEL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	B	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	C	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	D	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	E	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	F	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	G	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	H	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	I	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			
1	J	307	Total	C	N	O	S	0	0	0
			2502	1630	416	450	6			

There are 20 discrepancies between the modelled and reference sequences:

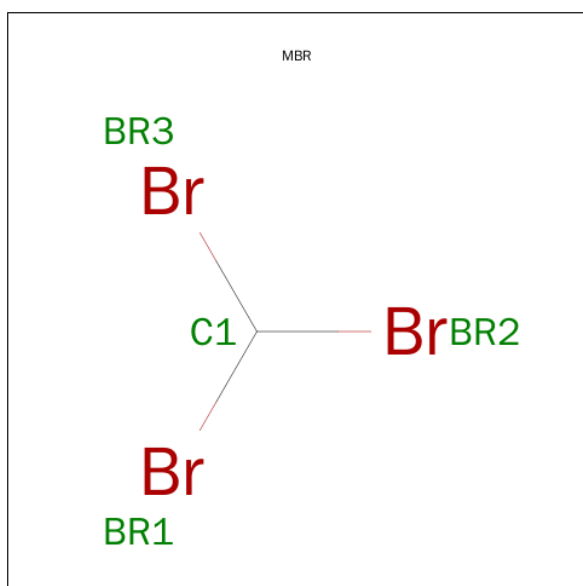
Chain	Residue	Modelled	Actual	Comment	Reference
A	164	GLY	-	INSERTION	UNP P0C7B7
A	289	ASN	MET	CONFLICT	UNP P0C7B7
B	164	GLY	-	INSERTION	UNP P0C7B7
B	289	ASN	MET	CONFLICT	UNP P0C7B7
C	164	GLY	-	INSERTION	UNP P0C7B7
C	289	ASN	MET	CONFLICT	UNP P0C7B7
D	164	GLY	-	INSERTION	UNP P0C7B7
D	289	ASN	MET	CONFLICT	UNP P0C7B7
E	164	GLY	-	INSERTION	UNP P0C7B7

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Chain	Residue	Modelled	Actual	Comment	Reference
E	289	ASN	MET	CONFLICT	UNP P0C7B7
F	164	GLY	-	INSERTION	UNP P0C7B7
F	289	ASN	MET	CONFLICT	UNP P0C7B7
G	164	GLY	-	INSERTION	UNP P0C7B7
G	289	ASN	MET	CONFLICT	UNP P0C7B7
H	164	GLY	-	INSERTION	UNP P0C7B7
H	289	ASN	MET	CONFLICT	UNP P0C7B7
I	164	GLY	-	INSERTION	UNP P0C7B7
I	289	ASN	MET	CONFLICT	UNP P0C7B7
J	164	GLY	-	INSERTION	UNP P0C7B7
J	289	ASN	MET	CONFLICT	UNP P0C7B7

- Molecule 2 is TRIBROMOMETHANE (three-letter code: MBR) (formula: CHBr_3).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Br 1 1	0	0
2	A	1	Total Br 1 1	0	0
2	A	1	Total Br 1 1	0	0
2	B	1	Total Br 1 1	0	0
2	B	1	Total Br 1 1	0	0
2	C	1	Total Br 1 1	0	0

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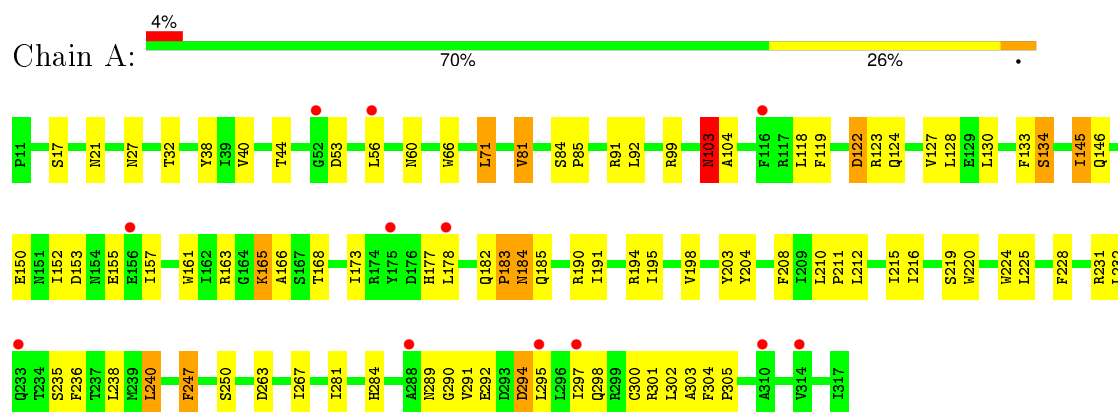
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	1	Total 1	Br 1	0	0
2	D	1	Total 1	Br 1	0	0
2	D	1	Total 1	Br 1	0	0
2	E	1	Total 1	Br 1	0	0
2	E	1	Total 1	Br 1	0	0
2	F	1	Total 1	Br 1	0	0
2	F	1	Total 1	Br 1	0	0
2	F	1	Total 1	Br 1	0	0
2	G	1	Total 1	Br 1	0	0
2	G	1	Total 1	Br 1	0	0
2	H	1	Total 1	Br 1	0	0
2	H	1	Total 1	Br 1	0	0
2	I	1	Total 1	Br 1	0	0
2	I	1	Total 1	Br 1	0	0
2	J	1	Total 1	Br 1	0	0
2	J	1	Total 1	Br 1	0	0

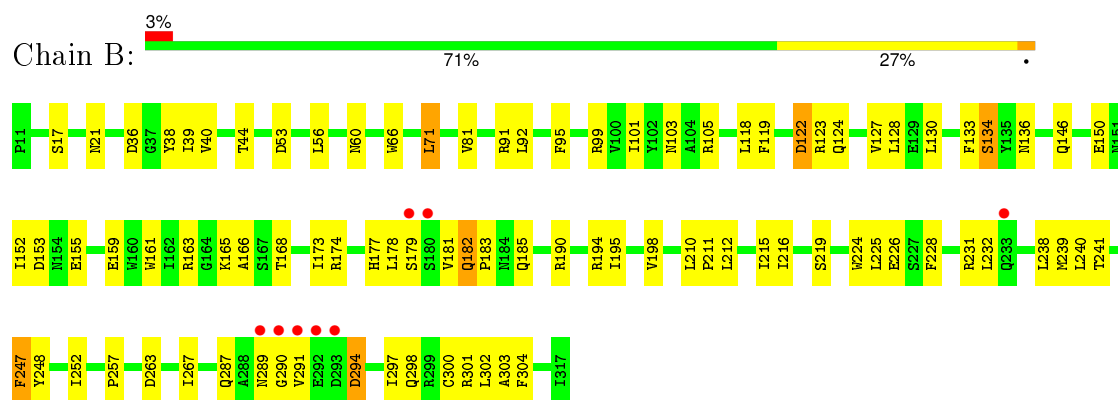
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

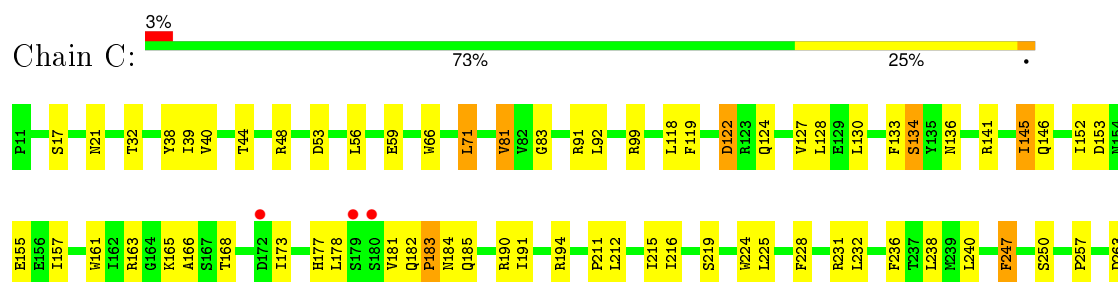
• Molecule 1: CYS-LOOP LIGAND-GATED ION CHANNEL

