



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:48 PM GMT

PDB ID : 1QK1
Title : CRYSTAL STRUCTURE OF HUMAN UBIQUITOUS MITOCHONDRIAL CREATINE KINASE
Authors : Eder, M.; Schlattner, U.; Fritz-Wolf, K.; Wallimann, T.; Kabsch, W.
Deposited on : 1999-07-08
Resolution : 2.70 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

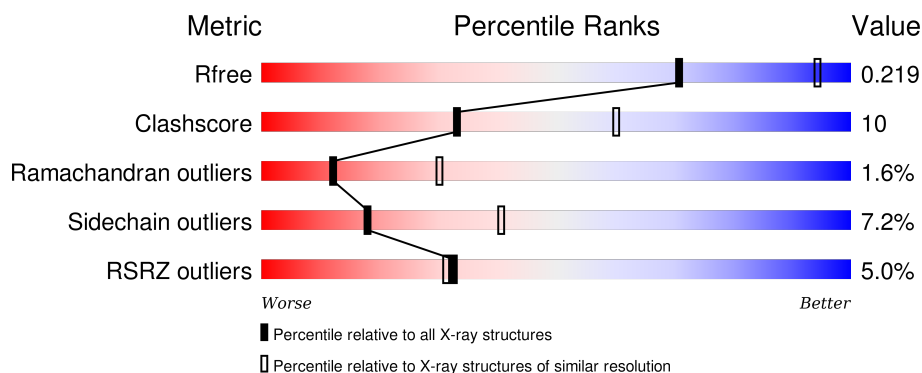
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

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






Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	379	<div> <div>5%</div> <div>77%</div> <div>20%</div> <div>.</div> </div>
1	B	379	<div> <div>5%</div> <div>77%</div> <div>20%</div> <div>.</div> </div>
1	C	379	<div> <div>5%</div> <div>74%</div> <div>22%</div> <div>..</div> </div>
1	D	379	<div> <div>4%</div> <div>78%</div> <div>17%</div> <div>.</div> </div>
1	E	379	<div> <div>4%</div> <div>74%</div> <div>21%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	379	 5% 75% 22% •
1	G	379	 7% 76% 21% •
1	H	379	 5% 75% 21% •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 24613 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 CREATINE KINASE, UBIQUITOUS MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	379	Total	C	N	O	S	0	0	0
			3035	1898	558	564	15			
1	B	379	Total	C	N	O	S	0	0	0
			3035	1898	558	564	15			
1	C	379	Total	C	N	O	S	0	0	0
			3035	1898	558	564	15			
1	D	379	Total	C	N	O	S	0	0	0
			3035	1898	558	564	15			
1	E	379	Total	C	N	O	S	0	0	0
			3035	1898	558	564	15			
1	F	379	Total	C	N	O	S	0	0	0
			3035	1898	558	564	15			
1	G	379	Total	C	N	O	S	0	0	0
			3035	1898	558	564	15			
1	H	379	Total	C	N	O	S	0	0	0
			3035	1898	558	564	15			

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		
2	G	1	Total	O	P	0	0
			5	4	1		
2	H	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	46	Total	O	0	0
			46	46		
3	B	36	Total	O	0	0
			36	36		
3	C	36	Total	O	0	0
			36	36		
3	D	40	Total	O	0	0
			40	40		

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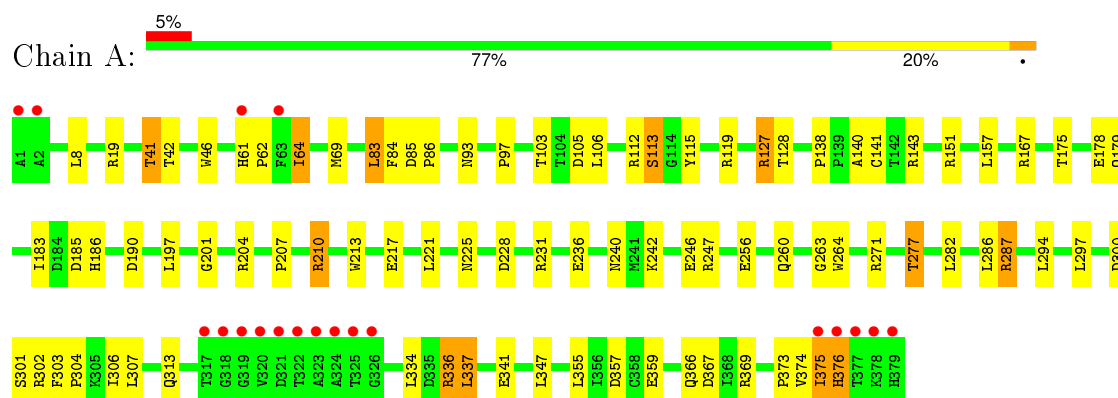
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	31	Total 31	O 31	0	0
3	F	34	Total 34	O 34	0	0
3	G	32	Total 32	O 32	0	0
3	H	38	Total 38	O 38	0	0

