



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:41 PM GMT

PDB ID : 1UPP
Title : SPINACH RUBISCO IN COMPLEX WITH 2-CARBOXYARABINITOL 2
BISPHOSPHATE AND CALCIUM.
Authors : Karkehabadi, S.; Taylor, T.C.; Andersson, I.
Deposited on : 2003-10-09
Resolution : 2.30 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

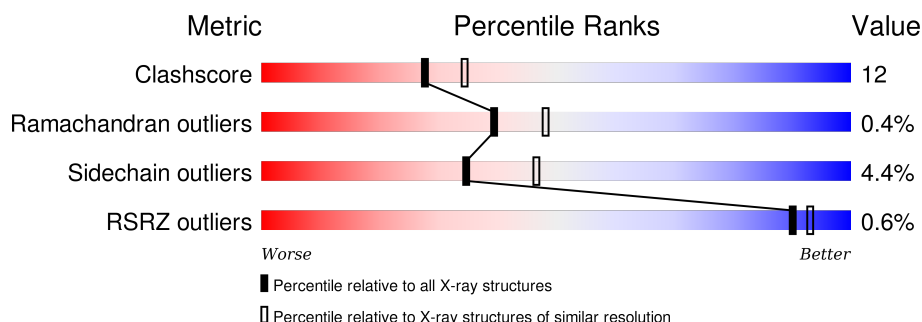
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	475	<div> <div></div> <div>63%30% . .</div> </div>
1	C	475	<div> <div></div> <div>66%28% . .</div> </div>
1	E	475	<div> <div></div> <div>66%28% . .</div> </div>
1	G	475	<div> <div></div> <div>67%26% . .</div> </div>
2	I	123	<div> <div></div> <div>64%31% . .</div> </div>
2	J	123	<div> <div></div> <div>61%33%6%</div> </div>
2	K	123	<div> <div></div> <div>60%36% . .</div> </div>

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Mol	Chain	Length	Quality of chain
2	L	123	

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
3	CA	E	476	-	-	-	X
3	CA	G	476	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 19504 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 RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	467	Total	C	N	O	S	0	0	0
			3656	2319	640	679	18			
1	C	467	Total	C	N	O	S	0	0	0
			3656	2319	640	679	18			
1	E	467	Total	C	N	O	S	0	0	0
			3656	2319	640	679	18			
1	G	467	Total	C	N	O	S	0	0	0
			3656	2319	640	679	18			

- Molecule 2 is a protein called RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	123	Total	C	N	O	S	0	0	0
			1032	673	167	185	7			
2	J	123	Total	C	N	O	S	0	0	0
			1032	673	167	185	7			
2	K	123	Total	C	N	O	S	0	0	0
			1032	673	167	185	7			
2	L	123	Total	C	N	O	S	0	0	0
			1032	673	167	185	7			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	2	GLN	LYS	CONFLICT	UNP Q43832
I	6	ILE	THR	CONFLICT	UNP Q43832
I	7	LEU	GLN	CONFLICT	UNP Q43832
I	9	LEU	MET	CONFLICT	UNP Q43832
I	11	LYS	ARG	CONFLICT	UNP Q43832
I	109	GLU	GLN	CONFLICT	UNP Q43832
I	113	ILE	VAL	CONFLICT	UNP Q43832

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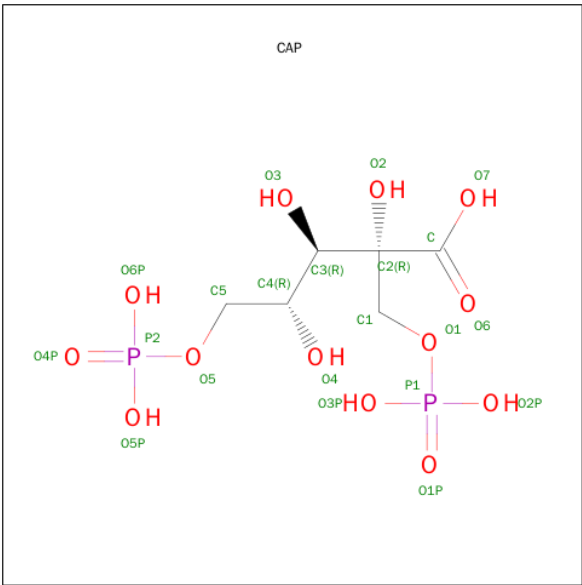
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Chain	Residue	Modelled	Actual	Comment	Reference
J	2	GLN	LYS	CONFLICT	UNP Q43832
J	6	ILE	THR	CONFLICT	UNP Q43832
J	7	LEU	GLN	CONFLICT	UNP Q43832
J	9	LEU	MET	CONFLICT	UNP Q43832
J	11	LYS	ARG	CONFLICT	UNP Q43832
J	109	GLU	GLN	CONFLICT	UNP Q43832
J	113	ILE	VAL	CONFLICT	UNP Q43832
K	2	GLN	LYS	CONFLICT	UNP Q43832
K	6	ILE	THR	CONFLICT	UNP Q43832
K	7	LEU	GLN	CONFLICT	UNP Q43832
K	9	LEU	MET	CONFLICT	UNP Q43832
K	11	LYS	ARG	CONFLICT	UNP Q43832
K	109	GLU	GLN	CONFLICT	UNP Q43832
K	113	ILE	VAL	CONFLICT	UNP Q43832
L	2	GLN	LYS	CONFLICT	UNP Q43832
L	6	ILE	THR	CONFLICT	UNP Q43832
L	7	LEU	GLN	CONFLICT	UNP Q43832
L	9	LEU	MET	CONFLICT	UNP Q43832
L	11	LYS	ARG	CONFLICT	UNP Q43832
L	109	GLU	GLN	CONFLICT	UNP Q43832
L	113	ILE	VAL	CONFLICT	UNP Q43832

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	1	Total Ca 1 1	0	0
3	A	1	Total Ca 1 1	0	0
3	C	1	Total Ca 1 1	0	0
3	E	1	Total Ca 1 1	0	0

- Molecule 4 is 2-CARBOXYARABINITOL-1,5-DIPHOSPHATE (three-letter code: CAP) (formula: C₆H₁₄O₁₃P₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	P	0	0
			21	6	13	2		
4	C	1	Total	C	O	P	0	0
			21	6	13	2		
4	E	1	Total	C	O	P	0	0
			21	6	13	2		
4	G	1	Total	C	O	P	0	0
			21	6	13	2		

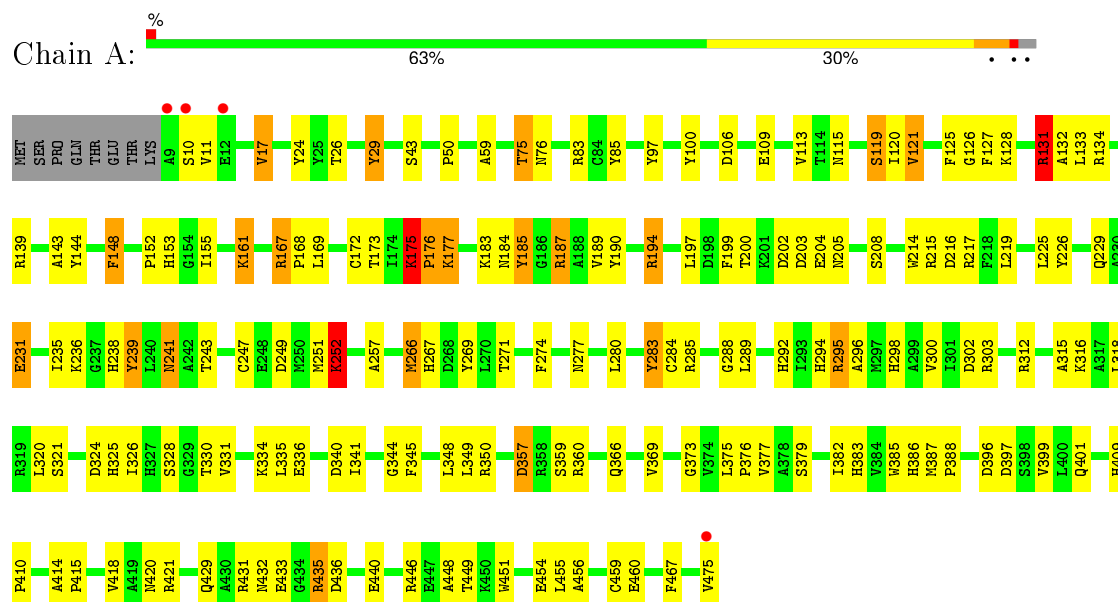
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	112	Total	O	0	0
			112	112		
5	C	121	Total	O	0	0
			121	121		
5	E	132	Total	O	0	0
			132	132		
5	G	133	Total	O	0	0
			133	133		
5	I	34	Total	O	0	0
			34	34		
5	J	44	Total	O	0	0
			44	44		
5	K	41	Total	O	0	0
			41	41		
5	L	47	Total	O	0	0
			47	47		

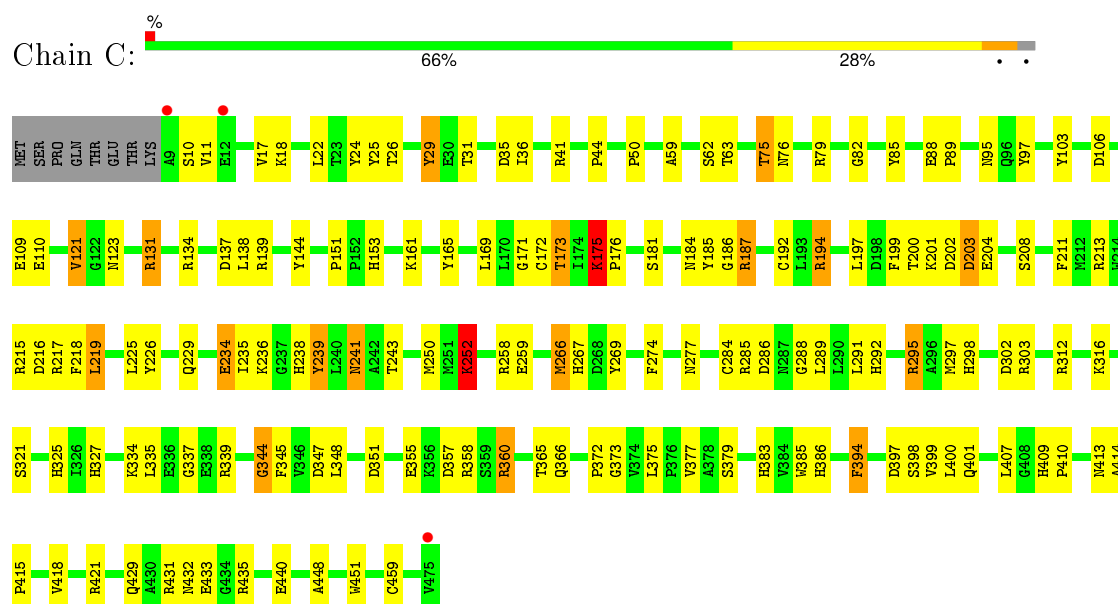
3 Residue-property plots

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.