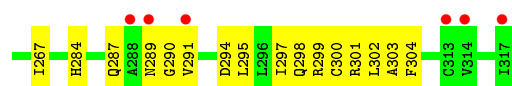


• Molecule 1: CYS-LOOP LIGAND-GATED ION CHANNEL

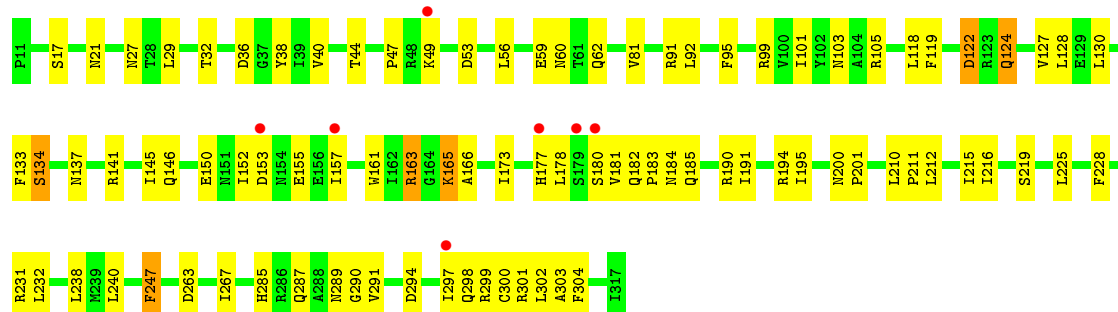


• Molecule 1: CYS-LOOP LIGAND-GATED ION CHANNEL

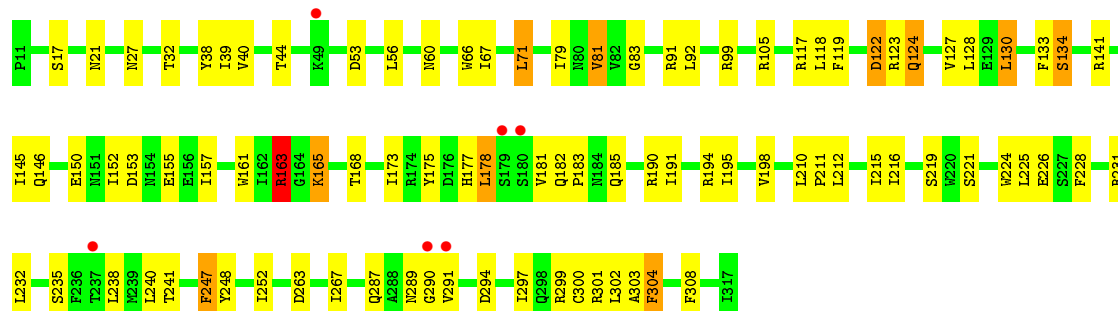




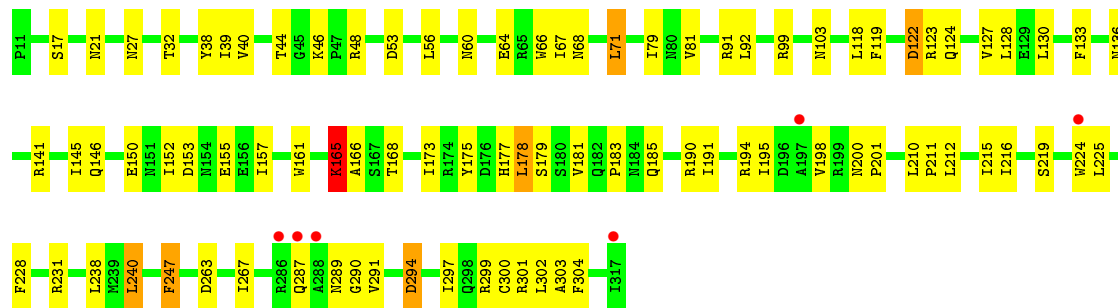
• Molecule 1: CYS-LOOP LIGAND-GATED ION CHANNEL



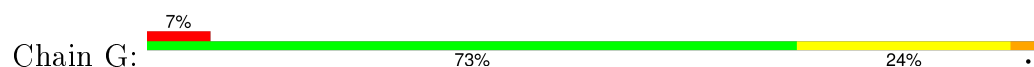
• Molecule 1: CYS-LOOP LIGAND-GATED ION CHANNEL

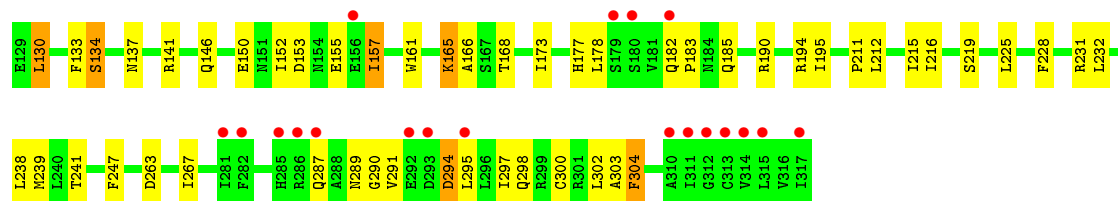


• Molecule 1: CYS-LOOP LIGAND-GATED ION CHANNEL

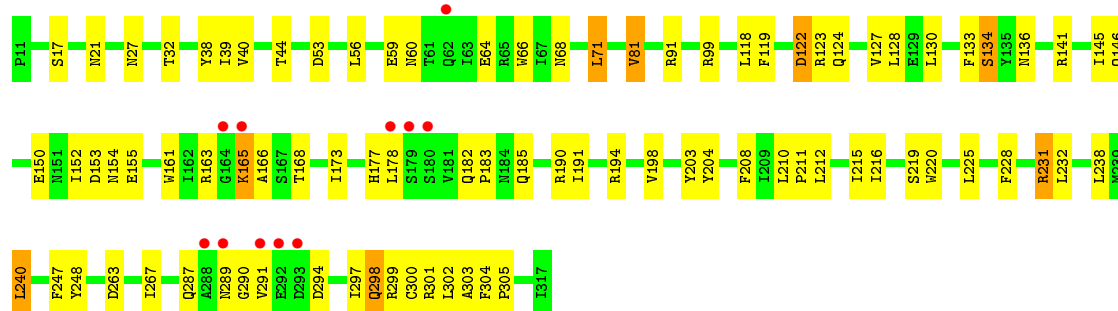


• Molecule 1: CYS-LOOP LIGAND-GATED ION CHANNEL

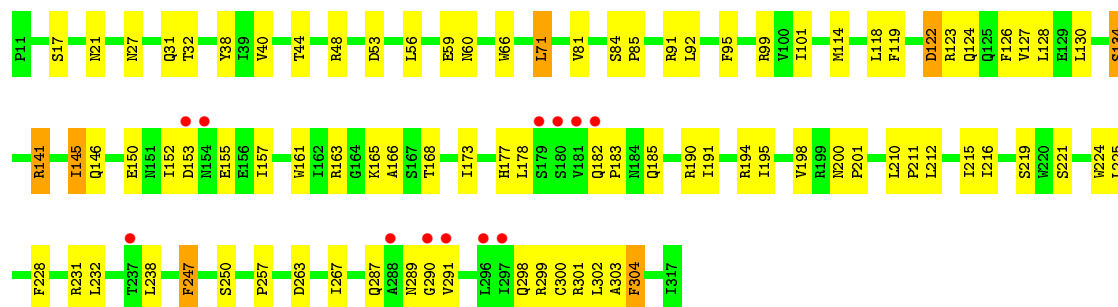




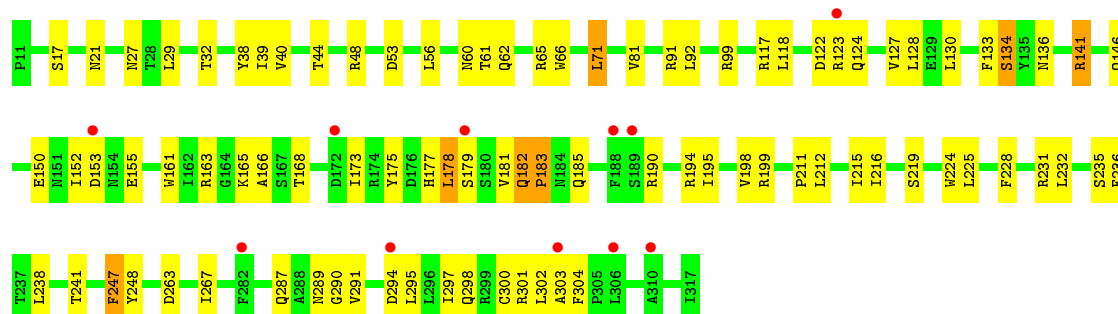
• Molecule 1: CYS-LOOP LIGAND-GATED ION CHANNEL



• Molecule 1: CYS-LOOP LIGAND-GATED ION CHANNEL



• Molecule 1: CYS-LOOP LIGAND-GATED ION CHANNEL



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	105.11Å 266.25Å 110.75Å 90.00° 109.78° 90.00°	Depositor
Resolution (Å)	44.08 – 3.65 44.08 – 3.65	Depositor EDS
% Data completeness (in resolution range)	98.9 (44.08-3.65) 98.8 (44.08-3.65)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 3.66Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.229 , 0.264 0.246 , 0.271	Depositor DCC
R_{free} test set	3189 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	108.2	Xtriage
Anisotropy	0.437	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 52.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	0 of 62752 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	25042	wwPDB-VP
Average B, all atoms (Å ²)	131.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MBR

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	0.41	2/2570 (0.1%)	0.66	0/3503
1	B	0.41	4/2570 (0.2%)	0.65	0/3503
1	C	0.38	0/2570	0.65	0/3503
1	D	0.46	4/2570 (0.2%)	0.75	5/3503 (0.1%)
1	E	0.42	2/2570 (0.1%)	0.80	6/3503 (0.2%)
1	F	0.41	2/2570 (0.1%)	0.93	8/3503 (0.2%)
1	G	0.45	3/2570 (0.1%)	0.68	0/3503
1	H	0.40	2/2570 (0.1%)	0.67	1/3503 (0.0%)
1	I	0.44	2/2570 (0.1%)	0.66	0/3503
1	J	0.37	0/2570	0.65	2/3503 (0.1%)
All	All	0.42	21/25700 (0.1%)	0.72	22/35030 (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	A	0	1
1	D	0	2
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
All	All	0	7

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	103	ASN	CG-ND2	-7.94	1.13	1.32
1	D	124	GLN	CD-NE2	-7.72	1.13	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	103	ASN	CG-OD1	-7.47	1.07	1.24
1	G	124	GLN	CD-NE2	-7.36	1.14	1.32
1	E	124	GLN	CD-NE2	-6.89	1.15	1.32
1	B	298	GLN	CD-NE2	-6.87	1.15	1.32
1	I	298	GLN	CD-NE2	-6.72	1.16	1.32
1	F	103	ASN	CG-ND2	-6.55	1.16	1.32
1	H	298	GLN	CD-NE2	-6.35	1.17	1.32
1	H	298	GLN	CD-OE1	-6.26	1.10	1.24
1	I	298	GLN	CD-OE1	-6.24	1.10	1.24
1	D	124	GLN	CD-OE1	-6.15	1.10	1.24
1	E	124	GLN	CD-OE1	-5.70	1.11	1.24
1	A	103	ASN	CG-ND2	-5.69	1.18	1.32
1	B	298	GLN	CD-OE1	-5.54	1.11	1.24
1	A	103	ASN	CG-OD1	-5.47	1.11	1.24
1	G	103	ASN	CG-ND2	-5.40	1.19	1.32
1	F	103	ASN	CG-OD1	-5.34	1.12	1.24
1	B	103	ASN	CG-ND2	-5.31	1.19	1.32
1	B	103	ASN	CG-OD1	-5.27	1.12	1.24
1	D	298	GLN	CD-NE2	-5.24	1.19	1.32