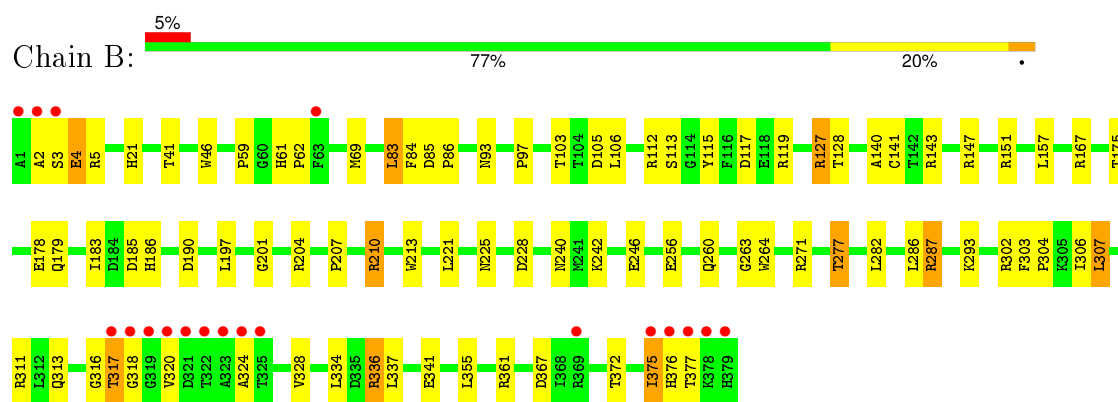
3 Residue-property plots

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.

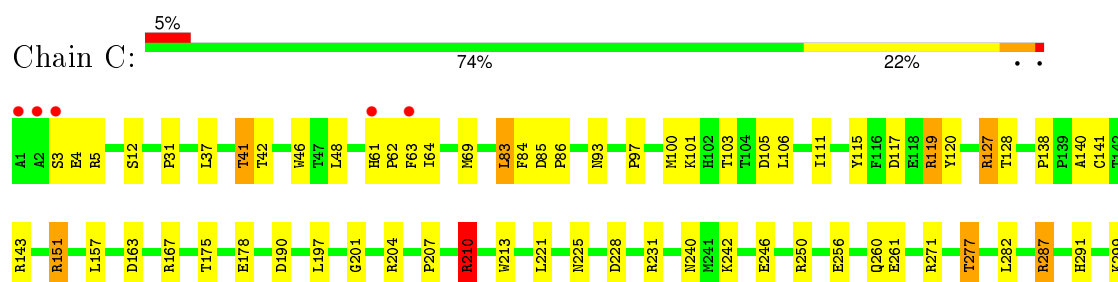
• Molecule 1: CREATINE KINASE, UBIQUITOUS MITOCHONDRIAL