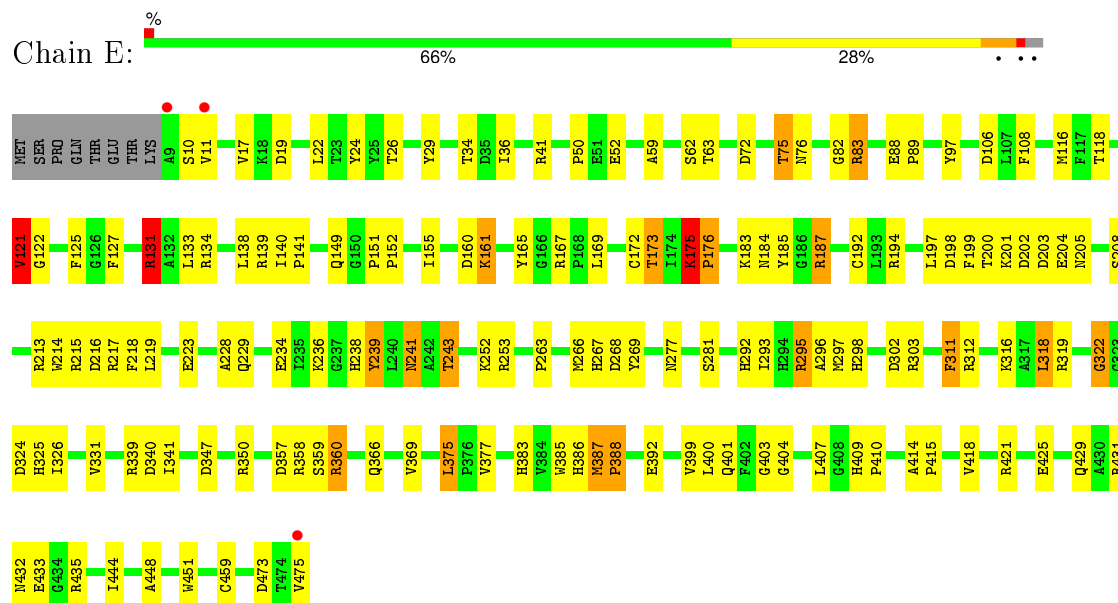
• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN



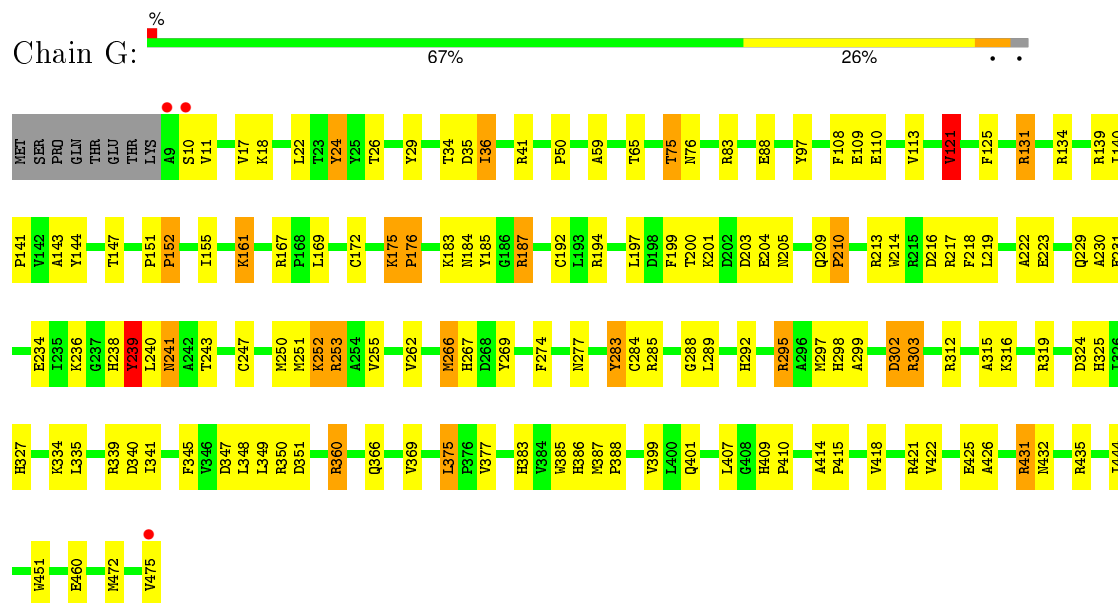
• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN



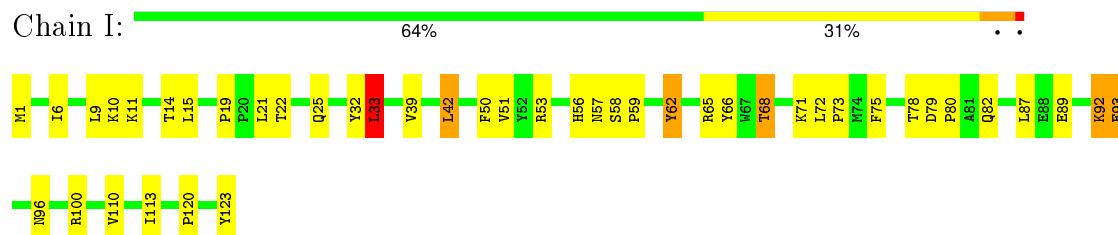
- Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN



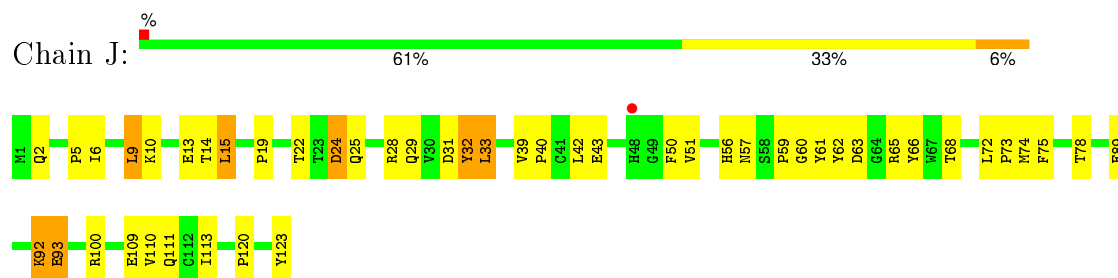
- Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN



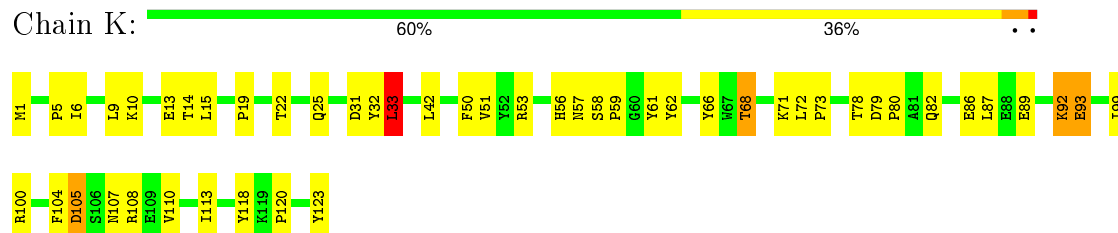
- Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN



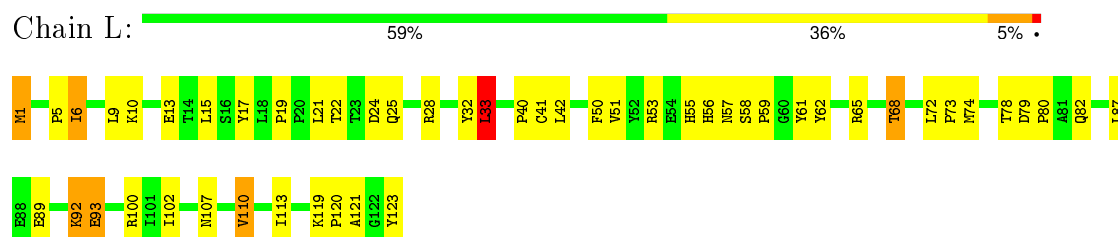
- Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN



• Molecule 2: RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN



• Molecule 2: RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	155.88Å 156.25Å 199.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 2.30 78.12 – 2.09	Depositor EDS
% Data completeness (in resolution range)	76.1 (100.00-2.30) 75.8 (78.12-2.09)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.41 (at 2.10Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.256 , 0.307 0.254 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	18.0	Xtriage
Anisotropy	0.123	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 17.9	EDS
Estimated twinning fraction	0.459 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	0 of 108167 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	19504	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.27 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.5641e-04.*

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: CA, CAP, KCX

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	0.87	1/3733 (0.0%)	1.75	75/5064 (1.5%)
1	C	0.84	2/3733 (0.1%)	1.84	77/5064 (1.5%)
1	E	0.86	0/3733	1.79	78/5064 (1.5%)
1	G	0.84	0/3733	1.70	69/5064 (1.4%)
2	I	0.69	0/1067	1.49	10/1453 (0.7%)
2	J	0.70	0/1067	1.53	21/1453 (1.4%)
2	K	0.66	0/1067	1.49	11/1453 (0.8%)
2	L	0.68	0/1067	1.45	8/1453 (0.6%)
All	All	0.82	3/19200 (0.0%)	1.71	349/26068 (1.3%)

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	2
1	C	0	1
1	E	0	2
1	G	0	3
2	I	0	1
All	All	0	9

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	176	PRO	N-CD	7.58	1.58	1.47
1	C	181	SER	CB-OG	5.80	1.49	1.42
1	A	43	SER	CB-OG	5.35	1.49	1.42