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	165	LYS	O-C-N	-27.07	79.38	122.70
1	F	165	LYS	CA-C-O	-19.47	79.22	120.10
1	E	163	ARG	NE-CZ-NH1	18.98	129.79	120.30
1	F	165	LYS	CA-C-N	18.34	157.54	117.20
1	E	163	ARG	NE-CZ-NH2	-14.78	112.91	120.30
1	D	163	ARG	NE-CZ-NH1	13.89	127.25	120.30
1	D	163	ARG	NE-CZ-NH2	-9.88	115.36	120.30
1	E	308	PHE	CB-CG-CD2	-8.36	114.95	120.80
1	E	163	ARG	CG-CD-NE	7.95	128.50	111.80
1	F	166	ALA	N-CA-CB	-7.62	99.43	110.10
1	E	163	ARG	CD-NE-CZ	7.12	133.57	123.60
1	D	163	ARG	CB-CG-CD	7.07	129.99	111.60
1	F	165	LYS	C-N-CA	6.44	137.80	121.70
1	E	308	PHE	CB-CG-CD1	6.32	125.22	120.80
1	F	166	ALA	N-CA-C	6.07	127.40	111.00
1	J	141	ARG	NE-CZ-NH2	6.03	123.32	120.30
1	F	141	ARG	NE-CZ-NH1	-5.98	117.31	120.30
1	F	141	ARG	NE-CZ-NH2	5.67	123.14	120.30
1	H	141	ARG	NE-CZ-NH2	-5.54	117.53	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	141	ARG	NE-CZ-NH1	-5.48	117.56	120.30
1	D	163	ARG	CD-NE-CZ	5.29	131.00	123.60
1	D	163	ARG	CG-CD-NE	5.12	122.56	111.80

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	165	LYS	Mainchain
1	D	165	LYS	Mainchain
1	D	47	PRO	Mainchain
1	E	165	LYS	Mainchain
1	F	165	LYS	Mainchain
1	G	165	LYS	Mainchain
1	H	165	LYS	Mainchain

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	A	2502	0	2469	60	1
1	B	2502	0	2469	49	0
1	C	2502	0	2469	53	0
1	D	2502	0	2469	50	1
1	E	2502	0	2469	67	0
1	F	2502	0	2469	53	0
1	G	2502	0	2469	50	0
1	H	2502	0	2469	49	0
1	I	2502	0	2469	54	0
1	J	2502	0	2469	51	0
2	A	3	0	0	4	0
2	B	2	0	0	3	0
2	C	2	0	0	3	0
2	D	2	0	0	3	0
2	E	2	0	0	8	0
2	F	3	0	0	6	0
2	G	2	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	2	0	0	4	0
2	I	2	0	0	5	0
2	J	2	0	0	4	0
All	All	25042	0	24690	456	1

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 9.