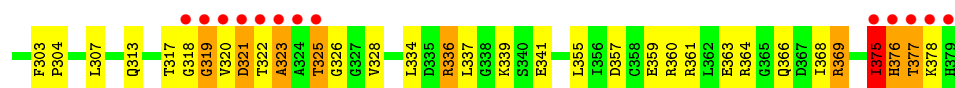


• Molecule 1: CREATINE KINASE, UBIQUITOUS MITOCHONDRIAL

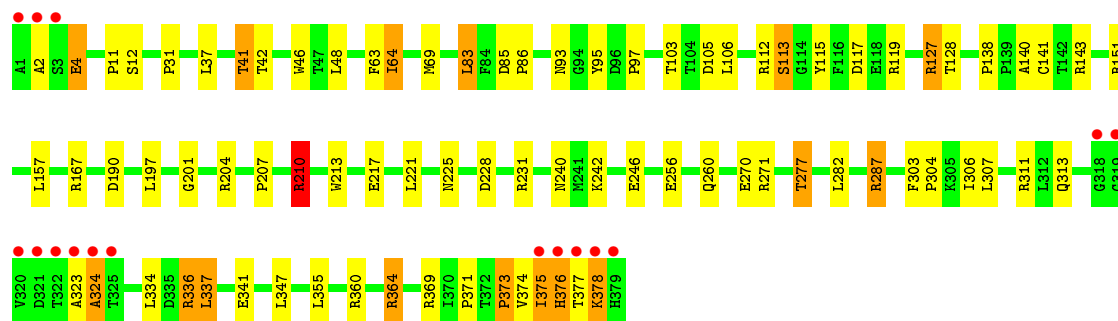
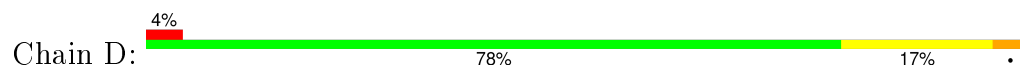


• Molecule 1: CREATINE KINASE, UBIQUITOUS MITOCHONDRIAL

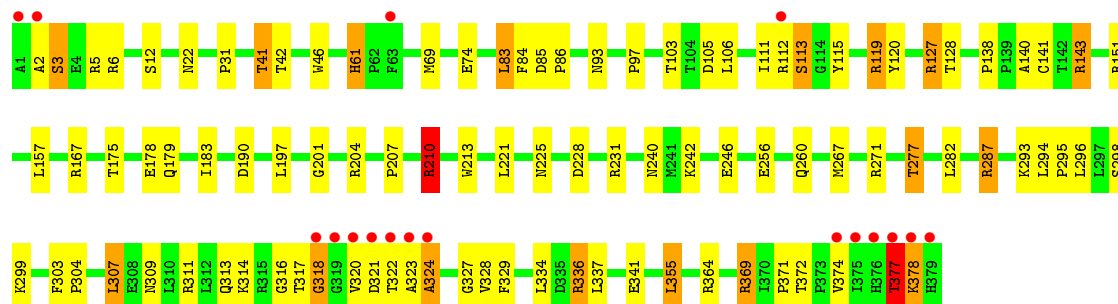
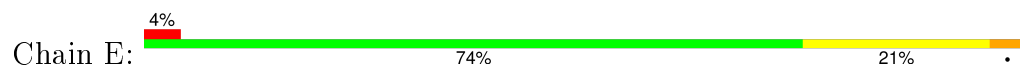




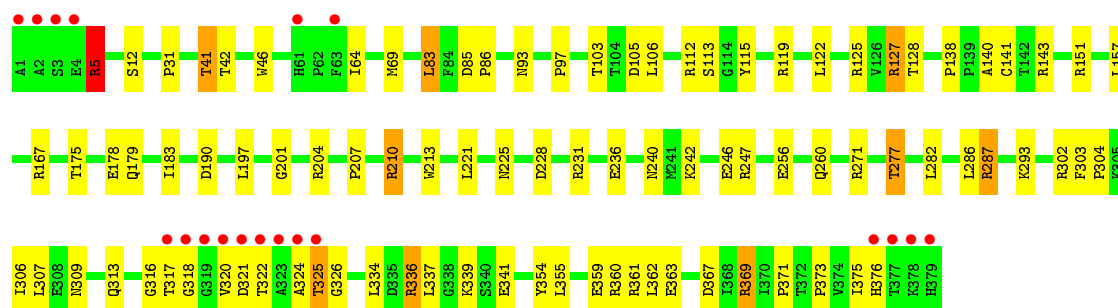
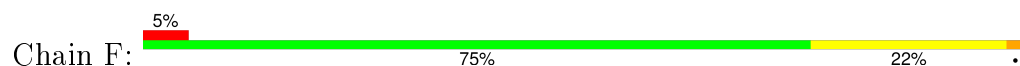
- Molecule 1: CREATINE KINASE, UBIQUITOUS MITOCHONDRIAL