All (349) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	312	ARG	NE-CZ-NH1	19.65	130.12	120.30
1	C	312	ARG	NE-CZ-NH2	-17.11	111.75	120.30
2	K	100	ARG	NE-CZ-NH2	-16.34	112.13	120.30
1	C	176	PRO	CA-N-CD	-16.10	88.96	111.50
1	C	303	ARG	NE-CZ-NH1	15.75	128.18	120.30
1	E	358	ARG	NE-CZ-NH2	-15.71	112.44	120.30
1	A	303	ARG	NE-CZ-NH2	-15.49	112.56	120.30
1	C	203	ASP	CB-CG-OD2	14.11	131.00	118.30
1	A	203	ASP	CB-CG-OD2	13.92	130.83	118.30
1	A	194	ARG	NE-CZ-NH1	-13.89	113.36	120.30
2	K	53	ARG	NE-CZ-NH1	-13.78	113.41	120.30
1	C	303	ARG	NE-CZ-NH2	-13.70	113.45	120.30
1	E	203	ASP	CB-CG-OD2	13.50	130.45	118.30
1	E	203	ASP	CB-CG-OD1	-13.35	106.28	118.30
1	G	312	ARG	NE-CZ-NH2	-13.26	113.67	120.30
1	A	312	ARG	NE-CZ-NH1	12.96	126.78	120.30
1	G	253	ARG	NE-CZ-NH2	-12.79	113.90	120.30
1	C	194	ARG	NE-CZ-NH1	-12.66	113.97	120.30
1	E	134	ARG	NE-CZ-NH1	12.58	126.59	120.30
1	C	187	ARG	CD-NE-CZ	12.54	141.16	123.60
1	C	216	ASP	CB-CG-OD1	12.35	129.41	118.30
1	A	131	ARG	CD-NE-CZ	12.25	140.75	123.60
1	E	215	ARG	NE-CZ-NH2	11.94	126.27	120.30
1	C	134	ARG	NE-CZ-NH1	11.90	126.25	120.30
1	C	295	ARG	NE-CZ-NH2	-11.89	114.36	120.30
1	C	106	ASP	CB-CG-OD2	11.85	128.97	118.30
2	L	100	ARG	NE-CZ-NH1	11.80	126.20	120.30
1	E	312	ARG	CD-NE-CZ	11.72	140.01	123.60
1	E	139	ARG	NE-CZ-NH1	-11.57	114.52	120.30
1	E	312	ARG	NE-CZ-NH2	-11.46	114.57	120.30
1	C	351	ASP	CB-CG-OD2	-11.45	107.99	118.30
1	C	213	ARG	NE-CZ-NH1	-11.29	114.66	120.30
1	G	303	ARG	NE-CZ-NH2	-11.17	114.71	120.30
1	A	203	ASP	CB-CG-OD1	-11.17	108.25	118.30
1	E	435	ARG	NE-CZ-NH2	-11.16	114.72	120.30
1	G	312	ARG	NE-CZ-NH1	11.08	125.84	120.30
1	C	421	ARG	NE-CZ-NH2	-11.04	114.78	120.30
1	A	350	ARG	NE-CZ-NH1	10.89	125.75	120.30
1	E	131	ARG	CD-NE-CZ	10.88	138.83	123.60
1	E	106	ASP	CB-CG-OD2	10.88	128.09	118.30
2	L	100	ARG	NE-CZ-NH2	-10.87	114.86	120.30
1	C	358	ARG	NE-CZ-NH2	-10.45	115.08	120.30
1	E	139	ARG	NE-CZ-NH2	10.36	125.48	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	167	ARG	CD-NE-CZ	10.33	138.06	123.60
2	I	65	ARG	NE-CZ-NH1	10.31	125.46	120.30
1	G	203	ASP	CB-CG-OD1	-10.28	109.05	118.30
1	A	397	ASP	CB-CG-OD1	10.20	127.48	118.30
1	C	203	ASP	CB-CG-OD1	-10.15	109.16	118.30
1	A	303	ARG	NE-CZ-NH1	10.06	125.33	120.30
1	E	319	ARG	NE-CZ-NH2	9.93	125.26	120.30
1	C	139	ARG	NE-CZ-NH2	9.93	125.26	120.30
1	G	176	PRO	CA-N-CD	-9.87	97.68	111.50
2	I	33	LEU	CA-CB-CG	9.84	137.93	115.30
2	J	100	ARG	CD-NE-CZ	9.75	137.25	123.60
1	C	139	ARG	NE-CZ-NH1	-9.56	115.52	120.30
1	A	177	LYS	CB-CG-CD	-9.41	87.14	111.60
1	G	253	ARG	NE-CZ-NH1	9.39	125.00	120.30
2	K	33	LEU	CA-CB-CG	9.33	136.77	115.30
2	J	33	LEU	CA-CB-CG	9.32	136.73	115.30
1	E	187	ARG	CD-NE-CZ	9.27	136.57	123.60
1	G	203	ASP	CB-CG-OD2	9.22	126.60	118.30
1	A	285	ARG	NE-CZ-NH1	9.20	124.90	120.30
1	A	134	ARG	NE-CZ-NH2	-9.19	115.70	120.30
1	G	187	ARG	CD-NE-CZ	9.09	136.33	123.60
1	G	131	ARG	CD-NE-CZ	9.06	136.29	123.60
1	C	285	ARG	CD-NE-CZ	9.03	136.24	123.60
1	A	134	ARG	NE-CZ-NH1	9.03	124.81	120.30
1	G	435	ARG	NE-CZ-NH1	8.97	124.78	120.30
1	G	176	PRO	N-CA-CB	8.93	114.02	103.30
1	A	312	ARG	NE-CZ-NH2	-8.91	115.84	120.30
1	C	131	ARG	CD-NE-CZ	8.90	136.06	123.60
2	L	33	LEU	CA-CB-CG	8.86	135.69	115.30
1	A	217	ARG	CG-CD-NE	8.86	130.40	111.80
1	A	176	PRO	CA-N-CD	-8.85	99.11	111.50
1	G	302	ASP	CB-CG-OD1	8.83	126.25	118.30
2	I	100	ARG	CD-NE-CZ	8.79	135.91	123.60
1	G	131	ARG	NE-CZ-NH2	8.57	124.59	120.30
1	A	397	ASP	OD1-CG-OD2	-8.56	107.04	123.30
1	E	339	ARG	NE-CZ-NH1	8.52	124.56	120.30
2	L	53	ARG	NE-CZ-NH1	-8.48	116.06	120.30
1	A	350	ARG	NE-CZ-NH2	-8.47	116.07	120.30
1	C	435	ARG	NE-CZ-NH2	-8.33	116.13	120.30
1	E	339	ARG	NE-CZ-NH2	-8.32	116.14	120.30
1	A	187	ARG	NE-CZ-NH2	-8.27	116.17	120.30
2	J	100	ARG	NE-CZ-NH1	8.27	124.43	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	41	ARG	NE-CZ-NH2	8.24	124.42	120.30
1	C	35	ASP	CB-CG-OD2	-8.23	110.89	118.30
1	G	350	ARG	NE-CZ-NH2	-8.21	116.20	120.30
2	K	66	TYR	CB-CG-CD1	-8.11	116.13	121.00
1	G	187	ARG	NE-CZ-NH2	-8.04	116.28	120.30
1	E	83	ARG	NE-CZ-NH2	-8.03	116.29	120.30
1	A	187	ARG	CD-NE-CZ	8.01	134.81	123.60
1	G	194	ARG	NE-CZ-NH2	7.97	124.28	120.30
1	A	397	ASP	CB-CG-OD2	7.97	125.47	118.30
1	G	339	ARG	NE-CZ-NH2	-7.95	116.33	120.30
1	A	324	ASP	CB-CG-OD1	-7.93	111.16	118.30
1	C	258	ARG	NE-CZ-NH2	-7.91	116.34	120.30
1	E	303	ARG	CD-NE-CZ	7.91	134.68	123.60
1	C	213	ARG	NE-CZ-NH2	7.90	124.25	120.30
2	I	1	MET	CA-CB-CG	7.88	126.70	113.30
1	E	295	ARG	NE-CZ-NH2	-7.87	116.37	120.30
1	C	286	ASP	CB-CG-OD1	7.80	125.32	118.30
1	E	303	ARG	NE-CZ-NH2	7.78	124.19	120.30
1	C	357	ASP	CB-CG-OD1	7.75	125.27	118.30
1	E	293	ILE	O-C-N	-7.75	110.31	122.70
1	C	216	ASP	CB-CG-OD2	-7.75	111.33	118.30
1	E	187	ARG	NE-CZ-NH2	-7.75	116.43	120.30
1	A	216	ASP	CB-CG-OD1	7.74	125.27	118.30
1	E	106	ASP	CB-CG-OD1	-7.73	111.35	118.30
1	G	312	ARG	CD-NE-CZ	7.72	134.41	123.60
1	A	295	ARG	NE-CZ-NH2	-7.71	116.44	120.30
1	E	217	ARG	CD-NE-CZ	7.71	134.40	123.60
1	A	300	VAL	CA-CB-CG1	7.71	122.46	110.90
1	C	176	PRO	N-CD-CG	-7.68	91.68	103.20
1	G	431	ARG	NE-CZ-NH1	7.66	124.13	120.30
1	E	165	TYR	CB-CG-CD1	-7.63	116.42	121.00
1	C	161	LYS	CA-CB-CG	7.62	130.17	113.40
1	E	217	ARG	NE-CZ-NH1	7.59	124.10	120.30
2	L	100	ARG	CD-NE-CZ	7.59	134.23	123.60
1	G	285	ARG	NE-CZ-NH1	7.56	124.08	120.30
1	C	351	ASP	CB-CG-OD1	7.45	125.00	118.30
1	E	213	ARG	NE-CZ-NH1	-7.38	116.61	120.30
1	A	396	ASP	CB-CG-OD1	7.36	124.93	118.30
1	E	131	ARG	NE-CZ-NH2	7.35	123.98	120.30
1	E	340	ASP	CB-CG-OD1	7.30	124.87	118.30
1	G	216	ASP	CB-CG-OD1	7.28	124.85	118.30
1	E	253	ARG	CD-NE-CZ	7.23	133.72	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	119	SER	O-C-N	-7.20	111.17	122.70
2	J	42	LEU	N-CA-CB	7.17	124.75	110.40
1	C	109	GLU	OE1-CD-OE2	-7.16	114.71	123.30
1	C	35	ASP	CB-CG-OD1	7.14	124.73	118.30
1	E	215	ARG	NH1-CZ-NH2	-7.13	111.55	119.40
1	C	103	TYR	CB-CG-CD2	7.13	125.28	121.00
1	G	375	LEU	CA-CB-CG	7.11	131.65	115.30
1	C	144	TYR	CB-CG-CD1	7.10	125.26	121.00
1	C	339	ARG	NE-CZ-NH1	7.09	123.85	120.30
2	J	43	GLU	OE1-CD-OE2	7.07	131.79	123.30
2	J	65	ARG	NE-CZ-NH1	7.05	123.83	120.30
1	A	176	PRO	N-CA-CB	7.05	111.76	103.30
1	G	213	ARG	NE-CZ-NH2	-7.00	116.80	120.30
1	E	268	ASP	CB-CG-OD1	7.00	124.60	118.30
1	E	375	LEU	CA-CB-CG	7.00	131.39	115.30
2	I	65	ARG	NE-CZ-NH2	-6.93	116.84	120.30
1	G	121	VAL	CB-CA-C	6.93	124.56	111.40
2	J	28	ARG	NE-CZ-NH1	6.91	123.76	120.30
1	G	421	ARG	NE-CZ-NH1	6.86	123.73	120.30
1	C	25	TYR	CB-CG-CD2	6.80	125.08	121.00
1	A	204	GLU	OE1-CD-OE2	-6.74	115.21	123.30
1	E	167	ARG	NE-CZ-NH1	6.72	123.66	120.30
1	E	360	ARG	CD-NE-CZ	6.71	133.00	123.60
1	E	350	ARG	NE-CZ-NH1	6.71	123.65	120.30
1	E	176	PRO	CA-N-CD	-6.68	102.15	111.50
1	C	131	ARG	NE-CZ-NH2	6.65	123.62	120.30
1	C	134	ARG	NE-CZ-NH2	-6.63	116.98	120.30
1	A	100	TYR	CB-CG-CD1	6.63	124.98	121.00
1	C	217	ARG	CD-NE-CZ	6.60	132.84	123.60
1	C	360	ARG	NE-CZ-NH1	6.60	123.60	120.30
1	G	269	TYR	CA-CB-CG	6.60	125.94	113.40
1	E	319	ARG	NE-CZ-NH1	-6.57	117.01	120.30
1	G	351	ASP	CB-CG-OD1	6.56	124.20	118.30
2	J	32	TYR	CB-CG-CD1	6.50	124.90	121.00
1	A	143	ALA	CB-CA-C	6.48	119.82	110.10
1	A	100	TYR	CB-CG-CD2	-6.47	117.12	121.00
2	K	108	ARG	NE-CZ-NH2	-6.46	117.07	120.30
2	J	32	TYR	CB-CG-CD2	-6.46	117.13	121.00
1	G	231	GLU	OE1-CD-OE2	-6.45	115.56	123.30
1	E	176	PRO	N-CA-CB	6.44	111.03	103.30
1	C	110	GLU	O-C-N	-6.42	112.29	123.20
1	E	72	ASP	CB-CG-OD2	-6.38	112.55	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	109	GLU	OE1-CD-OE2	-6.38	115.64	123.30
1	C	285	ARG	NE-CZ-NH1	6.36	123.48	120.30
1	G	143	ALA	CB-CA-C	6.35	119.62	110.10
1	A	249	ASP	CB-CG-OD1	6.33	124.00	118.30