All (456) 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:J:195:ILE:HD12	2:J:402:MBR:BR1	1.28	1.84
1:E:221:SER:HB3	2:E:401:MBR:BR1	1.37	1.76
1:I:195:ILE:HD12	2:I:402:MBR:BR1	1.57	1.56
1:C:128:LEU:HD13	2:C:402:MBR:BR1	1.61	1.52
1:J:195:ILE:CD1	2:J:402:MBR:BR1	2.19	1.44
1:E:221:SER:CB	2:E:401:MBR:BR1	2.18	1.43
1:G:128:LEU:CD1	2:G:402:MBR:BR1	2.24	1.40
1:H:128:LEU:HD13	2:H:402:MBR:BR1	1.77	1.39
1:H:128:LEU:CD1	2:H:402:MBR:BR1	2.29	1.36
1:D:128:LEU:HD13	2:D:402:MBR:BR1	1.82	1.33
1:A:128:LEU:HD13	2:A:402:MBR:BR1	1.86	1.31
1:G:128:LEU:HD13	2:G:402:MBR:BR1	1.84	1.28
1:C:128:LEU:CD1	2:C:402:MBR:BR1	2.35	1.27
1:F:195:ILE:HD12	2:F:402:MBR:BR1	1.90	1.27
1:B:195:ILE:HD12	2:B:402:MBR:BR1	1.96	1.21
1:F:128:LEU:HD13	2:F:402:MBR:BR1	1.96	1.19
1:E:128:LEU:HD13	2:E:402:MBR:BR1	2.02	1.14
1:I:195:ILE:CD1	2:I:402:MBR:BR1	2.53	1.10
1:A:128:LEU:CD1	2:A:402:MBR:BR1	2.56	1.08
1:D:128:LEU:CD1	2:D:402:MBR:BR1	2.59	1.04
1:G:128:LEU:HD12	2:G:402:MBR:BR1	2.14	1.00
1:D:195:ILE:HD12	2:D:402:MBR:BR1	2.18	0.99
1:E:128:LEU:CD1	2:E:402:MBR:BR1	2.65	0.99
1:A:195:ILE:HD12	2:A:402:MBR:BR1	2.17	0.98
1:F:128:LEU:CD1	2:F:402:MBR:BR1	2.72	0.92
1:H:128:LEU:HD11	2:H:402:MBR:BR1	2.27	0.87
1:F:195:ILE:CD1	2:F:402:MBR:BR1	2.78	0.86
1:C:91:ARG:HD2	1:D:134:SER:HB3	1.59	0.84
1:B:128:LEU:HD13	2:B:402:MBR:BR1	2.35	0.81
1:H:91:ARG:HD2	1:I:134:SER:HB3	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:195:ILE:HD12	2:E:402:MBR:BR1	2.36	0.81
1:C:128:LEU:HD12	2:C:402:MBR:BR1	2.34	0.81
1:D:181:VAL:HG21	1:D:185:GLN:HB2	1.63	0.80
1:G:91:ARG:HD2	1:H:134:SER:HB3	1.62	0.78
1:B:91:ARG:HD2	1:C:134:SER:HB3	1.65	0.77
1:A:91:ARG:HD2	1:B:134:SER:HB3	1.66	0.76
1:E:221:SER:HB2	2:E:401:MBR:BR1	2.37	0.74
1:I:91:ARG:HD2	1:J:134:SER:HB3	1.68	0.74
1:E:221:SER:CA	2:E:401:MBR:BR1	2.90	0.73
1:F:91:ARG:HD2	1:G:134:SER:HB3	1.69	0.73
1:D:91:ARG:HB2	1:E:133:PHE:HE2	1.54	0.71
1:E:155:GLU:OE2	1:E:163:ARG:NH2	2.24	0.71
1:A:219:SER:HA	1:A:238:LEU:HD21	1.73	0.70
1:G:128:LEU:HD11	2:G:402:MBR:BR1	2.41	0.70
1:J:128:LEU:HD13	2:J:402:MBR:BR1	2.46	0.69
1:A:103:ASN:HD22	1:A:104:ALA:N	1.90	0.69
1:B:128:LEU:CD1	2:B:402:MBR:BR1	2.96	0.69
1:C:219:SER:HA	1:C:238:LEU:HD21	1.74	0.69
1:A:133:PHE:HE2	1:E:91:ARG:HB2	1.57	0.69
1:D:155:GLU:OE2	1:D:163:ARG:NH2	2.26	0.68
1:B:219:SER:HA	1:B:238:LEU:HD21	1.75	0.68
1:I:225:LEU:HD21	1:J:232:LEU:HD22	1.74	0.68
1:E:219:SER:HA	1:E:238:LEU:HD21	1.76	0.68
1:J:219:SER:HA	1:J:238:LEU:HD21	1.75	0.67
1:H:219:SER:HA	1:H:238:LEU:HD21	1.74	0.67
1:G:219:SER:HA	1:G:238:LEU:HD21	1.77	0.67
1:I:219:SER:HA	1:I:238:LEU:HD21	1.76	0.67
1:F:219:SER:HA	1:F:238:LEU:HD21	1.77	0.67
1:D:219:SER:HA	1:D:238:LEU:HD21	1.76	0.67
1:D:91:ARG:HD2	1:E:134:SER:HB3	1.76	0.66
1:D:127:VAL:HG22	1:D:194:ARG:HG2	1.77	0.66
1:C:225:LEU:HD21	1:D:232:LEU:HD22	1.79	0.64
1:F:224:TRP:CZ3	2:F:401:MBR:BR1	3.05	0.64
1:F:91:ARG:HB2	1:G:133:PHE:HE2	1.61	0.64
1:A:225:LEU:HD21	1:B:232:LEU:HD22	1.78	0.64
1:A:240:LEU:HD23	1:E:241:THR:HA	1.80	0.63
1:G:294:ASP:HB2	1:G:297:ILE:HG22	1.81	0.62
1:F:44:THR:HA	1:F:99:ARG:HA	1.80	0.62
1:G:289:ASN:OD1	1:G:290:GLY:N	2.34	0.61
1:A:119:PHE:HA	1:A:122:ASP:OD1	2.00	0.61
1:H:128:LEU:HD12	2:H:402:MBR:BR1	2.49	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:91:ARG:HB2	1:H:133:PHE:HE2	1.66	0.61
1:A:134:SER:HB3	1:E:91:ARG:HD2	1.82	0.60
1:A:44:THR:HA	1:A:99:ARG:HA	1.83	0.60
1:A:289:ASN:OD1	1:A:290:GLY:N	2.32	0.60
1:C:212:LEU:O	1:C:216:ILE:HG12	2.02	0.60
1:A:127:VAL:HG22	1:A:194:ARG:HG2	1.84	0.59
1:G:195:ILE:HD12	2:G:402:MBR:BR1	2.58	0.59
1:H:127:VAL:HG22	1:H:194:ARG:HG2	1.84	0.59
1:D:91:ARG:HB2	1:E:133:PHE:CE2	2.37	0.59
1:D:59:GLU:OE2	1:E:134:SER:OG	2.21	0.59
1:H:173:ILE:HD13	1:H:190:ARG:HB3	1.84	0.59
1:E:212:LEU:O	1:E:216:ILE:HG12	2.03	0.59
1:A:263:ASP:O	1:A:267:ILE:HG12	2.03	0.58
1:A:294:ASP:HB2	1:A:297:ILE:HG22	1.84	0.58
1:F:133:PHE:HE2	1:J:91:ARG:HB2	1.67	0.58
1:I:44:THR:HA	1:I:99:ARG:HA	1.85	0.58
1:D:44:THR:HA	1:D:99:ARG:HA	1.85	0.58
1:F:212:LEU:O	1:F:216:ILE:HG12	2.04	0.58
1:D:212:LEU:O	1:D:216:ILE:HG12	2.03	0.58
1:D:263:ASP:O	1:D:267:ILE:HG12	2.04	0.58
1:F:175:TYR:HB2	1:F:178:LEU:HD21	1.86	0.57
1:A:173:ILE:HD13	1:A:190:ARG:HB3	1.86	0.57
1:J:212:LEU:O	1:J:216:ILE:HG12	2.05	0.57
1:C:173:ILE:HD13	1:C:190:ARG:HB3	1.86	0.57
1:E:127:VAL:HG22	1:E:194:ARG:HG2	1.87	0.57
1:F:179:SER:HB2	1:F:181:VAL:HG12	1.87	0.57
1:I:212:LEU:O	1:I:216:ILE:HG12	2.05	0.57
1:H:294:ASP:HB2	1:H:297:ILE:HG22	1.87	0.57
1:A:185:GLN:N	1:A:185:GLN:OE1	2.38	0.56
1:E:263:ASP:O	1:E:267:ILE:HG12	2.04	0.56
1:J:127:VAL:HG22	1:J:194:ARG:HG2	1.87	0.56
1:F:127:VAL:HG22	1:F:194:ARG:HG2	1.87	0.56
1:B:173:ILE:HD13	1:B:190:ARG:HB3	1.87	0.56
1:J:294:ASP:HB2	1:J:297:ILE:HG22	1.87	0.56
1:J:173:ILE:HD13	1:J:190:ARG:HB3	1.86	0.56
1:A:212:LEU:O	1:A:216:ILE:HG12	2.05	0.56
1:B:212:LEU:O	1:B:216:ILE:HG12	2.05	0.56
1:B:241:THR:HA	1:C:240:LEU:HD23	1.88	0.56
1:C:263:ASP:O	1:C:267:ILE:HG12	2.05	0.56
1:E:44:THR:HA	1:E:99:ARG:HA	1.88	0.56
1:E:289:ASN:OD1	1:E:290:GLY:N	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:127:VAL:HG22	1:I:194:ARG:HG2	1.86	0.56
1:H:225:LEU:HD21	1:I:232:LEU:HD22	1.87	0.56
1:I:221:SER:HB3	2:I:401:MBR:BR1	2.62	0.56
1:H:212:LEU:O	1:H:216:ILE:HG12	2.05	0.55
1:B:44:THR:HA	1:B:99:ARG:HA	1.87	0.55
1:F:119:PHE:HA	1:F:122:ASP:OD1	2.06	0.55
1:G:173:ILE:HD13	1:G:190:ARG:HB3	1.88	0.55
1:G:44:THR:HA	1:G:99:ARG:HA	1.88	0.54
1:F:175:TYR:O	1:F:178:LEU:HD11	2.08	0.54
1:I:173:ILE:HD13	1:I:190:ARG:HB3	1.90	0.54
1:B:263:ASP:O	1:B:267:ILE:HG12	2.08	0.54
1:F:173:ILE:HD13	1:F:190:ARG:HB3	1.89	0.54
1:C:181:VAL:HG21	1:C:185:GLN:HB2	1.90	0.54
1:G:212:LEU:O	1:G:216:ILE:HG12	2.08	0.53
1:C:289:ASN:OD1	1:C:290:GLY:N	2.40	0.53
1:J:155:GLU:O	1:J:161:TRP:NE1	2.41	0.53
1:F:240:LEU:HD23	1:J:241:THR:HA	1.90	0.53
1:D:119:PHE:HA	1:D:122:ASP:OD1	2.09	0.53
1:J:44:THR:HA	1:J:99:ARG:HA	1.88	0.53
1:C:44:THR:HA	1:C:99:ARG:HA	1.90	0.53
1:C:294:ASP:HB2	1:C:297:ILE:HG22	1.90	0.53
1:J:263:ASP:O	1:J:267:ILE:HG12	2.09	0.53
1:D:155:GLU:O	1:D:161:TRP:NE1	2.41	0.53
1:C:183:PRO:HB2	1:C:185:GLN:OE1	2.09	0.53
1:B:179:SER:HB2	1:B:181:VAL:HG12	1.90	0.53
1:I:91:ARG:HB2	1:J:133:PHE:HE2	1.72	0.53
1:H:59:GLU:OE2	1:I:134:SER:OG	2.27	0.53
1:F:123:ARG:HD2	1:F:198:VAL:HG22	1.91	0.53
1:H:263:ASP:O	1:H:267:ILE:HG12	2.09	0.53
1:H:228:PHE:HA	1:H:231:ARG:NH1	2.23	0.52
1:C:17:SER:HB2	1:C:40:VAL:HB	1.90	0.52
1:G:263:ASP:O	1:G:267:ILE:HG12	2.09	0.52
1:A:295:LEU:HD12	1:A:298:GLN:OE1	2.09	0.52
1:D:173:ILE:HD13	1:D:190:ARG:HB3	1.91	0.52
1:A:66:TRP:HB3	1:A:71:LEU:HD12	1.92	0.52
1:C:127:VAL:HG22	1:C:194:ARG:HG2	1.91	0.52
1:E:173:ILE:HD13	1:E:190:ARG:HB3	1.91	0.52
1:D:21:ASN:HD21	1:D:38:TYR:HE1	1.58	0.52
1:B:225:LEU:HB2	1:B:231:ARG:HG3	1.92	0.52