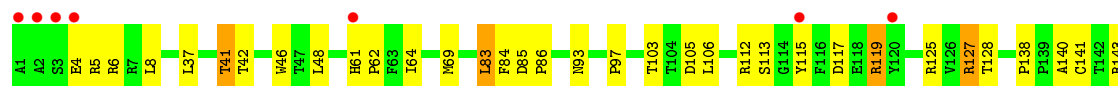
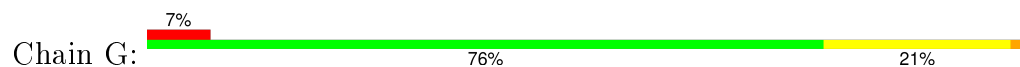
- Molecule 1: CREATINE KINASE, UBIQUITOUS MITOCHONDRIAL

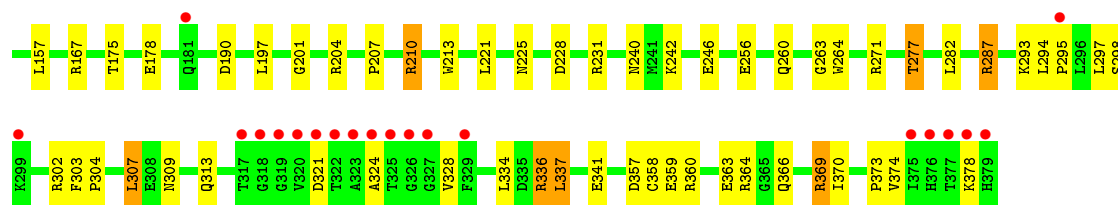


- Molecule 1: CREATINE KINASE, UBIQUITOUS MITOCHONDRIAL

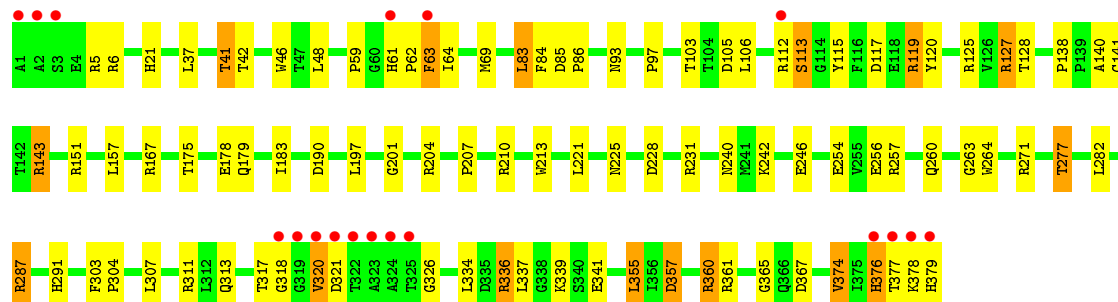
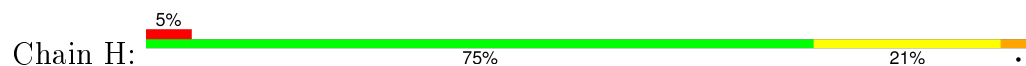


- Molecule 1: CREATINE KINASE, UBIQUITOUS MITOCHONDRIAL





• Molecule 1: CREATINE KINASE, UBIQUITOUS MITOCHONDRIAL



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.81Å 125.87Å 212.07Å 90.00° 96.71° 90.00°	Depositor
Resolution (Å)	50.00 – 2.70 48.10 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.4 (50.00-2.70) 99.6 (48.10-2.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 2.69Å)	Xtriage
Refinement program	CNS 0.5	Depositor
R, R_{free}	0.195 , 0.219 0.195 , 0.219	Depositor DCC
R_{free} test set	6548 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	43.9	Xtriage
Anisotropy	0.278	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 36.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 130944 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	24613	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.48% 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: PO4