1	E	357	ASP	CB-CG-OD1	6.33	124.00	118.30
1	C	252	LYS	CD-CE-NZ	6.33	126.25	111.70
1	G	187	ARG	NH1-CZ-NH2	6.30	126.33	119.40
1	A	215	ARG	NE-CZ-NH2	6.30	123.45	120.30
1	E	72	ASP	CB-CG-OD1	6.28	123.95	118.30
2	K	100	ARG	NH1-CZ-NH2	6.27	126.30	119.40
1	E	263	PRO	O-C-N	-6.25	112.69	122.70
1	E	198	ASP	CB-CG-OD1	-6.25	112.68	118.30
1	C	266	MET	CA-CB-CG	6.22	123.88	113.30
1	C	288	GLY	CA-C-O	-6.20	109.43	120.60
1	C	269	TYR	CA-CB-CG	6.20	125.17	113.40
1	A	360	ARG	NE-CZ-NH1	6.19	123.39	120.30
1	G	24	TYR	CB-CG-CD1	6.19	124.71	121.00
1	C	302	ASP	CB-CG-OD1	-6.18	112.74	118.30
1	E	218	PHE	CB-CG-CD1	6.18	125.12	120.80
2	K	105	ASP	CB-CG-OD1	6.17	123.86	118.30
1	A	269	TYR	CA-CB-CG	6.17	125.12	113.40
1	E	269	TYR	CA-CB-CG	6.17	125.12	113.40
1	G	65	THR	O-C-N	-6.16	112.84	122.70
1	A	283	TYR	CB-CG-CD2	-6.16	117.30	121.00
1	G	360	ARG	CD-NE-CZ	6.16	132.23	123.60
1	G	250	MET	CG-SD-CE	6.15	110.04	100.20
1	C	110	GLU	OE1-CD-OE2	-6.15	115.92	123.30
1	E	108	PHE	N-CA-CB	-6.15	99.53	110.60
2	I	42	LEU	CB-CG-CD2	-6.15	100.55	111.00
2	L	1	MET	CA-CB-CG	6.15	123.75	113.30
1	A	144	TYR	CB-CG-CD1	6.13	124.68	121.00
1	G	302	ASP	CB-CG-OD2	-6.13	112.78	118.30
1	E	131	ARG	CG-CD-NE	6.12	124.64	111.80
1	G	217	ARG	NE-CZ-NH1	6.11	123.35	120.30
1	A	217	ARG	NE-CZ-NH2	6.09	123.35	120.30
1	A	231	GLU	OE1-CD-OE2	-6.09	115.99	123.30
2	K	31	ASP	CB-CG-OD2	-6.07	112.84	118.30
1	A	357	ASP	CB-CG-OD1	6.05	123.74	118.30
2	J	100	ARG	NE-CZ-NH2	-6.05	117.28	120.30
1	C	339	ARG	NE-CZ-NH2	-6.03	117.29	120.30
2	J	33	LEU	CB-CG-CD1	6.00	121.21	111.00
1	E	421	ARG	NE-CZ-NH1	6.00	123.30	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	446	ARG	NE-CZ-NH1	5.99	123.30	120.30
1	C	175	LYS	O-C-N	-5.98	109.73	121.10
1	G	426	ALA	O-C-N	-5.97	113.14	122.70
1	A	302	ASP	CB-CG-OD1	5.95	123.66	118.30
1	C	218	PHE	CB-CG-CD1	5.94	124.96	120.80
1	A	340	ASP	CB-CG-OD1	5.93	123.64	118.30
1	C	153	HIS	CA-CB-CG	-5.93	103.52	113.60
1	G	35	ASP	CB-CG-OD1	5.91	123.62	118.30
1	G	252	LYS	CD-CE-NZ	5.90	125.27	111.70
1	G	319	ARG	NE-CZ-NH1	5.89	123.25	120.30
1	E	223	GLU	OE1-CD-OE2	-5.88	116.24	123.30
1	A	269	TYR	CB-CG-CD1	5.87	124.52	121.00
1	A	375	LEU	CA-CB-CG	5.87	128.81	115.30
1	A	435	ARG	NE-CZ-NH2	-5.87	117.36	120.30
1	A	139	ARG	NE-CZ-NH1	-5.86	117.37	120.30
1	A	247	CYS	CA-CB-SG	-5.85	103.47	114.00
1	E	118	THR	CA-CB-CG2	5.83	120.57	112.40
1	G	187	ARG	NE-CZ-NH1	-5.83	117.38	120.30
1	G	139	ARG	NE-CZ-NH2	5.83	123.22	120.30
2	K	66	TYR	CG-CD1-CE1	-5.83	116.64	121.30
1	A	106	ASP	CB-CG-OD2	5.81	123.53	118.30
1	E	340	ASP	CB-CG-OD2	-5.79	113.09	118.30
1	A	197	LEU	O-C-N	-5.79	113.44	122.70
1	A	83	ARG	NE-CZ-NH2	-5.78	117.41	120.30
2	J	65	ARG	NE-CZ-NH2	-5.77	117.41	120.30
1	G	266	MET	CA-CB-CG	5.77	123.10	113.30
1	E	311	PHE	CB-CG-CD1	-5.76	116.77	120.80
1	G	283	TYR	CB-CG-CD2	-5.74	117.56	121.00
1	A	357	ASP	CB-CG-OD2	-5.72	113.15	118.30
1	G	217	ARG	CG-CD-NE	5.72	123.82	111.80
1	C	175	LYS	C-N-CD	-5.71	108.03	120.60
1	A	29	TYR	CB-CG-CD2	-5.70	117.58	121.00
1	G	295	ARG	NE-CZ-NH2	-5.67	117.47	120.30
2	J	66	TYR	CB-CG-CD1	-5.67	117.60	121.00
1	G	88	GLU	OE1-CD-OE2	-5.66	116.51	123.30
2	J	93	GLU	OE1-CD-OE2	-5.66	116.51	123.30
2	J	109	GLU	OE1-CD-OE2	-5.65	116.52	123.30
1	A	17	VAL	CA-CB-CG2	5.65	119.37	110.90
1	E	357	ASP	CB-CG-OD2	-5.64	113.22	118.30
1	G	350	ARG	NE-CZ-NH1	5.64	123.12	120.30
2	J	66	TYR	O-C-N	5.64	131.72	122.70
1	C	121	VAL	CB-CA-C	5.62	122.08	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	41	ARG	NE-CZ-NH2	5.62	123.11	120.30
1	G	239	TYR	CB-CG-CD1	5.60	124.36	121.00
1	C	25	TYR	CB-CG-CD1	-5.59	117.65	121.00
1	G	324	ASP	O-C-N	-5.57	113.80	122.70
2	J	24	ASP	CB-CG-OD2	5.56	123.30	118.30
2	K	93	GLU	OE1-CD-OE2	-5.56	116.63	123.30
1	A	153	HIS	CA-CB-CG	-5.55	104.16	113.60
1	G	460	GLU	N-CA-CB	5.55	120.59	110.60
1	E	444	ILE	CA-C-O	5.54	131.74	120.10
1	E	41	ARG	NE-CZ-NH2	5.54	123.07	120.30
1	E	358	ARG	NE-CZ-NH1	5.54	123.07	120.30
2	L	93	GLU	OE1-CD-OE2	-5.54	116.66	123.30
1	A	252	LYS	CD-CE-NZ	5.53	124.42	111.70
1	A	435	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	C	291	LEU	CB-CG-CD1	-5.53	101.61	111.00
1	E	121	VAL	N-CA-CB	-5.53	99.34	111.50
1	C	215	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	G	161	LYS	CA-CB-CG	5.51	125.53	113.40
1	A	205	ASN	O-C-N	-5.50	113.89	122.70
1	A	132	ALA	N-CA-CB	5.48	117.77	110.10
1	G	247	CYS	CA-CB-SG	-5.47	104.15	114.00
1	C	204	GLU	OE1-CD-OE2	-5.46	116.75	123.30
1	E	293	ILE	C-N-CA	5.46	135.34	121.70
1	E	303	ARG	NH1-CZ-NH2	-5.45	113.41	119.40
2	J	31	ASP	CB-CG-OD1	5.44	123.19	118.30
1	C	226	TYR	CB-CG-CD2	5.43	124.26	121.00
2	I	93	GLU	OE1-CD-OE2	-5.43	116.79	123.30
1	C	303	ARG	CD-NE-CZ	5.40	131.16	123.60
1	E	253	ARG	CB-CG-CD	5.38	125.60	111.60
1	E	187	ARG	NH1-CZ-NH2	5.38	125.32	119.40
1	A	436	ASP	CB-CG-OD2	-5.38	113.46	118.30
1	E	324	ASP	CB-CG-OD1	-5.37	113.47	118.30
1	G	108	PHE	O-C-N	-5.37	114.11	122.70
1	G	283	TYR	CB-CG-CD1	5.36	124.22	121.00
1	E	435	ARG	NE-CZ-NH1	5.35	122.98	120.30
1	E	83	ARG	NH1-CZ-NH2	5.34	125.27	119.40
1	A	148	PHE	O-C-N	-5.33	114.17	122.70
1	G	144	TYR	CB-CG-CD2	-5.33	117.80	121.00
1	E	175	LYS	CA-C-O	-5.33	108.92	120.10
2	I	53	ARG	CD-NE-CZ	5.32	131.05	123.60
1	C	211	PHE	CB-CG-CD2	-5.31	117.08	120.80
1	C	397	ASP	O-C-N	-5.29	114.23	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	394	PHE	N-CA-CB	-5.29	101.08	110.60
1	A	161	LYS	CA-CB-CG	5.29	125.03	113.40
1	A	175	LYS	CB-CA-C	5.29	120.97	110.40
1	E	161	LYS	CA-CB-CG	5.29	125.03	113.40
1	C	82	GLY	N-CA-C	-5.28	99.89	113.10
1	E	263	PRO	N-CA-C	5.28	125.84	112.10
1	C	375	LEU	CA-CB-CG	5.28	127.44	115.30
1	C	250	MET	CA-CB-CG	5.26	122.24	113.30
1	G	167	ARG	NE-CZ-NH1	5.25	122.92	120.30
2	K	1	MET	CA-CB-CG	5.24	122.21	113.30
1	E	216	ASP	CB-CG-OD1	5.24	123.01	118.30
1	C	194	ARG	NE-CZ-NH2	5.23	122.92	120.30
1	A	225	LEU	CA-CB-CG	5.22	127.31	115.30
1	E	252	LYS	CD-CE-NZ	5.22	123.70	111.70
1	G	303	ARG	CG-CD-NE	5.22	122.75	111.80
1	A	215	ARG	CD-NE-CZ	5.21	130.90	123.60
1	G	194	ARG	NE-CZ-NH1	-5.21	117.69	120.30
1	G	369	VAL	CA-CB-CG2	5.21	118.71	110.90
1	E	121	VAL	CA-CB-CG1	5.20	118.70	110.90
1	G	218	PHE	CB-CG-CD2	-5.19	117.17	120.80
1	A	121	VAL	CB-CA-C	5.19	121.26	111.40
1	E	322	GLY	C-N-CA	5.19	133.20	122.30
2	J	109	GLU	CG-CD-OE1	5.19	128.67	118.30
1	A	257	ALA	O-C-N	-5.18	114.42	122.70
1	A	266	MET	CA-CB-CG	5.17	122.09	113.30
2	L	110	VAL	CB-CA-C	-5.17	101.58	111.40
1	E	228	ALA	N-CA-CB	5.16	117.33	110.10
1	C	398	SER	CA-CB-OG	-5.15	97.29	111.20
2	I	9	LEU	CB-CA-C	5.14	119.97	110.20
1	G	360	ARG	NE-CZ-NH2	-5.14	117.73	120.30
1	C	286	ASP	O-C-N	-5.14	114.48	122.70
1	C	79	ARG	NE-CZ-NH2	-5.13	117.73	120.30
1	A	369	VAL	CA-CB-CG2	5.12	118.58	110.90
1	A	128	LYS	CD-CE-NZ	-5.12	99.92	111.70
1	G	109	GLU	OE1-CD-OE2	-5.11	117.17	123.30
1	E	82	GLY	N-CA-C	-5.11	100.33	113.10
1	E	198	ASP	CB-CG-OD2	5.09	122.88	118.30
2	J	9	LEU	CA-CB-CG	5.09	127.00	115.30
1	G	134	ARG	NE-CZ-NH1	5.08	122.84	120.30
1	G	83	ARG	NE-CZ-NH1	5.08	122.84	120.30
1	C	234	GLU	CA-CB-CG	5.07	124.55	113.40
1	C	397	ASP	CA-C-O	5.05	130.70	120.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	421	ARG	NE-CZ-NH1	5.04	122.82	120.30
1	C	360	ARG	CD-NE-CZ	5.04	130.66	123.60
1	G	369	VAL	C-N-CA	5.04	134.30	121.70
1	C	208	SER	C-N-CA	5.04	134.29	121.70
1	G	239	TYR	CB-CG-CD2	-5.04	117.98	121.00
1	A	271	THR	O-C-N	-5.02	114.66	123.20
1	C	29	TYR	CB-CG-CD1	5.02	124.01	121.00
1	E	52	GLU	OE1-CD-OE2	-5.02	117.28	123.30
1	E	425	GLU	OE1-CD-OE2	-5.02	117.28	123.30
1	E	116	MET	CG-SD-CE	5.01	108.22	100.20
2	I	62	TYR	CB-CG-CD2	5.00	124.00	121.00
2	J	63	ASP	CB-CG-OD1	5.00	122.80	118.30