1:H:44:THR:HA	1:H:99:ARG:HA	1.90	0.52
1:E:123:ARG:HD2	1:E:198:VAL:HG22	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:GLU:O	1:A:161:TRP:NE1	2.40	0.51
1:G:127:VAL:HG22	1:G:194:ARG:HG2	1.92	0.51
1:I:157:ILE:HD11	1:J:117:ARG:HE	1.75	0.51
1:B:248:TYR:HD1	1:C:247:PHE:HA	1.74	0.51
1:A:247:PHE:HE2	1:E:247:PHE:CD2	2.28	0.51
1:E:66:TRP:HB3	1:E:71:LEU:HD12	1.92	0.51
1:B:294:ASP:HB2	1:B:297:ILE:HG22	1.92	0.51
1:F:289:ASN:OD1	1:F:290:GLY:N	2.40	0.51
1:H:119:PHE:HA	1:H:122:ASP:OD1	2.10	0.51
1:A:225:LEU:HB2	1:A:231:ARG:HG3	1.91	0.50
1:G:225:LEU:HB2	1:G:231:ARG:HG3	1.92	0.50
1:G:36:ASP:OD2	1:G:105:ARG:NH2	2.40	0.50
1:F:225:LEU:HB2	1:F:231:ARG:HG3	1.93	0.50
1:E:228:PHE:HA	1:E:231:ARG:NH1	2.26	0.50
1:A:133:PHE:CE2	1:E:91:ARG:HB2	2.43	0.50
1:G:225:LEU:HD21	1:H:232:LEU:HD22	1.92	0.50
1:I:263:ASP:O	1:I:267:ILE:HG12	2.11	0.50
1:F:263:ASP:O	1:F:267:ILE:HG12	2.12	0.50
1:A:128:LEU:HD12	2:A:402:MBR:BR1	2.60	0.50
1:B:123:ARG:HD2	1:B:198:VAL:HG22	1.93	0.50
1:I:119:PHE:HA	1:I:122:ASP:OD1	2.11	0.50
1:D:105:ARG:NH1	1:E:79:ILE:O	2.35	0.49
1:F:66:TRP:HB3	1:F:71:LEU:HD12	1.94	0.49
1:B:66:TRP:HB3	1:B:71:LEU:HD12	1.94	0.49
1:I:59:GLU:OE2	1:J:134:SER:OG	2.28	0.49
1:G:61:THR:HG21	1:H:64:GLU:CG	2.43	0.49
1:D:17:SER:HB2	1:D:40:VAL:HB	1.94	0.49
1:A:103:ASN:C	1:A:103:ASN:HD22	2.13	0.49
1:G:65:ARG:HD2	1:H:68:ASN:ND2	2.28	0.49
1:C:119:PHE:HA	1:C:122:ASP:OD1	2.11	0.49
1:H:155:GLU:O	1:H:161:TRP:NE1	2.46	0.49
1:C:48:ARG:NH1	1:C:48:ARG:HB2	2.28	0.49
1:C:228:PHE:HA	1:C:231:ARG:NH1	2.28	0.49
1:G:66:TRP:HB3	1:G:71:LEU:HD12	1.93	0.49
1:A:236:PHE:CD1	1:E:238:LEU:HD13	2.48	0.49
1:F:64:GLU:CG	1:J:61:THR:HG21	2.42	0.49
1:F:145:ILE:HD12	1:F:191:ILE:HG21	1.95	0.48
1:J:228:PHE:HA	1:J:231:ARG:NH1	2.28	0.48
1:G:228:PHE:HA	1:G:231:ARG:NH1	2.28	0.48
1:G:300:CYS:HB2	1:G:303:ALA:HB3	1.95	0.48
1:E:21:ASN:HD21	1:E:38:TYR:HE1	1.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:133:PHE:CE2	1:J:91:ARG:HB2	2.48	0.48
1:C:185:GLN:N	1:C:185:GLN:OE1	2.47	0.48
1:E:225:LEU:HB2	1:E:231:ARG:HG3	1.95	0.48
1:J:225:LEU:HB2	1:J:231:ARG:HG3	1.96	0.48
1:I:21:ASN:HD21	1:I:38:TYR:HE1	1.61	0.48
1:B:300:CYS:HB2	1:B:303:ALA:HB3	1.95	0.48
1:B:248:TYR:HE1	1:C:250:SER:OG	1.96	0.48
1:E:119:PHE:HA	1:E:122:ASP:OD1	2.14	0.48
1:F:48:ARG:NH1	1:F:48:ARG:HB2	2.28	0.48
1:D:185:GLN:N	1:D:185:GLN:OE1	2.47	0.48
1:F:91:ARG:HB2	1:G:133:PHE:CE2	2.44	0.48
1:D:211:PRO:O	1:D:215:ILE:HG12	2.14	0.48
1:J:216:ILE:O	1:J:219:SER:HB3	2.14	0.48
1:D:145:ILE:HD12	1:D:191:ILE:HG21	1.96	0.48
1:J:181:VAL:HG21	1:J:185:GLN:HB2	1.96	0.48
1:J:21:ASN:HD21	1:J:38:TYR:HE1	1.60	0.48
1:J:123:ARG:HD2	1:J:198:VAL:HG22	1.95	0.47
1:C:66:TRP:HB3	1:C:71:LEU:HD12	1.96	0.47
1:C:225:LEU:HB2	1:C:231:ARG:HG3	1.95	0.47
1:J:300:CYS:HB2	1:J:303:ALA:HB3	1.96	0.47
1:G:304:PHE:CD1	1:G:304:PHE:C	2.88	0.47
1:E:181:VAL:HG21	1:E:185:GLN:HB2	1.95	0.47
1:D:36:ASP:OD2	1:D:105:ARG:NH2	2.42	0.47
1:E:300:CYS:HB2	1:E:303:ALA:HB3	1.95	0.47
1:D:228:PHE:HA	1:D:231:ARG:NH1	2.30	0.47
1:H:21:ASN:HD21	1:H:38:TYR:HE1	1.62	0.47
1:F:247:PHE:HE2	1:J:247:PHE:CD2	2.31	0.47
1:F:300:CYS:HB2	1:F:303:ALA:HB3	1.97	0.47
1:B:127:VAL:HG22	1:B:194:ARG:HG2	1.96	0.47
1:H:66:TRP:HB3	1:H:71:LEU:HD12	1.96	0.47
1:G:155:GLU:O	1:G:161:TRP:NE1	2.46	0.47
1:C:155:GLU:O	1:C:161:TRP:NE1	2.44	0.47
1:J:66:TRP:HB3	1:J:71:LEU:HD12	1.95	0.47
1:C:92:LEU:HD23	1:C:92:LEU:HA	1.81	0.47
1:H:211:PRO:O	1:H:215:ILE:HG12	2.15	0.47
1:F:155:GLU:O	1:F:161:TRP:NE1	2.44	0.47
1:H:123:ARG:HD2	1:H:198:VAL:HG22	1.97	0.47
1:E:232:LEU:O	1:E:235:SER:OG	2.30	0.47
1:B:119:PHE:HA	1:B:122:ASP:OD1	2.15	0.47
1:A:216:ILE:O	1:A:219:SER:HB3	2.15	0.47
1:I:247:PHE:CD2	1:J:247:PHE:HE2	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:81:VAL:HG13	1:C:83:GLY:O	2.15	0.47
1:D:289:ASN:OD1	1:D:290:GLY:N	2.40	0.47
1:C:91:ARG:CD	1:D:134:SER:HB3	2.40	0.46
1:B:238:LEU:HD13	1:C:236:PHE:HD2	1.80	0.46
1:A:211:PRO:O	1:A:215:ILE:HG12	2.15	0.46
1:J:155:GLU:OE2	1:J:163:ARG:NH1	2.47	0.46
1:A:294:ASP:HB2	1:A:297:ILE:CG2	2.46	0.46
1:F:228:PHE:HA	1:F:231:ARG:NH1	2.29	0.46
1:J:289:ASN:OD1	1:J:290:GLY:N	2.42	0.46
1:H:91:ARG:CD	1:I:134:SER:HB3	2.38	0.46
1:I:145:ILE:HD12	1:I:191:ILE:HG21	1.96	0.46
1:E:27:ASN:HB3	1:E:32:THR:HB	1.97	0.46
1:F:247:PHE:HA	1:J:248:TYR:HD1	1.80	0.46
1:A:204:TYR:O	1:A:208:PHE:HB2	2.15	0.46
1:I:211:PRO:O	1:I:215:ILE:HG12	2.15	0.46
1:I:228:PHE:HA	1:I:231:ARG:NH1	2.31	0.46
1:H:300:CYS:HB2	1:H:303:ALA:HB3	1.98	0.46
1:I:225:LEU:HB2	1:I:231:ARG:HG3	1.97	0.46
1:B:225:LEU:HD21	1:C:232:LEU:HD22	1.97	0.46
1:G:304:PHE:C	1:G:304:PHE:HD1	2.18	0.46
1:B:36:ASP:OD2	1:B:105:ARG:NH2	2.47	0.46
1:F:46:LYS:H	1:F:46:LYS:HG2	1.53	0.46
1:B:252:ILE:HG13	1:C:250:SER:HB3	1.97	0.46
1:D:225:LEU:HB2	1:D:231:ARG:HG3	1.98	0.46
1:G:295:LEU:HA	1:G:298:GLN:OE1	2.15	0.46
1:A:247:PHE:CD2	1:B:247:PHE:HE2	2.34	0.46
1:I:155:GLU:O	1:I:161:TRP:NE1	2.46	0.46
1:F:67:ILE:HG22	1:J:62:GLN:NE2	2.31	0.46
1:C:211:PRO:O	1:C:215:ILE:HG12	2.16	0.46
1:J:48:ARG:NH1	1:J:48:ARG:HB2	2.31	0.46
1:F:216:ILE:O	1:F:219:SER:HB3	2.16	0.45
1:G:294:ASP:HB2	1:G:297:ILE:CG2	2.46	0.45
1:D:247:PHE:CD2	1:E:247:PHE:HE2	2.34	0.45
1:B:21:ASN:HD21	1:B:38:TYR:HE1	1.62	0.45
1:D:157:ILE:HD11	1:E:117:ARG:HE	1.81	0.45
1:F:68:ASN:ND2	1:J:65:ARG:HD2	2.31	0.45
1:E:175:TYR:HB2	1:E:178:LEU:HD21	1.97	0.45
1:I:66:TRP:HB3	1:I:71:LEU:HD12	1.98	0.45
1:C:300:CYS:HB2	1:C:303:ALA:HB3	1.97	0.45
1:D:216:ILE:O	1:D:219:SER:HB3	2.16	0.45
1:I:163:ARG:HD3	1:I:163:ARG:HA	1.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:216:ILE:O	1:G:219:SER:HB3	2.16	0.45
1:A:295:LEU:HA	1:A:298:GLN:OE1	2.17	0.45
1:E:211:PRO:O	1:E:215:ILE:HG12	2.16	0.45
1:E:17:SER:HB2	1:E:40:VAL:HB	1.99	0.45
1:J:295:LEU:HA	1:J:298:GLN:OE1	2.17	0.45
1:A:228:PHE:HA	1:A:231:ARG:NH1	2.32	0.45
1:G:105:ARG:NH2	1:H:81:VAL:O	2.50	0.45
1:H:27:ASN:HB3	1:H:32:THR:HB	1.98	0.45
1:G:119:PHE:HA	1:G:122:ASP:OD1	2.15	0.45
1:D:294:ASP:HB2	1:D:297:ILE:HG22	1.97	0.45
1:J:195:ILE:HD11	2:J:402:MBR:BR1	2.51	0.45
1:G:17:SER:HB2	1:G:40:VAL:HB	1.99	0.45
1:C:163:ARG:HD3	1:C:163:ARG:HA	1.65	0.45
1:C:216:ILE:O	1:C:219:SER:HB3	2.16	0.45
1:D:62:GLN:NE2	1:E:67:ILE:HG22	2.32	0.45
1:G:103:ASN:HD22	1:G:104:ALA:N	2.15	0.45
1:F:157:ILE:HA	1:F:157:ILE:HD13	1.80	0.45
1:I:126:PHE:O	2:I:402:MBR:BR1	2.89	0.45
1:I:289:ASN:OD1	1:I:290:GLY:N	2.41	0.45
1:E:155:GLU:O	1:E:161:TRP:NE1	2.46	0.45
1:A:300:CYS:HB2	1:A:303:ALA:HB3	1.99	0.45
1:C:157:ILE:HD13	1:C:157:ILE:HA	1.81	0.45
1:I:300:CYS:HB2	1:I:303:ALA:HB3	1.99	0.45
1:F:211:PRO:O	1:F:215:ILE:HG12	2.17	0.44
1:G:137:ASN:N	1:G:137:ASN:OD1	2.49	0.44
1:A:123:ARG:HD2	1:A:198:VAL:HG22	2.00	0.44
1:A:155:GLU:OE2	1:A:163:ARG:NH1	2.50	0.44
1:C:224:TRP:CH2	1:C:301:ARG:HB3	2.52	0.44