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	0.48	0/3099	0.71	1/4189 (0.0%)
1	B	0.47	0/3099	0.72	0/4189
1	C	0.50	0/3099	0.72	3/4189 (0.1%)
1	D	0.48	0/3099	0.72	2/4189 (0.0%)
1	E	0.49	0/3099	0.73	2/4189 (0.0%)
1	F	0.48	0/3099	0.73	1/4189 (0.0%)
1	G	0.47	0/3099	0.72	1/4189 (0.0%)
1	H	0.48	0/3099	0.72	1/4189 (0.0%)
All	All	0.48	0/24792	0.72	11/33512 (0.0%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	210	ARG	NE-CZ-NH2	-5.85	117.38	120.30
1	C	210	ARG	NE-CZ-NH2	-5.52	117.54	120.30
1	C	210	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	E	210	ARG	NE-CZ-NH2	-5.25	117.68	120.30
1	G	337	LEU	CA-CB-CG	5.20	127.27	115.30
1	A	337	LEU	CA-CB-CG	5.18	127.22	115.30
1	F	5	ARG	N-CA-C	-5.14	97.12	111.00
1	E	143	ARG	NE-CZ-NH2	-5.09	117.75	120.30
1	C	291	HIS	N-CA-C	-5.06	97.33	111.00
1	D	210	ARG	NE-CZ-NH1	5.04	122.82	120.30
1	H	143	ARG	NE-CZ-NH2	-5.01	117.80	120.30

There are no chirality outliers.

There are no planarity outliers.