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	175	LYS	Peptide
1	A	330	THR	Mainchain
1	C	175	LYS	Mainchain
1	E	175	LYS	Peptide
1	E	243	THR	Mainchain
1	G	152	PRO	Mainchain
1	G	175	LYS	Peptide
1	G	201	KCX	Peptide
2	I	11	LYS	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3656	0	3565	94	0
1	C	3656	0	3565	80	0
1	E	3656	0	3564	76	0
1	G	3656	0	3564	79	0
2	I	1032	0	990	35	0
2	J	1032	0	990	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	K	1032	0	990	36	0
2	L	1032	0	990	38	1
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
4	A	21	0	7	0	0
4	C	21	0	6	1	0
4	E	21	0	7	0	0
4	G	21	0	7	0	0
5	A	112	0	0	13	0
5	C	121	0	0	15	0
5	E	132	0	0	11	0
5	G	133	0	0	10	3
5	I	34	0	0	1	0
5	J	44	0	0	3	0
5	K	41	0	0	6	0
5	L	47	0	0	6	0
All	All	19504	0	18245	439	4

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (439) 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:G:303:ARG:HG3	5:G:2084:HOH:O	1.58	1.03
2:K:22:THR:H	2:K:25:GLN:HE21	1.06	1.02
1:A:177:LYS:CD	5:A:2040:HOH:O	2.10	0.97
2:J:29:GLN:HB2	5:J:2016:HOH:O	1.67	0.95
2:J:22:THR:H	2:J:25:GLN:HE21	0.98	0.94
2:I:22:THR:H	2:I:25:GLN:HE21	1.03	0.92
2:K:42:LEU:HD22	5:K:2025:HOH:O	1.72	0.89
1:A:267:HIS:HD2	1:A:277:ASN:HD22	1.23	0.86
2:J:2:GLN:HG3	5:J:2001:HOH:O	1.75	0.86
1:A:177:LYS:HD2	5:A:2040:HOH:O	1.69	0.85
1:C:26:THR:HG22	1:C:29:TYR:HB2	1.62	0.82
1:G:267:HIS:CD2	1:G:277:ASN:HD22	1.97	0.82
1:G:414:ALA:HB3	1:G:415:PRO:HD3	1.62	0.80
1:E:140:ILE:HB	5:E:2105:HOH:O	1.82	0.80
1:A:267:HIS:CD2	1:A:277:ASN:HD22	2.00	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:22:THR:H	2:L:25:GLN:HE21	1.27	0.79
1:C:267:HIS:CD2	1:C:277:ASN:HD22	2.01	0.78
1:E:383:HIS:H	1:E:386:HIS:HD2	1.32	0.78
2:J:22:THR:N	2:J:25:GLN:HE21	1.80	0.77
1:G:267:HIS:HD2	1:G:277:ASN:HD22	1.33	0.77
1:E:267:HIS:CD2	1:E:277:ASN:HD22	2.04	0.76
1:E:26:THR:HG22	1:E:29:TYR:HB2	1.66	0.76
2:I:96:ASN:HB2	5:I:2025:HOH:O	1.86	0.75
1:E:241:ASN:ND2	1:E:243:THR:H	1.85	0.75
1:C:400:LEU:HD21	5:C:2106:HOH:O	1.86	0.75
1:A:26:THR:HG22	1:A:29:TYR:HB2	1.68	0.75
2:L:40:PRO:HG2	2:L:74:MET:HB2	1.69	0.74
2:K:89:GLU:HA	5:K:2032:HOH:O	1.88	0.74
1:E:414:ALA:HB3	1:E:415:PRO:HD3	1.68	0.74
1:E:239:TYR:HE2	1:E:401:GLN:HE22	1.33	0.73
2:I:22:THR:H	2:I:25:GLN:NE2	1.84	0.73
2:I:22:THR:N	2:I:25:GLN:HE21	1.82	0.73
1:E:292:HIS:HA	1:E:325:HIS:HB2	1.70	0.72
2:J:24:ASP:HB2	5:J:2013:HOH:O	1.88	0.72
1:G:113:VAL:HG11	1:G:274:PHE:CD1	2.25	0.72
1:C:383:HIS:H	1:C:386:HIS:HD2	1.38	0.71
1:A:414:ALA:HB3	1:A:415:PRO:HD3	1.71	0.71
2:K:22:THR:N	2:K:25:GLN:HE21	1.87	0.70
2:K:99:ILE:HG23	5:K:2018:HOH:O	1.92	0.70
1:A:383:HIS:H	1:A:386:HIS:HD2	1.36	0.69
1:A:241:ASN:HD22	1:A:243:THR:H	1.38	0.69
2:J:22:THR:H	2:J:25:GLN:NE2	1.81	0.69
1:G:26:THR:HG22	1:G:29:TYR:HB2	1.74	0.69
1:A:239:TYR:HE2	1:A:401:GLN:HE22	1.40	0.69
1:C:414:ALA:HB3	1:C:415:PRO:HD3	1.76	0.68
1:A:241:ASN:ND2	1:A:243:THR:H	1.92	0.67
1:A:177:LYS:CE	5:A:2040:HOH:O	2.40	0.67
1:A:75:THR:HG22	1:A:76:ASN:H	1.59	0.67
1:C:241:ASN:ND2	1:C:243:THR:H	1.93	0.67
1:E:295:ARG:HG3	1:E:298:HIS:CD2	2.31	0.66
2:I:32:TYR:CE2	2:I:113:ILE:HD11	2.30	0.66
2:I:68:THR:HG21	2:J:6:ILE:HD11	1.76	0.66
1:E:267:HIS:HD2	1:E:277:ASN:HD22	1.41	0.66
1:G:292:HIS:HA	1:G:325:HIS:HB2	1.77	0.66
1:A:328:SER:HB3	5:A:2069:HOH:O	1.95	0.66
2:J:32:TYR:CE2	2:J:113:ILE:HD11	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:161:LYS:HE2	1:G:219:LEU:HD23	1.77	0.65
1:C:267:HIS:HD2	1:C:277:ASN:HD22	1.44	0.65
1:C:321:SER:HB2	5:C:2088:HOH:O	1.95	0.65
1:C:239:TYR:HE2	1:C:401:GLN:HE22	1.43	0.65
1:G:431:ARG:HH21	1:G:432:ASN:HD21	1.43	0.65
1:C:394:PHE:HB2	5:C:2106:HOH:O	1.96	0.65
1:A:379:SER:HB2	1:A:401:GLN:HB2	1.77	0.65
5:E:2064:HOH:O	2:K:10:LYS:HE3	1.95	0.65
2:L:92:LYS:HD2	2:L:93:GLU:N	2.12	0.65
1:G:303:ARG:HD2	5:G:2083:HOH:O	1.96	0.64
1:G:239:TYR:HE2	1:G:401:GLN:HE22	1.44	0.64
1:C:75:THR:HG22	1:C:76:ASN:H	1.62	0.64
2:L:89:GLU:HG2	2:L:92:LYS:HE2	1.78	0.63
1:C:440:GLU:HG2	5:C:2115:HOH:O	1.99	0.63
1:G:75:THR:HG22	1:G:76:ASN:H	1.62	0.63
2:K:32:TYR:CE2	2:K:113:ILE:HD11	2.32	0.63
1:C:292:HIS:HA	1:C:325:HIS:HB2	1.80	0.62
2:J:92:LYS:HD2	2:J:93:GLU:N	2.14	0.62
1:A:115:ASN:HB2	5:A:2030:HOH:O	1.99	0.62
2:K:92:LYS:HD2	2:K:93:GLU:N	2.14	0.62
1:A:161:LYS:HE2	1:C:219:LEU:HD23	1.81	0.62
1:C:173:THR:HB	1:C:175:LYS:HE2	1.81	0.62
1:E:241:ASN:HD22	1:E:243:THR:H	1.47	0.62
2:J:32:TYR:HE2	2:J:113:ILE:HD11	1.64	0.62
1:A:241:ASN:HA	1:A:266:MET:HG3	1.82	0.62
1:C:274:PHE:CD1	5:C:2088:HOH:O	2.51	0.62
2:L:32:TYR:CE2	2:L:113:ILE:HD11	2.34	0.62
2:J:89:GLU:HG2	2:J:92:LYS:HE2	1.83	0.61
2:K:42:LEU:HB3	5:K:2018:HOH:O	2.00	0.61
2:L:107:ASN:HB2	5:L:2041:HOH:O	1.98	0.61
1:E:385:TRP:CZ2	1:E:459:CYS:HB3	2.36	0.61
1:E:241:ASN:HA	1:E:266:MET:HG3	1.82	0.61
1:E:229:GLN:HE21	1:E:236:LYS:H	1.47	0.61
1:A:376:PRO:HA	5:A:2069:HOH:O	1.99	0.61
1:G:229:GLN:HE21	1:G:236:LYS:H	1.48	0.60
1:A:177:LYS:CG	5:A:2040:HOH:O	2.43	0.60
1:E:409:HIS:CG	1:E:410:PRO:HD2	2.36	0.60
1:E:173:THR:HB	1:E:175:LYS:HE2	1.84	0.60
1:E:155:ILE:HG12	1:E:375:LEU:HD13	1.84	0.60
1:G:234:GLU:HB3	2:L:13:GLU:OE2	2.02	0.60
1:C:123:ASN:HA	5:C:2044:HOH:O	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:72:LEU:HB3	2:I:73:PRO:HD2	1.84	0.60
2:K:86:GLU:HB3	5:K:2025:HOH:O	2.01	0.60
1:E:366:GLN:NE2	5:E:2105:HOH:O	2.35	0.60
1:G:377:VAL:HG22	1:G:399:VAL:HB	1.84	0.60
1:G:340:ASP:HB2	5:G:2092:HOH:O	2.01	0.59
1:E:122:GLY:HA3	5:E:2037:HOH:O	2.01	0.59
1:C:345:PHE:HA	1:C:348:LEU:HD12	1.84	0.59
1:G:230:ALA:HA	5:G:2066:HOH:O	2.02	0.59
1:G:140:ILE:H	1:G:140:ILE:HD12	1.68	0.58
1:C:360:ARG:NH2	5:C:2098:HOH:O	2.35	0.58
2:I:32:TYR:HE2	2:I:113:ILE:HD11	1.65	0.58
2:L:58:SER:HB2	2:L:59:PRO:HD2	1.84	0.58
1:E:429:GLN:O	1:E:433:GLU:HG3	2.03	0.58
1:A:318:LEU:HG	1:A:326:ILE:HD12	1.85	0.58
2:K:89:GLU:HG2	2:K:92:LYS:HE2	1.84	0.58
1:A:429:GLN:O	1:A:433:GLU:HG3	2.04	0.58
2:L:32:TYR:HE2	2:L:113:ILE:HD11	1.68	0.57
2:K:32:TYR:HE2	2:K:113:ILE:HD11	1.70	0.57
2:I:92:LYS:HD2	2:I:93:GLU:N	2.19	0.57
1:E:318:LEU:HG	1:E:326:ILE:HD12	1.86	0.57
1:A:385:TRP:CZ2	1:A:459:CYS:HB3	2.40	0.56
2:K:22:THR:H	2:K:25:GLN:NE2	1.90	0.56
2:L:121:ALA:HB3	5:L:2047:HOH:O	2.04	0.56
1:E:387:MET:HB3	1:E:388:PRO:HD3	1.88	0.56
1:C:175:LYS:H	1:C:407:LEU:HD22	1.71	0.56
2:I:89:GLU:HG2	2:I:92:LYS:HE2	1.87	0.56
1:E:204:GLU:HG2	1:E:205:ASN:N	2.21	0.55
1:G:200:THR:OG1	1:G:238:HIS:HD2	1.90	0.55
2:K:33:LEU:HB2	2:K:113:ILE:HG13	1.89	0.55
1:G:341:ILE:HD11	1:G:475:VAL:HG23	1.88	0.55
1:C:429:GLN:O	1:C:433:GLU:HG3	2.07	0.55
1:G:204:GLU:HG2	1:G:205:ASN:N	2.22	0.55
2:L:22:THR:N	2:L:25:GLN:HE21	2.01	0.55
1:C:284:CYS:HB3	1:C:289:LEU:O	2.07	0.55
1:C:316:LYS:HE2	1:C:366:GLN:HG2	1.88	0.55