1:B:155:GLU:O	1:B:161:TRP:NE1	2.48	0.44
1:I:185:GLN:OE1	1:I:185:GLN:N	2.50	0.44
1:H:216:ILE:O	1:H:219:SER:HB3	2.17	0.44
1:I:216:ILE:O	1:I:219:SER:HB3	2.17	0.44
1:H:294:ASP:HB2	1:H:297:ILE:CG2	2.47	0.44
1:A:21:ASN:HD21	1:A:38:TYR:HE1	1.64	0.44
1:B:226:GLU:OE2	1:C:284:HIS:HE1	2.01	0.44
1:I:91:ARG:HB2	1:J:133:PHE:CE2	2.52	0.44
1:B:216:ILE:O	1:B:219:SER:HB3	2.17	0.44
1:C:91:ARG:HB2	1:D:133:PHE:HE2	1.83	0.44
1:I:157:ILE:HA	1:I:157:ILE:HD13	1.82	0.44
1:H:17:SER:HB2	1:H:40:VAL:HB	1.99	0.44
1:D:95:PHE:HE1	1:D:101:ILE:HD12	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:228:PHE:HA	1:B:231:ARG:NH1	2.32	0.44
1:D:200:ASN:HA	1:D:201:PRO:HD3	1.86	0.44
1:D:137:ASN:OD1	1:D:137:ASN:N	2.51	0.44
1:C:295:LEU:HA	1:C:298:GLN:OE1	2.18	0.44
1:F:17:SER:HB2	1:F:40:VAL:HB	2.00	0.44
1:G:211:PRO:O	1:G:215:ILE:HG12	2.18	0.44
1:F:299:ARG:C	1:F:301:ARG:H	2.20	0.43
1:A:210:LEU:HB3	1:A:211:PRO:HD3	1.99	0.43
1:G:241:THR:HA	1:H:240:LEU:HD23	2.00	0.43
1:E:224:TRP:CH2	1:E:301:ARG:HB3	2.53	0.43
1:H:204:TYR:O	1:H:208:PHE:HB2	2.18	0.43
1:F:225:LEU:HD21	1:G:232:LEU:HD22	1.99	0.43
1:A:232:LEU:HD22	1:E:225:LEU:HD21	1.99	0.43
1:C:21:ASN:HD21	1:C:38:TYR:HE1	1.65	0.43
1:A:157:ILE:HA	1:A:157:ILE:HD13	1.85	0.43
1:H:185:GLN:OE1	1:H:185:GLN:N	2.50	0.43
1:B:91:ARG:HB2	1:C:133:PHE:HE2	1.84	0.43
1:A:17:SER:HB2	1:A:40:VAL:HB	2.00	0.43
1:G:157:ILE:HD13	1:G:157:ILE:HA	1.77	0.43
1:B:211:PRO:O	1:B:215:ILE:HG12	2.18	0.43
1:J:27:ASN:HB3	1:J:32:THR:HB	2.01	0.43
1:H:228:PHE:HA	1:H:231:ARG:HH11	1.83	0.43
1:C:99:ARG:NH2	1:D:180:SER:HB2	2.33	0.43
1:B:17:SER:HB2	1:B:40:VAL:HB	1.99	0.43
1:E:157:ILE:HD13	1:E:157:ILE:HA	1.78	0.43
1:E:92:LEU:HD23	1:E:92:LEU:HA	1.82	0.43
1:H:225:LEU:HB2	1:H:231:ARG:HG3	2.00	0.43
1:A:92:LEU:HA	1:A:92:LEU:HD23	1.81	0.43
1:I:92:LEU:HD23	1:I:92:LEU:HA	1.83	0.43
1:E:216:ILE:O	1:E:219:SER:HB3	2.18	0.43
1:B:174:ARG:HH22	1:I:141:ARG:HD3	1.84	0.43
1:B:289:ASN:OD1	1:B:290:GLY:N	2.47	0.43
1:J:17:SER:HB2	1:J:40:VAL:HB	1.99	0.43
1:I:200:ASN:HA	1:I:201:PRO:HD3	1.86	0.43
1:F:294:ASP:HB2	1:F:297:ILE:HG22	2.01	0.43
1:G:185:GLN:N	1:G:185:GLN:OE1	2.52	0.43
1:E:304:PHE:HD1	1:E:304:PHE:C	2.22	0.43
1:H:294:ASP:O	1:H:298:GLN:HG2	2.19	0.43
1:E:304:PHE:CD1	1:E:304:PHE:C	2.92	0.43
1:A:81:VAL:O	1:E:105:ARG:NH2	2.52	0.43
1:G:95:PHE:HE1	1:G:101:ILE:HD12	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:289:ASN:OD1	1:H:290:GLY:N	2.45	0.43
1:B:163:ARG:HD3	1:B:163:ARG:HA	1.67	0.43
1:A:183:PRO:O	1:A:184:ASN:HB2	2.18	0.43
1:E:145:ILE:HD12	1:E:191:ILE:HG21	2.01	0.43
1:D:300:CYS:HB2	1:D:303:ALA:HB3	2.01	0.42
1:H:163:ARG:HD3	1:H:163:ARG:HA	1.58	0.42
1:E:225:LEU:O	1:E:231:ARG:HD2	2.19	0.42
1:D:210:LEU:HB3	1:D:211:PRO:HD3	2.01	0.42
1:D:27:ASN:HB3	1:D:32:THR:HB	2.01	0.42
1:A:232:LEU:O	1:A:235:SER:OG	2.35	0.42
1:A:250:SER:HB3	1:E:252:ILE:HG13	2.01	0.42
1:A:145:ILE:HD12	1:A:191:ILE:HG21	2.01	0.42
1:F:21:ASN:HD21	1:F:38:TYR:HE1	1.66	0.42
1:J:232:LEU:O	1:J:235:SER:OG	2.35	0.42
1:C:294:ASP:HB2	1:C:297:ILE:CG2	2.49	0.42
1:C:145:ILE:HD12	1:C:191:ILE:HG21	2.02	0.42
1:J:182:GLN:HG3	1:J:183:PRO:HD3	2.01	0.42
1:A:122:ASP:OD1	1:A:122:ASP:N	2.51	0.42
1:D:157:ILE:HD13	1:D:157:ILE:HA	1.84	0.42
1:G:130:LEU:HD23	1:G:130:LEU:HA	1.89	0.42
1:E:128:LEU:HD11	2:E:402:MBR:BR1	2.68	0.42
1:I:145:ILE:HG23	1:I:168:THR:HG21	2.02	0.42
1:H:299:ARG:C	1:H:301:ARG:H	2.23	0.42
1:F:185:GLN:OE1	1:F:185:GLN:N	2.53	0.42
1:E:238:LEU:HD12	1:E:238:LEU:HA	1.89	0.42
1:F:224:TRP:HZ3	2:F:401:MBR:BR1	2.57	0.42
1:C:299:ARG:C	1:C:301:ARG:H	2.23	0.42
1:A:91:ARG:HB2	1:B:133:PHE:HE2	1.85	0.42
1:B:248:TYR:CD1	1:C:247:PHE:HA	2.52	0.42
1:J:211:PRO:O	1:J:215:ILE:HG12	2.19	0.42
1:A:284:HIS:HE1	1:E:226:GLU:OE2	2.03	0.42
1:I:123:ARG:HD2	1:I:198:VAL:HG22	2.01	0.42
1:I:128:LEU:HD13	2:I:402:MBR:BR1	2.75	0.42
1:G:91:ARG:HB2	1:H:133:PHE:CE2	2.49	0.42
1:J:295:LEU:HD12	1:J:298:GLN:OE1	2.20	0.42
1:I:84:SER:HA	1:I:85:PRO:HD3	1.83	0.42
1:A:203:TYR:HB2	1:B:257:PRO:C	2.41	0.42
1:A:220:TRP:CE3	1:A:305:PRO:HB3	2.55	0.42
1:I:17:SER:HB2	1:I:40:VAL:HB	2.01	0.42
1:F:122:ASP:OD1	1:F:122:ASP:N	2.52	0.41
1:G:33:TYR:OH	1:G:127:VAL:N	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:210:LEU:HB3	1:E:211:PRO:HD3	2.02	0.41
1:A:224:TRP:CH2	1:A:301:ARG:HB3	2.55	0.41
1:G:27:ASN:HB3	1:G:32:THR:HB	2.02	0.41
1:F:92:LEU:HD23	1:F:92:LEU:HA	1.85	0.41
1:A:84:SER:HA	1:A:85:PRO:HD3	1.86	0.41
1:C:59:GLU:OE2	1:D:134:SER:OG	2.34	0.41
1:B:247:PHE:CD2	1:C:247:PHE:HE2	2.37	0.41
1:A:281:ILE:HD11	1:E:221:SER:HB2	2.01	0.41
1:B:224:TRP:CH2	1:B:301:ARG:HB3	2.55	0.41
1:C:224:TRP:CE2	1:C:301:ARG:HD3	2.55	0.41
1:J:224:TRP:CH2	1:J:301:ARG:HB3	2.55	0.41
1:I:27:ASN:HB3	1:I:32:THR:HB	2.02	0.41
1:D:92:LEU:HD23	1:D:92:LEU:HA	1.83	0.41
1:H:231:ARG:HH11	1:H:231:ARG:HD3	1.61	0.41
1:B:294:ASP:HB2	1:B:297:ILE:CG2	2.50	0.41
1:B:159:GLU:HG3	1:C:257:PRO:HB3	2.03	0.41
1:D:29:LEU:HA	1:D:29:LEU:HD23	1.85	0.41
1:E:130:LEU:HD23	1:E:130:LEU:HA	1.85	0.41
1:I:238:LEU:HD13	1:J:236:PHE:CD2	2.56	0.41
1:E:185:GLN:N	1:E:185:GLN:OE1	2.53	0.41
1:F:210:LEU:HB3	1:F:211:PRO:HD3	2.03	0.41
1:H:145:ILE:HD12	1:H:191:ILE:HG21	2.03	0.41
1:I:31:GLN:HG2	1:I:114:MET:HB2	2.02	0.41
1:B:185:GLN:N	1:B:185:GLN:OE1	2.53	0.41
1:F:224:TRP:CH2	1:F:301:ARG:HB3	2.55	0.41
1:A:247:PHE:HA	1:E:248:TYR:HD1	1.86	0.41
1:D:157:ILE:HG12	1:E:117:ARG:HH21	1.86	0.41
1:B:95:PHE:HE1	1:B:101:ILE:HD12	1.84	0.41
1:E:81:VAL:HG13	1:E:83:GLY:O	2.21	0.41
1:H:210:LEU:HB3	1:H:211:PRO:HD3	2.01	0.41
1:A:27:ASN:HB3	1:A:32:THR:HB	2.03	0.41
1:B:92:LEU:HA	1:B:92:LEU:HD23	1.79	0.41
1:G:21:ASN:HD21	1:G:38:TYR:HE1	1.68	0.41
1:G:81:VAL:HG13	1:G:83:GLY:O	2.21	0.41
1:G:92:LEU:HD23	1:G:92:LEU:HA	1.80	0.41
1:D:299:ARG:C	1:D:301:ARG:H	2.24	0.41
1:F:200:ASN:HA	1:F:201:PRO:HD3	1.91	0.41
1:I:210:LEU:HB3	1:I:211:PRO:HD3	2.03	0.40
1:H:248:TYR:HE1	1:I:250:SER:OG	2.05	0.40
1:J:175:TYR:HB2	1:J:178:LEU:HD21	2.03	0.40
1:I:48:ARG:NH1	1:I:48:ARG:HB2	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:304:PHE:C	1:I:304:PHE:CD1	2.95	0.40
1:D:225:LEU:O	1:D:231:ARG:HD2	2.21	0.40
1:E:294:ASP:HB2	1:E:297:ILE:HG22	2.03	0.40
1:A:247:PHE:CE2	1:E:247:PHE:CG	3.09	0.40
1:J:92:LEU:HD23	1:J:92:LEU:HA	1.82	0.40
1:F:79:ILE:HD13	1:F:79:ILE:HA	1.96	0.40
1:I:95:PHE:HE1	1:I:101:ILE:HD12	1.86	0.40
1:F:27:ASN:HB3	1:F:32:THR:HB	2.03	0.40
1:E:299:ARG:C	1:E:301:ARG:H	2.25	0.40
1:B:210:LEU:HB3	1:B:211:PRO:HD3	2.02	0.40
1:I:224:TRP:CH2	1:I:301:ARG:HB3	2.56	0.40
1:I:299:ARG:C	1:I:301:ARG:H	2.25	0.40
1:H:203:TYR:HB2	1:I:257:PRO:C	2.42	0.40
1:H:220:TRP:CE3	1:H:305:PRO:HB3	2.56	0.40
1:J:179:SER:C	1:J:181:VAL:H	2.25	0.40
1:J:122:ASP:OD2	1:J:199:ARG:NE	2.46	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:292:GLU:OE1	1:D:49:LYS:NZ[1_556]	2.01	0.19