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	3035	0	3010	64	0
1	B	3035	0	3010	58	0
1	C	3035	0	3010	86	0
1	D	3035	0	3010	54	0
1	E	3035	0	3010	66	0
1	F	3035	0	3010	64	0
1	G	3035	0	3010	68	0
1	H	3035	0	3010	73	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
2	G	5	0	0	1	0
2	H	5	0	0	0	0
3	A	46	0	0	2	0
3	B	36	0	0	2	0
3	C	36	0	0	2	0
3	D	40	0	0	3	0
3	E	31	0	0	1	0
3	F	34	0	0	1	0
3	G	32	0	0	2	0
3	H	38	0	0	1	0
All	All	24613	0	24080	499	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (499) 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:C:151:ARG:HG2	1:E:151:ARG:HH11	1.15	1.10
1:F:5:ARG:HG3	1:F:5:ARG:HH11	1.31	0.95
1:C:318:GLY:HA2	1:C:323:ALA:HB2	1.54	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:151:ARG:HG2	1:B:151:ARG:HH11	1.41	0.86
1:G:302:ARG:HB3	1:G:370:ILE:HD11	1.56	0.85
1:G:117:ASP:OD1	1:G:119:ARG:HG3	1.75	0.85
1:C:361:ARG:HD3	1:C:368:ILE:HG22	1.61	0.82
1:C:303:PHE:HB3	1:C:304:PRO:HD3	1.62	0.80
1:C:151:ARG:HG2	1:E:151:ARG:NH1	1.94	0.80
1:D:360:ARG:O	1:D:364:ARG:HD2	1.83	0.79
1:F:303:PHE:HB3	1:F:304:PRO:HD3	1.65	0.78
1:E:293:LYS:HG2	1:E:328:VAL:HG22	1.65	0.78
1:G:6:ARG:HD2	3:G:2001:HOH:O	1.83	0.77
1:E:377:THR:HG23	1:E:378:LYS:H	1.49	0.77
1:E:303:PHE:HB3	1:E:304:PRO:HD3	1.66	0.76
1:B:303:PHE:HB3	1:B:304:PRO:HD3	1.66	0.76
1:F:339:LYS:HE2	1:F:376:HIS:HB2	1.67	0.75
1:A:373:PRO:HB2	1:A:375:ILE:HG12	1.67	0.74
1:G:303:PHE:HB3	1:G:304:PRO:HD3	1.68	0.74
1:A:61:HIS:HD2	1:A:62:PRO:HD2	1.51	0.74
1:F:119:ARG:O	1:F:293:LYS:HE3	1.88	0.73
1:B:117:ASP:OD1	1:B:119:ARG:HG2	1.89	0.73
1:D:374:VAL:HG13	1:D:375:ILE:HG12	1.68	0.73
1:F:375:ILE:O	1:F:375:ILE:HD12	1.89	0.72
1:C:318:GLY:CA	1:C:323:ALA:HB2	2.20	0.71
1:B:3:SER:O	1:B:5:ARG:N	2.24	0.71
1:A:64:ILE:HD13	1:A:64:ILE:H	1.55	0.70
1:D:117:ASP:OD1	1:D:119:ARG:HG2	1.91	0.70
1:B:106:LEU:HD23	1:B:341:GLU:HG3	1.74	0.69
1:H:61:HIS:CD2	1:H:63:PHE:HB2	2.27	0.69
1:E:106:LEU:HD23	1:E:341:GLU:HG3	1.75	0.69
1:B:2:ALA:HB1	1:B:4:GLU:HG3	1.74	0.69
1:F:339:LYS:HE2	1:F:376:HIS:CB	2.23	0.68
1:B:151:ARG:NH1	1:B:151:ARG:HG2	2.09	0.68
1:E:22:ASN:ND2	1:E:61:HIS:O	2.27	0.68
1:H:61:HIS:HB3	1:H:64:ILE:HD11	1.76	0.67
1:E:369:ARG:HH11	1:E:369:ARG:HB3	1.59	0.67
1:F:359:GLU:O	1:F:363:GLU:HG3	1.93	0.67
1:A:151:ARG:HD2	1:H:151:ARG:HD3	1.76	0.67
1:C:339:LYS:HG2	1:C:377:THR:CB	2.23	0.67
1:C:127:ARG:HG2	1:C:128:THR:N	2.10	0.67
1:C:375:ILE:HD12	1:C:375:ILE:H	1.60	0.67
1:H:61:HIS:HB3	1:H:64:ILE:CD1	2.25	0.66
1:C:61:HIS:HB3	1:C:64:ILE:HG13	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:5:ARG:CG	1:F:5:ARG:HH11	2.06	0.66
1:D:127:ARG:HG2	1:D:128:THR:N	2.11	0.66
1:E:31:PRO:HG3	1:H:263:GLY:HA2	1.78	0.66