1:E:194:ARG:NH1	2:K:6:ILE:HD12	2.22	0.55
1:A:316:LYS:HE2	1:A:366:GLN:HG2	1.88	0.55
1:A:284:CYS:HB3	1:A:289:LEU:O	2.07	0.55
1:E:26:THR:CG2	1:E:29:TYR:HB2	2.37	0.54
1:C:414:ALA:O	1:C:418:VAL:HG23	2.07	0.54
1:C:409:HIS:CG	1:C:410:PRO:HD2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:241:ASN:ND2	1:G:243:THR:H	2.06	0.54
1:E:208:SER:HB2	1:E:214:TRP:HB3	1.90	0.54
1:E:400:LEU:HD21	5:E:2108:HOH:O	2.06	0.54
1:E:24:TYR:CD2	1:E:59:ALA:HB2	2.43	0.54
1:A:219:LEU:HG	5:L:2026:HOH:O	2.07	0.54
1:C:62:SER:OG	1:C:63:THR:N	2.41	0.54
1:G:175:LYS:H	1:G:407:LEU:HD22	1.73	0.54
1:E:173:THR:HG23	1:E:201:KCX:HG2	1.89	0.53
1:E:202:ASP:OD1	1:E:238:HIS:HE1	1.91	0.53
1:A:50:PRO:HG3	1:A:97:TYR:CZ	2.43	0.53
1:C:373:GLY:N	5:C:2104:HOH:O	2.41	0.53
1:G:316:LYS:HE2	1:G:366:GLN:HG2	1.91	0.53
1:E:173:THR:HA	1:E:201:KCX:HG3	1.90	0.53
1:G:315:ALA:HB1	1:G:349:LEU:HD21	1.91	0.53
1:G:284:CYS:HB3	1:G:289:LEU:O	2.08	0.53
1:A:229:GLN:HE21	1:A:236:LYS:H	1.56	0.53
1:C:50:PRO:HG3	1:C:97:TYR:CZ	2.43	0.53
1:G:18:LYS:HB3	1:G:22:LEU:HD12	1.90	0.53
1:G:267:HIS:HD2	1:G:277:ASN:ND2	2.06	0.53
1:E:75:THR:HG22	1:E:76:ASN:H	1.73	0.53
1:E:473:ASP:HB3	5:E:2091:HOH:O	2.09	0.53
1:A:155:ILE:HG13	1:A:373:GLY:O	2.10	0.52
2:I:33:LEU:HB2	2:I:113:ILE:HG13	1.91	0.52
2:I:58:SER:HB2	2:I:59:PRO:HD2	1.91	0.52
1:A:409:HIS:CG	1:A:410:PRO:HD2	2.44	0.52
1:C:274:PHE:HD1	5:C:2088:HOH:O	1.90	0.52
1:E:318:LEU:CG	1:E:326:ILE:HD12	2.40	0.52
2:K:14:THR:O	2:K:15:LEU:HB2	2.09	0.52
1:A:467:PHE:HA	5:A:2106:HOH:O	2.09	0.52
1:C:431:ARG:HH21	1:C:432:ASN:HD21	1.57	0.52
2:L:120:PRO:HG2	2:L:123:TYR:CD2	2.44	0.52
1:C:241:ASN:HA	1:C:266:MET:HG3	1.91	0.52
1:G:113:VAL:HG11	1:G:274:PHE:CE1	2.44	0.52
1:A:414:ALA:O	1:A:418:VAL:HG23	2.10	0.52
1:G:241:ASN:HD22	1:G:243:THR:H	1.56	0.52
1:G:209:GLN:HB3	1:G:210:PRO:HD2	1.92	0.52
2:I:21:LEU:HA	2:I:25:GLN:NE2	2.25	0.52
1:A:190:TYR:CZ	1:A:194:ARG:HD3	2.45	0.52
1:C:337:GLY:HA2	5:C:2092:HOH:O	2.09	0.51
2:I:6:ILE:HD11	2:L:68:THR:HG21	1.92	0.51
1:G:155:ILE:HG12	1:G:375:LEU:HD13	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:334:LYS:HG3	1:A:335:LEU:HG	1.92	0.51
2:K:104:PHE:HB3	5:K:2034:HOH:O	2.09	0.51
1:A:382:ILE:HA	1:A:386:HIS:CD2	2.46	0.51
2:J:40:PRO:HG2	2:J:74:MET:HB2	1.92	0.51
2:I:51:VAL:HG13	2:I:62:TYR:HB3	1.92	0.51
1:E:451:TRP:CH2	2:K:19:PRO:HD3	2.46	0.51
1:A:451:TRP:CZ3	2:I:19:PRO:HD3	2.46	0.50
1:C:26:THR:CG2	1:C:29:TYR:HB2	2.37	0.50
1:C:186:GLY:HA3	2:I:66:TYR:OH	2.11	0.50
1:A:295:ARG:HG3	1:A:298:HIS:CD2	2.46	0.50
1:C:448:ALA:HA	1:C:451:TRP:NE1	2.27	0.50
2:J:10:LYS:HB3	2:J:50:PHE:CZ	2.46	0.50
1:G:295:ARG:HG3	1:G:298:HIS:CD2	2.47	0.50
1:A:24:TYR:CD2	1:A:59:ALA:HB2	2.47	0.50
1:C:137:ASP:OD1	1:C:138:LEU:N	2.43	0.50
2:I:39:VAL:HG11	2:I:75:PHE:CD1	2.47	0.50
1:E:392:GLU:HA	5:E:2109:HOH:O	2.10	0.49
2:L:22:THR:H	2:L:25:GLN:NE2	2.05	0.49
1:E:431:ARG:HH21	1:E:432:ASN:HD21	1.60	0.49
1:C:44:PRO:HD2	1:C:95:ASN:O	2.12	0.49
2:K:71:LYS:HD3	2:L:1:MET:HG2	1.94	0.49
1:G:383:HIS:H	1:G:386:HIS:HD2	1.59	0.49
1:C:241:ASN:HD22	1:C:243:THR:H	1.58	0.49
1:A:26:THR:CG2	1:A:29:TYR:HB2	2.39	0.49
1:G:451:TRP:CZ3	2:L:19:PRO:HD3	2.48	0.49
1:E:62:SER:OG	1:E:63:THR:N	2.44	0.49
1:G:431:ARG:HE	1:G:432:ASN:ND2	2.11	0.48
1:C:289:LEU:HD23	2:J:59:PRO:HB3	1.94	0.48
1:A:383:HIS:CE1	1:A:385:TRP:HB2	2.48	0.48
1:A:357:ASP:HA	5:A:2083:HOH:O	2.12	0.48
1:G:50:PRO:HG3	1:G:97:TYR:CZ	2.48	0.48
2:K:42:LEU:HD21	2:K:87:LEU:HA	1.94	0.48
1:A:185:TYR:O	1:A:189:VAL:HG23	2.12	0.48
1:G:472:MET:CB	5:G:2084:HOH:O	2.61	0.48
1:G:303:ARG:CD	5:G:2083:HOH:O	2.59	0.48
1:G:241:ASN:HA	1:G:266:MET:HG3	1.96	0.48
1:A:387:MET:HB3	1:A:388:PRO:HD3	1.95	0.48
1:A:125:PHE:CG	1:A:133:LEU:HD23	2.49	0.48
1:E:451:TRP:CZ3	2:K:19:PRO:HD3	2.49	0.48
1:G:327:HIS:CG	5:G:2088:HOH:O	2.67	0.48
1:G:431:ARG:HE	1:G:432:ASN:HD22	1.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:318:LEU:CG	1:A:326:ILE:HD12	2.44	0.48
1:C:385:TRP:CZ2	1:C:459:CYS:HB3	2.49	0.48
1:A:208:SER:HB2	1:A:214:TRP:HB3	1.96	0.47
1:A:456:ALA:O	1:A:460:GLU:HG3	2.14	0.47
1:C:171:GLY:HA2	1:C:199:PHE:O	2.13	0.47
1:A:194:ARG:HD2	1:A:231:GLU:OE2	2.15	0.47
1:A:451:TRP:CH2	2:I:19:PRO:HD3	2.49	0.47
1:G:184:ASN:ND2	1:G:187:ARG:HH11	2.12	0.47
1:A:294:HIS:CE1	1:A:296:ALA:HB2	2.49	0.47
2:L:65:ARG:NH2	5:L:2026:HOH:O	2.45	0.47
1:A:341:ILE:HD11	1:A:475:VAL:HG23	1.95	0.47
1:A:292:HIS:HA	1:A:325:HIS:HB2	1.97	0.47
1:A:219:LEU:HD11	2:L:61:TYR:HB2	1.96	0.47
1:C:234:GLU:HB3	2:J:13:GLU:OE2	2.15	0.47
5:C:2054:HOH:O	2:J:60:GLY:HA3	2.13	0.47
1:E:281:SER:OG	1:E:322:GLY:HA3	2.15	0.47
2:I:89:GLU:HG2	2:I:92:LYS:CE	2.44	0.47
1:A:251:MET:HE1	1:A:283:TYR:CD1	2.50	0.47
1:E:184:ASN:ND2	1:E:187:ARG:HH11	2.13	0.47
2:I:68:THR:HG21	2:J:6:ILE:CD1	2.43	0.47
2:K:10:LYS:HB3	2:K:50:PHE:CZ	2.50	0.47
2:K:51:VAL:HG13	2:K:62:TYR:HB3	1.96	0.47
1:E:302:ASP:OD2	1:E:311:PHE:HB2	2.15	0.47
1:E:160:ASP:HB3	1:G:183:LYS:HD3	1.97	0.47
1:C:31:THR:N	5:C:2015:HOH:O	2.48	0.47
1:C:451:TRP:CZ3	2:J:19:PRO:HD3	2.50	0.46
2:L:10:LYS:HB3	2:L:50:PHE:CZ	2.50	0.46
1:C:297:MET:O	1:C:297:MET:HG2	2.15	0.46
1:A:187:ARG:HD2	5:A:2042:HOH:O	2.15	0.46
1:E:131:ARG:HG2	5:E:2040:HOH:O	2.15	0.46
1:G:303:ARG:HA	5:G:2083:HOH:O	2.14	0.46
1:C:26:THR:O	1:C:85:TYR:HA	2.15	0.46
1:A:431:ARG:HE	1:A:432:ASN:ND2	2.12	0.46
2:K:72:LEU:HB3	2:K:73:PRO:HD2	1.97	0.46
1:E:377:VAL:HG22	1:E:399:VAL:HB	1.96	0.46
1:C:165:TYR:CD1	2:J:111:GLN:HB2	2.51	0.46
1:E:50:PRO:HG3	1:E:97:TYR:CZ	2.50	0.46
1:E:26:THR:HG22	1:E:26:THR:O	2.16	0.46
1:G:219:LEU:HD11	2:K:61:TYR:HB2	1.98	0.46
2:K:68:THR:HG21	2:L:6:ILE:HD11	1.97	0.46
2:I:14:THR:O	2:I:15:LEU:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:316:LYS:HE2	1:E:366:GLN:HG2	1.98	0.46
1:E:83:ARG:NH1	5:E:2024:HOH:O	2.37	0.46
1:A:148:PHE:CD2	1:A:320:LEU:HB3	2.51	0.46
2:L:33:LEU:HB2	2:L:113:ILE:HG13	1.98	0.46
1:C:431:ARG:HE	1:C:432:ASN:ND2	2.14	0.46
1:C:184:ASN:ND2	1:C:187:ARG:HH11	2.14	0.46
1:G:347:ASP:OD2	1:G:360:ARG:NH1	2.48	0.45
1:E:414:ALA:O	1:E:418:VAL:HG23	2.15	0.45
1:A:229:GLN:HG2	5:A:2051:HOH:O	2.15	0.45
1:G:169:LEU:HD13	1:G:199:PHE:CE2	2.51	0.45
1:C:18:LYS:HB3	1:C:22:LEU:HD12	1.98	0.45
1:C:295:ARG:HG3	1:C:298:HIS:CD2	2.51	0.45
1:A:113:VAL:HG11	1:A:274:PHE:CD1	2.52	0.45
1:A:267:HIS:HD2	1:A:277:ASN:ND2	2.03	0.45
1:E:175:LYS:H	1:E:407:LEU:HD22	1.81	0.45
2:J:5:PRO:HG2	2:J:9:LEU:HD11	1.98	0.45
1:G:151:PRO:HA	1:G:152:PRO:HD3	1.91	0.45
1:G:36:ILE:N	1:G:36:ILE:HD12	2.32	0.45
2:J:51:VAL:HG13	2:J:62:TYR:HB3	1.98	0.45
2:L:24:ASP:HB2	5:L:2010:HOH:O	2.16	0.45
1:C:379:SER:HB2	1:C:401:GLN:HB2	1.97	0.45
1:A:169:LEU:HD13	1:A:199:PHE:CE2	2.52	0.45
1:C:229:GLN:HE21	1:C:236:LYS:H	1.65	0.45
1:G:24:TYR:CD2	1:G:59:ALA:HB2	2.52	0.45