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 X-ray entries followed by that with respect to entries of similar resolution.

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	305/307 (99%)	276 (90%)	20 (7%)	9 (3%)	5	46
1	B	305/307 (99%)	275 (90%)	21 (7%)	9 (3%)	5	46
1	C	305/307 (99%)	276 (90%)	23 (8%)	6 (2%)	9	54
1	D	305/307 (99%)	275 (90%)	22 (7%)	8 (3%)	7	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	305/307 (99%)	273 (90%)	26 (8%)	6 (2%)	9	54
1	F	305/307 (99%)	275 (90%)	23 (8%)	7 (2%)	8	52
1	G	305/307 (99%)	276 (90%)	21 (7%)	8 (3%)	7	48
1	H	305/307 (99%)	273 (90%)	25 (8%)	7 (2%)	8	52
1	I	305/307 (99%)	274 (90%)	24 (8%)	7 (2%)	8	52
1	J	305/307 (99%)	275 (90%)	23 (8%)	7 (2%)	8	52
All	All	3050/3070 (99%)	2748 (90%)	228 (8%)	74 (2%)	7	51

All (74) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
1	B	53	ASP
1	B	60	ASN
1	B	166	ALA
1	C	166	ALA
1	D	53	ASP
1	D	60	ASN
1	E	53	ASP
1	E	60	ASN
1	F	60	ASN
1	G	53	ASP
1	G	60	ASN
1	G	166	ALA
1	H	60	ASN
1	I	60	ASN
1	J	53	ASP
1	J	60	ASN
1	J	166	ALA
1	A	53	ASP
1	A	152	ILE
1	B	152	ILE
1	C	53	ASP
1	C	152	ILE
1	D	152	ILE
1	E	152	ILE
1	F	53	ASP
1	F	152	ILE
1	G	152	ILE
1	G	183	PRO

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Mol	Chain	Res	Type
1	H	53	ASP
1	H	152	ILE
1	H	166	ALA
1	I	53	ASP
1	I	152	ILE
1	J	152	ILE
1	A	183	PRO
1	A	184	ASN
1	A	294	ASP
1	B	150	GLU
1	C	183	PRO
1	D	166	ALA
1	D	183	PRO
1	E	183	PRO
1	H	153	ASP
1	H	183	PRO
1	I	183	PRO
1	B	153	ASP
1	B	294	ASP
1	C	153	ASP
1	D	150	GLU
1	F	153	ASP
1	F	183	PRO
1	F	294	ASP
1	G	150	GLU
1	H	150	GLU
1	I	150	GLU
1	I	166	ALA
1	J	150	GLU
1	J	183	PRO
1	A	150	GLU
1	A	153	ASP
1	A	166	ALA
1	C	184	ASN
1	D	153	ASP
1	D	184	ASN
1	E	150	GLU
1	E	153	ASP
1	F	150	GLU
1	G	294	ASP
1	J	153	ASP
1	G	153	ASP

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Mol	Chain	Res	Type
1	I	153	ASP
1	B	183	PRO
1	B	182	GLN

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 X-ray entries followed by that with respect to entries of similar resolution.

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	274/275 (100%)	253 (92%)	21 (8%)	16	57
1	B	274/275 (100%)	251 (92%)	23 (8%)	14	53
1	C	274/275 (100%)	250 (91%)	24 (9%)	12	51
1	D	274/275 (100%)	254 (93%)	20 (7%)	17	59
1	E	274/275 (100%)	251 (92%)	23 (8%)	14	53
1	F	274/275 (100%)	254 (93%)	20 (7%)	17	59
1	G	274/275 (100%)	251 (92%)	23 (8%)	14	53
1	H	274/275 (100%)	250 (91%)	24 (9%)	12	51
1	I	274/275 (100%)	254 (93%)	20 (7%)	17	59
1	J	274/275 (100%)	252 (92%)	22 (8%)	15	55
All	All	2740/2750 (100%)	2520 (92%)	220 (8%)	15	55

All (220) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	LEU
1	A	71	LEU
1	A	81	VAL
1	A	103	ASN
1	A	118	LEU
1	A	122	ASP
1	A	124	GLN
1	A	130	LEU
1	A	134	SER
1	A	145	ILE

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Mol	Chain	Res	Type
1	A	146	GLN
1	A	165	LYS
1	A	168	THR
1	A	177	HIS
1	A	178	LEU
1	A	182	GLN
1	A	240	LEU
1	A	247	PHE
1	A	291	VAL
1	A	302	LEU
1	A	304	PHE
1	B	39	ILE
1	B	56	LEU
1	B	71	LEU
1	B	81	VAL
1	B	118	LEU
1	B	122	ASP
1	B	124	GLN
1	B	130	LEU
1	B	134	SER
1	B	136	ASN
1	B	146	GLN
1	B	165	LYS
1	B	168	THR
1	B	177	HIS
1	B	178	LEU
1	B	182	GLN
1	B	239	MET
1	B	240	LEU
1	B	247	PHE
1	B	287	GLN
1	B	291	VAL
1	B	302	LEU
1	B	304	PHE
1	C	32	THR
1	C	39	ILE
1	C	56	LEU
1	C	71	LEU
1	C	81	VAL
1	C	118	LEU
1	C	122	ASP
1	C	124	GLN

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Mol	Chain	Res	Type
1	C	130	LEU
1	C	134	SER
1	C	136	ASN
1	C	141	ARG
1	C	145	ILE
1	C	146	GLN
1	C	165	LYS
1	C	168	THR
1	C	177	HIS
1	C	178	LEU
1	C	182	GLN
1	C	247	PHE
1	C	287	GLN
1	C	291	VAL
1	C	302	LEU
1	C	304	PHE
1	D	56	LEU
1	D	81	VAL
1	D	118	LEU
1	D	122	ASP
1	D	124	GLN
1	D	130	LEU
1	D	134	SER
1	D	141	ARG
1	D	146	GLN
1	D	165	LYS
1	D	177	HIS
1	D	178	LEU
1	D	182	GLN
1	D	240	LEU
1	D	247	PHE
1	D	285	HIS
1	D	287	GLN
1	D	291	VAL
1	D	302	LEU
1	D	304	PHE
1	E	39	ILE
1	E	56	LEU
1	E	71	LEU
1	E	81	VAL
1	E	118	LEU
1	E	122	ASP