1:G:61:HIS:HD2	1:G:62:PRO:HD2	1.59	0.66
1:G:369:ARG:N	1:G:369:ARG:HD3	2.10	0.66
1:E:311:ARG:HG3	1:E:374:VAL:CG2	2.24	0.65
1:C:151:ARG:CG	1:E:151:ARG:HH11	2.03	0.65
1:A:106:LEU:HD23	1:A:341:GLU:HG3	1.79	0.65
1:B:263:GLY:HA2	1:C:31:PRO:HG3	1.78	0.65
1:E:127:ARG:HG2	1:E:128:THR:N	2.11	0.65
1:A:127:ARG:HG2	1:A:128:THR:N	2.11	0.64
1:G:61:HIS:CD2	1:G:62:PRO:HD2	2.33	0.64
1:G:106:LEU:HD23	1:G:341:GLU:HG3	1.80	0.64
1:F:106:LEU:HD23	1:F:341:GLU:HG3	1.80	0.64
1:H:106:LEU:HD23	1:H:341:GLU:HG3	1.79	0.64
1:H:127:ARG:HG2	1:H:128:THR:N	2.13	0.64
1:A:8:LEU:HD23	1:G:8:LEU:HD23	1.79	0.63
1:F:167:ARG:HH11	1:F:167:ARG:HG3	1.61	0.63
1:D:4:GLU:HA	1:D:4:GLU:OE1	1.98	0.63
1:B:317:THR:O	1:B:317:THR:HG22	1.99	0.63
1:B:61:HIS:HD2	1:B:62:PRO:HD2	1.63	0.63
1:D:106:LEU:HD23	1:D:341:GLU:HG3	1.80	0.63
1:H:64:ILE:O	1:H:64:ILE:HD12	1.98	0.62
1:E:112:ARG:O	1:E:113:SER:HB3	1.98	0.62
1:H:167:ARG:HG3	1:H:167:ARG:HH11	1.64	0.62
1:H:61:HIS:ND1	1:H:62:PRO:HD2	2.14	0.62
1:F:31:PRO:HG3	1:G:263:GLY:HA2	1.82	0.62
1:D:311:ARG:HG3	1:D:374:VAL:CG1	2.29	0.62
1:B:106:LEU:CD2	1:B:341:GLU:HG3	2.29	0.62
1:A:263:GLY:HA2	1:D:31:PRO:HG3	1.82	0.61
1:C:106:LEU:HD23	1:C:341:GLU:HG3	1.81	0.61
1:D:167:ARG:HG3	1:D:167:ARG:HH11	1.65	0.61
1:C:167:ARG:HH11	1:C:167:ARG:HG3	1.65	0.61
1:B:127:ARG:HG2	1:B:128:THR:N	2.14	0.61
1:E:167:ARG:HG3	1:E:167:ARG:HH11	1.64	0.61
1:C:143:ARG:NH2	3:C:2013:HOH:O	2.33	0.61
1:G:167:ARG:HG3	1:G:167:ARG:HH11	1.66	0.61
1:B:61:HIS:CD2	1:B:62:PRO:HD2	2.36	0.61
1:C:101:LYS:H	1:C:378:LYS:HE2	1.66	0.61
1:F:112:ARG:O	1:F:113:SER:HB3	2.01	0.60
1:B:167:ARG:HH11	1:B:167:ARG:HG3	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:256:GLU:O	1:F:260:GLN:HG3	2.01	0.60
1:A:167:ARG:HG3	1:A:167:ARG:HH11	1.66	0.60
1:C:317:THR:H	1:C:323:ALA:HA	1.65	0.60
1:D:303:PHE:HB3	1:D:304:PRO:HD3	1.83	0.60
1:F:127:ARG:HG2	1:F:128:THR:N	2.14	0.60
1:E:106:LEU:CD2	1:E:341:GLU:HG3	2.31	0.60
1:E:143:ARG:NH2	3:E:2015:HOH:O	2.33	0.60
1:B:316:GLY:HA3	1:B:320:VAL:HG21	1.84	0.59
1:B:105:ASP:O	1:B:341:GLU:HG2	2.02	0.59
1:C:256:GLU:O	1:C:260:GLN:HG3	2.03	0.59
1:C:369:ARG:HG3	1:C:369:ARG:NH1	2.16	0.59
1:A:106:LEU:CD2	1:A:341:GLU:HG3	2.33	0.59
1:D:256:GLU:O	1:D:260:GLN:HG3	2.01	0.59
1:C:325:THR:HG22	1:C:328:VAL:HB	1.84	0.58
1:G:127:ARG:HG2	1:G:128:THR:N	2.16	0.58
1:C:141:CYS:O	1:C:204:ARG:NH2	2.30	0.58
1:G:369:ARG:H	1:G:369:ARG:HD3	1.68	0.58
1:C:376:HIS:O	1:C:377:THR:HG23	2.03	0.58
1:A:141:CYS:O	1:A:204:ARG:NH2	2.30	0.58
1:A:201:GLY:O	1:A:204:ARG:HD3	2.04	0.58
1:F:317:THR:HG22	1:F:324:ALA:O	2.04	0.58
1:H:112:ARG:O	1:H:113:SER:HB3	2.03	0.58
1:G:201:GLY:O	1:G:204:ARG:HD3	2.03	0.58
1:H:106:LEU:CD2	1:H:341:GLU:HG3	2.35	0.57
1:F:106:LEU:CD2	1:F:341:GLU:HG3	2.34	0.57