2:L:79:ASP:HB3	2:L:82:GLN:HG3	1.99	0.45
1:G:252:LYS:HB3	1:G:252:LYS:HE3	1.79	0.45
1:A:289:LEU:HD23	2:I:59:PRO:HB3	1.98	0.45
1:C:267:HIS:HD2	1:C:277:ASN:ND2	2.14	0.44
1:A:345:PHE:HA	1:A:348:LEU:HD12	1.98	0.44
2:L:51:VAL:HG13	2:L:62:TYR:HB3	1.98	0.44
1:E:149:GLN:HG2	1:E:149:GLN:O	2.17	0.44
2:L:21:LEU:HA	2:L:25:GLN:HE21	1.82	0.44
1:E:448:ALA:HA	1:E:451:TRP:NE1	2.32	0.44
1:C:169:LEU:HD13	1:C:199:PHE:CE2	2.53	0.44
1:A:435:ARG:HD2	1:A:440:GLU:OE1	2.17	0.44
1:E:36:ILE:HD12	1:E:36:ILE:N	2.33	0.44
1:C:192:CYS:O	1:C:197:LEU:HD12	2.17	0.44
1:A:119:SER:O	1:A:120:ILE:C	2.55	0.44
1:G:192:CYS:HB3	1:G:197:LEU:HD12	1.98	0.44
1:A:455:LEU:HG	1:A:459:CYS:SG	2.58	0.44
1:A:184:ASN:ND2	1:A:187:ARG:HH11	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:267:HIS:HD2	1:E:277:ASN:ND2	2.13	0.44
5:C:2053:HOH:O	2:J:111:GLN:HG3	2.17	0.44
2:L:5:PRO:HB2	2:L:9:LEU:CD1	2.48	0.44
1:A:202:ASP:OD1	1:A:238:HIS:HE1	2.01	0.44
1:C:194:ARG:NH1	2:J:6:ILE:HD12	2.33	0.44
1:A:431:ARG:HH21	1:A:432:ASN:HD21	1.66	0.44
2:I:22:THR:N	2:I:25:GLN:HB2	2.33	0.43
1:E:138:LEU:O	1:E:316:LYS:NZ	2.48	0.43
2:L:21:LEU:HD22	2:L:25:GLN:HB3	1.99	0.43
1:G:214:TRP:CE3	1:G:253:ARG:HG2	2.53	0.43
1:E:383:HIS:CE1	1:E:385:TRP:HB2	2.52	0.43
1:A:448:ALA:HA	1:A:451:TRP:NE1	2.33	0.43
1:E:169:LEU:HD13	1:E:199:PHE:CE2	2.53	0.43
2:L:72:LEU:HB3	2:L:73:PRO:HD2	2.00	0.43
1:C:225:LEU:C	1:C:225:LEU:HD12	2.39	0.43
1:C:151:PRO:HG2	1:C:372:PRO:O	2.19	0.43
1:A:336:GLU:HG3	5:A:2074:HOH:O	2.18	0.43
1:G:26:THR:CG2	1:G:29:TYR:HB2	2.46	0.43
1:C:75:THR:HG22	1:C:76:ASN:N	2.31	0.43
2:J:89:GLU:HG2	2:J:92:LYS:CE	2.47	0.43
1:C:407:LEU:HG	1:C:413:ASN:OD1	2.17	0.43
1:A:173:THR:HB	1:A:175:LYS:HE2	2.00	0.43
1:G:387:MET:HB3	1:G:388:PRO:HD3	2.01	0.43
1:A:113:VAL:HG21	1:A:321:SER:HB2	1.99	0.43
2:K:105:ASP:OD1	2:K:107:ASN:N	2.52	0.43
1:E:347:ASP:OD2	1:E:360:ARG:NH1	2.47	0.43
1:C:451:TRP:CH2	2:J:19:PRO:HD3	2.54	0.43
1:G:345:PHE:HA	1:G:348:LEU:HD12	2.01	0.43
2:I:89:GLU:O	2:I:92:LYS:HG3	2.17	0.43
2:K:79:ASP:HA	2:K:80:PRO:HD2	1.92	0.43
1:G:299:ALA:HA	1:G:302:ASP:OD1	2.18	0.43
2:L:42:LEU:HD21	2:L:87:LEU:HA	2.00	0.43
1:A:420:ASN:HD22	1:A:420:ASN:HA	1.66	0.43
1:A:26:THR:O	1:A:85:TYR:HA	2.19	0.43
2:K:58:SER:HB2	2:K:59:PRO:HD2	2.01	0.43
1:G:240:LEU:HD12	1:G:262:VAL:HG21	2.01	0.43
1:C:327:HIS:CG	5:C:2082:HOH:O	2.71	0.43
1:E:234:GLU:HB3	2:K:13:GLU:OE2	2.18	0.43
2:J:14:THR:O	2:J:15:LEU:HB2	2.18	0.42
1:G:297:MET:HG2	1:G:297:MET:O	2.19	0.42
2:I:120:PRO:HG2	2:I:123:TYR:CD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:234:GLU:OE2	2:J:13:GLU:HA	2.19	0.42
1:G:222:ALA:O	1:G:223:GLU:C	2.57	0.42
1:A:315:ALA:HB1	1:A:349:LEU:HD21	2.01	0.42
1:G:414:ALA:O	1:G:418:VAL:HG23	2.20	0.42
2:L:22:THR:OG1	2:L:25:GLN:HG3	2.19	0.42
2:K:14:THR:O	2:K:15:LEU:CB	2.66	0.42
1:G:209:GLN:HB3	1:G:210:PRO:CD	2.48	0.42
1:G:444:ILE:HG23	5:G:2113:HOH:O	2.18	0.42
1:E:192:CYS:HB3	1:E:197:LEU:HD12	2.01	0.42
1:A:376:PRO:HB3	5:A:2069:HOH:O	2.18	0.42
1:E:200:THR:OG1	1:E:238:HIS:HD2	2.02	0.42
1:A:294:HIS:ND1	1:A:296:ALA:HB2	2.35	0.42
1:C:252:LYS:HB3	1:C:252:LYS:HE3	1.83	0.42
2:I:72:LEU:HD23	2:I:72:LEU:HA	1.87	0.42
1:C:202:ASP:OD1	1:C:238:HIS:HE1	2.02	0.42
1:C:377:VAL:HG22	1:C:399:VAL:HB	2.01	0.42
2:K:99:ILE:HB	2:K:118:TYR:HB3	2.02	0.42
1:C:50:PRO:HB3	1:C:97:TYR:CD1	2.54	0.42
1:G:383:HIS:CE1	1:G:385:TRP:HB2	2.54	0.42
1:A:377:VAL:HG22	1:A:399:VAL:HB	2.02	0.42
1:A:267:HIS:HB2	1:A:280:LEU:HD23	2.01	0.42
2:I:71:LYS:NZ	2:I:89:GLU:OE2	2.47	0.42
1:G:241:ASN:ND2	1:G:243:THR:OG1	2.45	0.42
1:G:284:CYS:O	1:G:288:GLY:N	2.52	0.42
1:A:229:GLN:HE21	1:A:235:ILE:HA	1.84	0.42
2:I:14:THR:O	2:I:15:LEU:CB	2.67	0.42
2:K:120:PRO:HG2	2:K:123:TYR:CD2	2.54	0.42
1:G:121:VAL:HG22	1:G:125:PHE:CE1	2.55	0.42
1:A:219:LEU:HD23	1:G:161:LYS:HE2	2.02	0.42
1:E:88:GLU:HA	1:E:89:PRO:HD3	1.85	0.42
1:G:251:MET:O	1:G:255:VAL:HG23	2.19	0.42
1:G:425:GLU:OE1	2:L:17:TYR:HB2	2.19	0.42
1:G:418:VAL:O	1:G:422:VAL:HG23	2.19	0.42
1:C:235:ILE:HD11	2:J:51:VAL:HG21	2.01	0.42
1:C:200:THR:OG1	1:C:238:HIS:HD2	2.03	0.42
1:C:88:GLU:HA	1:C:89:PRO:HD3	1.84	0.42
1:E:341:ILE:HD11	1:E:475:VAL:HG23	2.02	0.42
1:A:131:ARG:HB3	1:A:131:ARG:HH21	1.84	0.42
2:I:89:GLU:HG2	2:I:92:LYS:NZ	2.35	0.41
1:A:284:CYS:O	1:A:288:GLY:N	2.53	0.41
1:A:200:THR:OG1	1:A:238:HIS:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:79:ASP:HB3	2:K:82:GLN:HG3	2.02	0.41
2:I:42:LEU:HD21	2:I:87:LEU:HA	2.02	0.41
2:J:72:LEU:HB3	2:J:73:PRO:HD2	2.01	0.41
1:E:151:PRO:HA	1:E:152:PRO:HD3	1.88	0.41
1:E:34:THR:O	1:E:141:PRO:HG3	2.19	0.41
2:L:5:PRO:HB2	2:L:9:LEU:HD11	2.03	0.41
1:A:126:GLY:O	1:A:127:PHE:C	2.59	0.41
1:C:259:GLU:HB2	5:C:2071:HOH:O	2.20	0.41
1:G:334:LYS:HG3	1:G:335:LEU:HG	2.01	0.41
1:G:26:THR:HG22	1:G:26:THR:O	2.20	0.41
2:J:120:PRO:HG2	2:J:123:TYR:CD2	2.56	0.41
1:G:34:THR:O	1:G:141:PRO:HG3	2.20	0.41
1:E:403:GLY:O	1:E:404:GLY:C	2.58	0.41
1:C:173:THR:HG23	1:C:201:KCX:HG2	2.01	0.41
1:A:383:HIS:HE1	1:A:385:TRP:HB2	1.85	0.41
1:A:383:HIS:N	1:A:386:HIS:HD2	2.13	0.41
1:A:226:TYR:HB3	2:L:55:HIS:CE1	2.56	0.41
1:G:386:HIS:HA	5:G:2107:HOH:O	2.20	0.41
2:L:119:LYS:HE2	5:L:2045:HOH:O	2.19	0.41
1:E:22:LEU:HD11	5:E:2005:HOH:O	2.19	0.41
1:C:355:GLU:HA	1:C:365:THR:HG23	2.03	0.41
2:L:21:LEU:HA	2:L:25:GLN:NE2	2.35	0.41
1:E:201:KCX:HE3	1:E:201:KCX:HB3	1.87	0.41
2:L:79:ASP:HA	2:L:80:PRO:HD2	1.92	0.41
1:A:167:ARG:HG3	1:A:168:PRO:O	2.21	0.41
1:E:121:VAL:HG22	1:E:125:PHE:CE1	2.55	0.41
2:L:89:GLU:HG2	2:L:92:LYS:CE	2.46	0.41
2:I:72:LEU:HB3	2:I:73:PRO:CD	2.50	0.41
1:G:251:MET:HE1	1:G:283:TYR:CD1	2.56	0.41
2:I:10:LYS:HB3	2:I:50:PHE:CZ	2.56	0.41
2:K:5:PRO:HG2	2:K:9:LEU:HD11	2.01	0.41
2:L:41:CYS:HB3	2:L:102:ILE:CG1	2.51	0.41
1:C:24:TYR:CD2	1:C:59:ALA:HB2	2.56	0.41
1:A:194:ARG:HH11	1:A:194:ARG:HD2	1.56	0.41
2:J:39:VAL:HG11	2:J:75:PHE:CD1	2.56	0.41
2:J:61:TYR:CD1	2:J:61:TYR:C	2.95	0.41
1:A:454:GLU:H	1:A:454:GLU:CD	2.24	0.41
2:K:89:GLU:HG2	2:K:92:LYS:CE	2.50	0.40
1:A:449:THR:HG22	1:A:455:LEU:HG	2.03	0.40
1:C:344:GLY:O	1:C:347:ASP:HB2	2.21	0.40
1:A:26:THR:O	1:A:26:THR:HG22	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:175:LYS:HE3	4:C:477:CAP:O1P	2.21	0.40
2:I:79:ASP:HB3	2:I:82:GLN:HG3	2.03	0.40
1:G:110:GLU:HB3	1:G:147:THR:HB	2.03	0.40
1:A:252:LYS:HE3	1:A:252:LYS:HB3	1.73	0.40
2:I:79:ASP:HA	2:I:80:PRO:HD2	1.87	0.40
1:C:36:ILE:HD12	1:C:36:ILE:N	2.36	0.40
1:E:239:TYR:CE2	1:E:401:GLN:NE2	2.87	0.40
1:E:296:ALA:O	1:E:297:MET:HB3	2.22	0.40
1:G:409:HIS:CG	1:G:410:PRO:HD2	2.57	0.40
1:E:359:SER:HA	5:E:2101:HOH:O	2.20	0.40
1:C:26:THR:HG22	1:C:26:THR:O	2.22	0.40
1:E:19:ASP:HB2	1:E:22:LEU:HG	2.04	0.40
1:E:125:PHE:CD1	1:E:133:LEU:HD23	2.56	0.40
1:C:334:LYS:HG3	1:C:335:LEU:HG	2.02	0.40