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Mol	Chain	Res	Type
1	E	124	GLN
1	E	130	LEU
1	E	134	SER
1	E	141	ARG
1	E	146	GLN
1	E	163	ARG
1	E	165	LYS
1	E	168	THR
1	E	177	HIS
1	E	178	LEU
1	E	182	GLN
1	E	240	LEU
1	E	247	PHE
1	E	287	GLN
1	E	291	VAL
1	E	302	LEU
1	E	304	PHE
1	F	39	ILE
1	F	56	LEU
1	F	71	LEU
1	F	81	VAL
1	F	118	LEU
1	F	122	ASP
1	F	124	GLN
1	F	130	LEU
1	F	136	ASN
1	F	146	GLN
1	F	165	LYS
1	F	168	THR
1	F	177	HIS
1	F	178	LEU
1	F	240	LEU
1	F	247	PHE
1	F	287	GLN
1	F	291	VAL
1	F	302	LEU
1	F	304	PHE
1	G	39	ILE
1	G	56	LEU
1	G	71	LEU
1	G	81	VAL
1	G	118	LEU

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Mol	Chain	Res	Type
1	G	122	ASP
1	G	124	GLN
1	G	130	LEU
1	G	134	SER
1	G	141	ARG
1	G	146	GLN
1	G	157	ILE
1	G	165	LYS
1	G	168	THR
1	G	177	HIS
1	G	178	LEU
1	G	182	GLN
1	G	239	MET
1	G	247	PHE
1	G	287	GLN
1	G	291	VAL
1	G	302	LEU
1	G	304	PHE
1	H	39	ILE
1	H	56	LEU
1	H	71	LEU
1	H	81	VAL
1	H	118	LEU
1	H	122	ASP
1	H	124	GLN
1	H	130	LEU
1	H	134	SER
1	H	136	ASN
1	H	146	GLN
1	H	154	ASN
1	H	165	LYS
1	H	168	THR
1	H	177	HIS
1	H	178	LEU
1	H	182	GLN
1	H	231	ARG
1	H	240	LEU
1	H	247	PHE
1	H	287	GLN
1	H	291	VAL
1	H	302	LEU
1	H	304	PHE

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Mol	Chain	Res	Type
1	I	56	LEU
1	I	71	LEU
1	I	81	VAL
1	I	118	LEU
1	I	122	ASP
1	I	124	GLN
1	I	130	LEU
1	I	134	SER
1	I	141	ARG
1	I	145	ILE
1	I	146	GLN
1	I	165	LYS
1	I	177	HIS
1	I	178	LEU
1	I	182	GLN
1	I	247	PHE
1	I	287	GLN
1	I	291	VAL
1	I	302	LEU
1	I	304	PHE
1	J	29	LEU
1	J	39	ILE
1	J	56	LEU
1	J	71	LEU
1	J	81	VAL
1	J	118	LEU
1	J	124	GLN
1	J	130	LEU
1	J	134	SER
1	J	136	ASN
1	J	141	ARG
1	J	146	GLN
1	J	165	LYS
1	J	168	THR
1	J	177	HIS
1	J	178	LEU
1	J	182	GLN
1	J	247	PHE
1	J	287	GLN
1	J	291	VAL
1	J	302	LEU
1	J	304	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	103	ASN
1	D	103	ASN
1	E	124	GLN
1	E	298	GLN
1	F	103	ASN
1	F	298	GLN
1	G	103	ASN
1	I	177	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 22 ligands modelled in this entry, 22 are modelled with single atom - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	307/307 (100%)	-0.06	12 (3%)	43	28	73, 122, 214, 290	0
1	B	307/307 (100%)	-0.07	8 (2%)	59	42	73, 118, 212, 284	0
1	C	307/307 (100%)	-0.02	9 (2%)	55	38	74, 117, 214, 284	0
1	D	307/307 (100%)	-0.08	7 (2%)	64	46	77, 118, 215, 285	0
1	E	307/307 (100%)	-0.10	6 (1%)	68	51	77, 122, 213, 287	0
1	F	307/307 (100%)	-0.14	6 (1%)	68	51	80, 122, 214, 285	0
1	G	307/307 (100%)	-0.06	21 (6%)	20	12	77, 116, 214, 288	0
1	H	307/307 (100%)	-0.09	11 (3%)	46	31	78, 118, 210, 285	0
1	I	307/307 (100%)	-0.10	12 (3%)	43	28	73, 118, 214, 304	0
1	J	307/307 (100%)	-0.05	11 (3%)	46	31	86, 123, 217, 313	0
All	All	3070/3070 (100%)	-0.08	103 (3%)	49	33	73, 119, 215, 313	0

All (103) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	289	ASN	7.4
1	G	315	LEU	6.6
1	I	180	SER	6.6
1	E	290	GLY	6.2
1	H	291	VAL	5.4
1	G	314	VAL	5.4
1	H	165	LYS	5.2
1	C	180	SER	4.9
1	B	291	VAL	4.8
1	G	293	ASP	4.7
1	I	179	SER	4.6
1	C	317	ILE	4.6
1	J	303	ALA	4.5

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Mol	Chain	Res	Type	RSRZ
1	I	181	VAL	4.4
1	H	289	ASN	4.4
1	B	293	ASP	4.3
1	B	290	GLY	4.3
1	H	164	GLY	4.1
1	E	291	VAL	4.1
1	A	297	ILE	4.1
1	H	180	SER	3.9
1	B	289	ASN	3.9
1	I	290	GLY	3.7
1	G	313	CYS	3.7
1	D	153	ASP	3.7
1	D	49	LYS	3.7
1	J	153	ASP	3.5
1	I	154	ASN	3.5
1	D	179	SER	3.4
1	F	317	ILE	3.4
1	I	296	LEU	3.4
1	H	179	SER	3.4
1	C	288	ALA	3.2
1	B	179	SER	3.2
1	F	224	TRP	3.1
1	F	288	ALA	3.1
1	E	179	SER	3.0
1	I	182	GLN	3.0
1	H	288	ALA	3.0
1	I	237	THR	3.0
1	C	291	VAL	2.9
1	B	180	SER	2.9
1	D	177	HIS	2.9
1	G	182	GLN	2.9
1	J	189	SER	2.8
1	F	286	ARG	2.8
1	E	180	SER	2.8
1	H	62	GLN	2.8
1	J	306	LEU	2.8
1	C	313	CYS	2.7
1	A	310	ALA	2.7
1	G	312	GLY	2.7
1	G	295	LEU	2.7
1	C	179	SER	2.7
1	H	292	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	G	126	PHE	2.6
1	J	172	ASP	2.6
1	G	286	ARG	2.6
1	G	287	GLN	2.6
1	D	297	ILE	2.5
1	A	52	GLY	2.5
1	D	157	ILE	2.5
1	G	285	HIS	2.5
1	A	56	LEU	2.5
1	A	175	TYR	2.4
1	C	172	ASP	2.4
1	F	197	ALA	2.4
1	G	179	SER	2.4
1	B	292	GLU	2.4
1	J	294	ASP	2.4
1	G	180	SER	2.4
1	I	297	ILE	2.4
1	I	153	ASP	2.4
1	A	156	GLU	2.4
1	G	281	ILE	2.4
1	D	180	SER	2.4
1	G	311	ILE	2.3
1	J	282	PHE	2.3
1	A	295	LEU	2.3
1	H	178	LEU	2.3
1	H	293	ASP	2.2
1	I	288	ALA	2.2
1	A	233	GLN	2.2
1	A	116	PHE	2.2
1	G	282	PHE	2.2
1	E	237	THR	2.2
1	C	314	VAL	2.2
1	A	178	LEU	2.1
1	G	317	ILE	2.1
1	J	123	ARG	2.1
1	E	49	LYS	2.1
1	J	188	PHE	2.1
1	A	288	ALA	2.1
1	G	156	GLU	2.1
1	G	292	GLU	2.1
1	G	49	LYS	2.1
1	I	291	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	314	VAL	2.1
1	G	310	ALA	2.1
1	B	233	GLN	2.1
1	F	287	GLN	2.0
1	J	310	ALA	2.0
1	J	179	SER	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	MBR	E	402	1/4	0.56	2.32	51.62	211,211,211,211	0
2	MBR	J	402	1/4	0.78	2.96	35.92	202,202,202,202	0
2	MBR	H	402	1/4	0.86	2.26	32.37	198,198,198,198	0
2	MBR	B	402	1/4	0.79	2.23	29.88	195,195,195,195	0
2	MBR	I	402	1/4	0.83	2.47	29.06	212,212,212,212	0
2	MBR	F	402	1/4	0.82	2.68	21.45	196,196,196,196	0
2	MBR	C	402	1/4	0.85	2.32	19.37	195,195,195,195	0
2	MBR	D	402	1/4	0.76	2.29	17.09	185,185,185,185	0
2	MBR	A	402	1/4	0.87	1.75	14.62	201,201,201,201	0
2	MBR	G	402	1/4	0.69	2.74	14.40	186,186,186,186	0
2	MBR	C	401	1/4	0.89	0.49	9.05	193,193,193,193	0
2	MBR	E	401	1/4	0.63	0.38	6.13	190,190,190,190	0
2	MBR	J	401	1/4	-0.00	0.60	4.21	212,212,212,212	0
2	MBR	I	401	1/4	0.35	0.42	1.72	186,186,186,186	0
2	MBR	G	401	1/4	0.73	0.14	-0.96	190,190,190,190	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	MBR	B	401	1/4	0.68	0.30	-	200,200,200,200	0
2	MBR	A	401	1/4	0.08	0.57	-	210,210,210,210	0
2	MBR	D	401	1/4	0.31	0.54	-	186,186,186,186	0
2	MBR	A	403	1/4	0.77	0.47	-	154,154,154,154	0
2	MBR	F	401	1/4	0.40	2.00	-	201,201,201,201	0
2	MBR	H	401	1/4	0.73	0.17	-	195,195,195,195	0
2	MBR	F	403	1/4	0.89	1.14	-	166,166,166,166	0

6.5 Other polymers [i](#)

There are no such residues in this entry.