All (4) 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)
5:G:2077:HOH:O	5:G:2077:HOH:O[3_555]	1.65	0.55
5:G:2081:HOH:O	5:G:2081:HOH:O[3_555]	1.89	0.31
2:L:24:ASP:OD1	2:L:28:ARG:NH2[4_555]	2.05	0.15
5:G:2086:HOH:O	5:G:2086:HOH:O[3_555]	2.12	0.08

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	464/475 (98%)	439 (95%)	22 (5%)	3 (1%)	30 36
1	C	464/475 (98%)	445 (96%)	18 (4%)	1 (0%)	52 64
1	E	464/475 (98%)	437 (94%)	24 (5%)	3 (1%)	30 36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	464/475 (98%)	439 (95%)	24 (5%)	1 (0%)	52	64
2	I	121/123 (98%)	114 (94%)	7 (6%)	0	100	100
2	J	121/123 (98%)	112 (93%)	8 (7%)	1 (1%)	24	27
2	K	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
2	L	121/123 (98%)	112 (93%)	8 (7%)	1 (1%)	24	27
All	All	2340/2392 (98%)	2209 (94%)	121 (5%)	10 (0%)	39	48

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	176	PRO
1	E	176	PRO
1	G	176	PRO
1	C	344	GLY
2	J	15	LEU
2	L	15	LEU
1	E	369	VAL
1	A	344	GLY
1	A	331	VAL
1	E	331	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 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	378/386 (98%)	364 (96%)	14 (4%)	41	55
1	C	378/386 (98%)	364 (96%)	14 (4%)	41	55
1	E	378/386 (98%)	361 (96%)	17 (4%)	34	46
1	G	378/386 (98%)	366 (97%)	12 (3%)	46	62
2	I	112/112 (100%)	105 (94%)	7 (6%)	22	29
2	J	112/112 (100%)	105 (94%)	7 (6%)	22	29
2	K	112/112 (100%)	105 (94%)	7 (6%)	22	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	L	112/112 (100%)	104 (93%)	8 (7%)	18	23
All	All	1960/1992 (98%)	1874 (96%)	86 (4%)	35	46

All (86) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	SER
1	A	11	VAL
1	A	17	VAL
1	A	75	THR
1	A	121	VAL
1	A	131	ARG
1	A	152	PRO
1	A	172	CYS
1	A	183	LYS
1	A	185	TYR
1	A	239	TYR
1	A	241	ASN
1	A	252	LYS
1	A	359	SER
1	C	10	SER
1	C	11	VAL
1	C	17	VAL
1	C	75	THR
1	C	121	VAL
1	C	131	ARG
1	C	172	CYS
1	C	173	THR
1	C	185	TYR
1	C	203	ASP
1	C	219	LEU
1	C	239	TYR
1	C	241	ASN
1	C	252	LYS
1	E	10	SER
1	E	11	VAL
1	E	17	VAL
1	E	75	THR
1	E	121	VAL
1	E	127	PHE
1	E	131	ARG
1	E	172	CYS

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Mol	Chain	Res	Type
1	E	173	THR
1	E	183	LYS
1	E	185	TYR
1	E	219	LEU
1	E	239	TYR
1	E	241	ASN
1	E	318	LEU
1	E	387	MET
1	E	388	PRO
1	G	10	SER
1	G	11	VAL
1	G	17	VAL
1	G	36	ILE
1	G	75	THR
1	G	121	VAL
1	G	131	ARG
1	G	172	CYS
1	G	185	TYR
1	G	210	PRO
1	G	239	TYR
1	G	241	ASN
2	I	33	LEU
2	I	56	HIS
2	I	57	ASN
2	I	68	THR
2	I	78	THR
2	I	92	LYS
2	I	110	VAL
2	J	33	LEU
2	J	56	HIS
2	J	57	ASN
2	J	68	THR
2	J	78	THR
2	J	92	LYS
2	J	110	VAL
2	K	33	LEU
2	K	56	HIS
2	K	57	ASN
2	K	68	THR
2	K	78	THR
2	K	92	LYS
2	K	110	VAL

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Mol	Chain	Res	Type
2	L	6	ILE
2	L	33	LEU
2	L	56	HIS
2	L	57	ASN
2	L	68	THR
2	L	78	THR
2	L	92	LYS
2	L	110	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (55) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	156	GLN
1	A	163	ASN
1	A	184	ASN
1	A	207	ASN
1	A	229	GLN
1	A	238	HIS
1	A	241	ASN
1	A	267	HIS
1	A	386	HIS
1	A	420	ASN
1	A	432	ASN
1	C	153	HIS
1	C	163	ASN
1	C	184	ASN
1	C	229	GLN
1	C	238	HIS
1	C	241	ASN
1	C	267	HIS
1	C	304	GLN
1	C	386	HIS
1	C	401	GLN
1	C	420	ASN
1	C	432	ASN
1	E	86	HIS
1	E	156	GLN
1	E	184	ASN
1	E	229	GLN
1	E	238	HIS
1	E	241	ASN
1	E	267	HIS

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Mol	Chain	Res	Type
1	E	304	GLN
1	E	386	HIS
1	E	401	GLN
1	E	432	ASN
1	G	163	ASN
1	G	184	ASN
1	G	207	ASN
1	G	229	GLN
1	G	238	HIS
1	G	241	ASN
1	G	267	HIS
1	G	386	HIS
1	G	420	ASN
1	G	432	ASN
2	I	25	GLN
2	I	29	GLN
2	J	25	GLN
2	J	29	GLN
2	J	55	HIS
2	J	57	ASN
2	K	25	GLN
2	K	29	GLN
2	L	25	GLN
2	L	29	GLN
2	L	107	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	KCX	A	201	1,3	7,11,12	1.16	0	7,12,14	3.13	1 (14%)
1	KCX	C	201	1,3	7,11,12	1.22	1 (14%)	7,12,14	1.81	1 (14%)
1	KCX	E	201	1,3	7,11,12	0.82	0	7,12,14	2.49	1 (14%)
1	KCX	G	201	1,3	7,11,12	1.26	1 (14%)	7,12,14	6.33	2 (28%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	KCX	A	201	1,3	-	0/6/10/12	0/0/0/0
1	KCX	C	201	1,3	-	0/6/10/12	0/0/0/0
1	KCX	E	201	1,3	-	0/6/10/12	0/0/0/0
1	KCX	G	201	1,3	-	0/6/10/12	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	201	KCX	CB-CA	2.33	1.56	1.53
1	G	201	KCX	CB-CA	2.64	1.56	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	201	KCX	CD-CG-CB	-2.18	105.92	113.66
1	C	201	KCX	CE-NZ-CX	4.02	128.04	123.49
1	E	201	KCX	CE-NZ-CX	5.63	129.87	123.49
1	A	201	KCX	CE-NZ-CX	8.05	132.61	123.49
1	G	201	KCX	CE-NZ-CX	16.47	142.15	123.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	201	KCX	1	0
1	E	201	KCX	3	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
4	CAP	A	477	3	14,20,20	1.83	4 (28%)	15,31,31	2.02	3 (20%)
4	CAP	C	477	3	14,20,20	2.16	5 (35%)	15,31,31	2.28	8 (53%)
4	CAP	E	477	3	14,20,20	1.83	3 (21%)	15,31,31	2.00	5 (33%)
4	CAP	G	477	3	14,20,20	2.02	4 (28%)	15,31,31	2.00	5 (33%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	CAP	A	477	3	-	0/23/29/29	0/0/0/0
4	CAP	C	477	3	-	0/23/29/29	0/0/0/0
4	CAP	E	477	3	-	0/23/29/29	0/0/0/0
4	CAP	G	477	3	-	0/23/29/29	0/0/0/0

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	477	CAP	O4-C4	-5.07	1.32	1.43
4	C	477	CAP	O3-C3	-4.17	1.34	1.42
4	E	477	CAP	O3-C3	-3.91	1.34	1.42
4	C	477	CAP	O2-C2	-3.55	1.38	1.43
4	E	477	CAP	O4-C4	-3.54	1.35	1.43
4	A	477	CAP	O4-C4	-3.50	1.35	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	477	CAP	O4-C4	-3.40	1.35	1.43
4	A	477	CAP	O3-C3	-3.35	1.35	1.42
4	C	477	CAP	P2-O6P	-3.23	1.43	1.54
4	E	477	CAP	O2-C2	-2.87	1.39	1.43
4	C	477	CAP	P1-O1P	-2.86	1.41	1.51
4	G	477	CAP	O2-C2	-2.76	1.39	1.43
4	G	477	CAP	O3-C3	-2.71	1.37	1.42
4	A	477	CAP	P2-O6P	-2.45	1.45	1.54
4	A	477	CAP	P1-O1P	-2.44	1.43	1.51
4	G	477	CAP	P1-O1P	-2.08	1.44	1.51

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	477	CAP	O4-C4-C3	-4.99	96.53	109.50
4	A	477	CAP	O4-C4-C3	-4.47	97.87	109.50
4	C	477	CAP	O4-C4-C3	-3.89	99.39	109.50
4	G	477	CAP	O4-C4-C3	-3.61	100.11	109.50
4	E	477	CAP	O3P-P1-O1	-3.36	96.89	106.56
4	G	477	CAP	O3-C3-C4	-3.23	101.98	108.91
4	C	477	CAP	O5-P2-O4P	-2.98	99.55	107.14
4	G	477	CAP	O2P-P1-O1	-2.74	98.68	106.56
4	C	477	CAP	O3P-P1-O1	-2.69	98.81	106.56
4	A	477	CAP	O2P-P1-O1	-2.51	99.33	106.56
4	C	477	CAP	O3-C3-C4	-2.46	103.64	108.91
4	C	477	CAP	O5P-P2-O5	-2.16	100.34	106.56
4	C	477	CAP	O1-P1-O1P	-2.12	101.73	107.14
4	E	477	CAP	O2P-P1-O1	2.03	112.41	106.56
4	E	477	CAP	O5P-P2-O5	2.03	112.41	106.56
4	G	477	CAP	O2P-P1-O1P	2.04	117.14	110.58
4	C	477	CAP	O6P-P2-O4P	2.35	118.15	110.58
4	E	477	CAP	O3P-P1-O1P	3.07	120.46	110.58
4	A	477	CAP	O3P-P1-O1P	4.13	123.88	110.58
4	G	477	CAP	O3P-P1-O1P	4.19	124.06	110.58
4	C	477	CAP	O3P-P1-O1P	4.22	124.15	110.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	477	CAP	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 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	466/475 (98%)	-0.82	4 (0%) 85 89	11, 20, 44, 85	0
1	C	466/475 (98%)	-0.82	3 (0%) 90 93	11, 20, 44, 85	0
1	E	466/475 (98%)	-0.80	3 (0%) 90 93	11, 20, 44, 85	0
1	G	466/475 (98%)	-0.82	3 (0%) 90 93	11, 20, 45, 85	0
2	I	123/123 (100%)	-0.47	0 100 100	12, 32, 53, 67	0
2	J	123/123 (100%)	-0.53	1 (0%) 87 90	12, 32, 53, 67	0
2	K	123/123 (100%)	-0.45	0 100 100	11, 32, 53, 67	0
2	L	123/123 (100%)	-0.50	0 100 100	12, 32, 53, 67	0
All	All	2356/2392 (98%)	-0.75	14 (0%) 90 93	11, 21, 48, 85	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	9	ALA	7.6
1	C	9	ALA	5.8
1	E	9	ALA	5.1
1	E	475	VAL	4.3
1	A	9	ALA	4.1
1	G	10	SER	4.0
1	A	475	VAL	3.1
1	G	475	VAL	3.1
1	C	475	VAL	2.9
1	C	12	GLU	2.5
1	E	11	VAL	2.4
1	A	12	GLU	2.3
2	J	48	HIS	2.2
1	A	10	SER	2.2

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	KCX	G	201	12/13	0.98	0.06	-	12,14,18,18	0
1	KCX	E	201	12/13	0.97	0.09	-	13,14,18,19	0
1	KCX	C	201	12/13	0.96	0.09	-	12,15,18,18	0
1	KCX	A	201	12/13	0.97	0.06	-	13,14,18,18	0

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
3	CA	G	476	1/1	0.98	0.12	3.71	36,36,36,36	0
3	CA	E	476	1/1	0.99	0.12	2.92	36,36,36,36	0
4	CAP	A	477	21/21	0.97	0.08	0.02	16,18,22,23	0
4	CAP	G	477	21/21	0.97	0.08	0.00	15,19,23,24	0
4	CAP	E	477	21/21	0.97	0.07	-0.40	15,19,22,23	0
4	CAP	C	477	21/21	0.98	0.07	-0.64	15,19,22,23	0
3	CA	C	476	1/1	0.97	0.06	-1.15	38,38,38,38	0
3	CA	A	476	1/1	0.98	0.06	-2.45	38,38,38,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.