1:D:377:THR:O	1:D:378:LYS:HB2	2.03	0.57
1:E:256:GLU:O	1:E:260:GLN:HG3	2.04	0.57
1:C:364:ARG:NE	1:C:366:GLN:OE1	2.38	0.57
1:C:359:GLU:O	1:C:363:GLU:HG3	2.05	0.57
1:B:313:GLN:HB3	1:B:334:LEU:HD23	1.87	0.57
1:G:106:LEU:CD2	1:G:341:GLU:HG3	2.35	0.57
1:C:201:GLY:O	1:C:204:ARG:HD3	2.05	0.57
1:B:256:GLU:O	1:B:260:GLN:HG3	2.05	0.57
1:D:106:LEU:CD2	1:D:341:GLU:HG3	2.35	0.56
1:H:313:GLN:HB3	1:H:334:LEU:HD23	1.87	0.56
1:G:105:ASP:O	1:G:341:GLU:HG2	2.06	0.56
1:D:201:GLY:O	1:D:204:ARG:HD3	2.05	0.56
1:B:320:VAL:HG13	1:B:324:ALA:HB2	1.86	0.56
1:F:325:THR:O	1:F:325:THR:HG22	2.06	0.56
1:F:313:GLN:HB3	1:F:334:LEU:HD23	1.88	0.56
1:C:5:ARG:HG3	1:C:5:ARG:HH11	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:302:ARG:O	1:A:306:ILE:HG13	2.06	0.56
1:D:374:VAL:HG13	1:D:375:ILE:N	2.20	0.56
1:C:117:ASP:OD1	1:C:119:ARG:HB3	2.06	0.56
1:E:141:CYS:O	1:E:204:ARG:NH2	2.31	0.56
1:C:320:VAL:HG23	1:C:321:ASP:OD1	2.07	0.56
1:B:201:GLY:O	1:B:204:ARG:HD3	2.05	0.56
1:F:141:CYS:O	1:F:204:ARG:NH2	2.29	0.55
1:G:5:ARG:HH11	1:G:5:ARG:HB3	1.71	0.55
1:H:141:CYS:O	1:H:204:ARG:NH2	2.28	0.55
1:C:106:LEU:CD2	1:C:341:GLU:HG3	2.36	0.55
1:H:201:GLY:O	1:H:204:ARG:HD3	2.06	0.55
1:F:12:SER:CB	1:G:264:TRP:CD2	2.89	0.55
1:H:256:GLU:O	1:H:260:GLN:HG3	2.06	0.55
1:C:317:THR:HB	1:C:322:THR:C	2.26	0.55
1:F:324:ALA:O	1:F:325:THR:HB	2.06	0.55
1:H:303:PHE:HB3	1:H:304:PRO:HD3	1.86	0.55
1:G:309:ASN:O	1:G:374:VAL:HG23	2.06	0.55
1:E:201:GLY:O	1:E:204:ARG:HD3	2.07	0.55
1:F:228:ASP:OD1	1:F:277:THR:HG23	2.07	0.55
1:E:313:GLN:HB3	1:E:334:LEU:HD23	1.88	0.55
1:H:117:ASP:OD1	1:H:119:ARG:CD	2.55	0.55
1:C:339:LYS:HE2	1:C:377:THR:OG1	2.06	0.55
1:C:313:GLN:HB3	1:C:334:LEU:HD23	1.88	0.55
1:A:143:ARG:NH2	3:A:2023:HOH:O	2.40	0.54
1:C:339:LYS:HG2	1:C:377:THR:HB	1.88	0.54
1:H:105:ASP:O	1:H:341:GLU:HG2	2.07	0.54
1:F:143:ARG:NH2	3:F:2017:HOH:O	2.40	0.54
1:G:313:GLN:HB3	1:G:334:LEU:HD23	1.89	0.54
1:G:256:GLU:O	1:G:260:GLN:HG3	2.07	0.54
1:A:228:ASP:OD1	1:A:277:THR:HG23	2.08	0.54
1:A:151:ARG:NH1	1:H:151:ARG:CD	2.71	0.54
1:A:151:ARG:HH11	1:H:151:ARG:HD3	1.73	0.54
1:H:291:HIS:CE1	1:H:317:THR:HG23	2.43	0.54
1:E:311:ARG:HG3	1:E:374:VAL:HG21	1.87	0.54
1:A:313:GLN:HB3	1:A:334:LEU:HD23	1.89	0.54
1:D:228:ASP:OD1	1:D:277:THR:HG23	2.08	0.53
1:G:302:ARG:HB3	1:G:370:ILE:CD1	2.31	0.53
1:A:61:HIS:HD2	1:A:62:PRO:CD	2.21	0.53
1:F:105:ASP:O	1:F:341:GLU:HG2	2.08	0.53
1:G:141:CYS:O	1:G:204:ARG:NH2	2.30	0.53
1:F:201:GLY:O	1:F:204:ARG:HD3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:85:ASP:HB2	1:C:86:PRO:HD3	1.90	0.53
1:F:302:ARG:O	1:F:306:ILE:HG13	2.08	0.53
1:G:242:LYS:O	1:G:246:GLU:HG3	2.08	0.53
1:A:151:ARG:NH1	1:H:151:ARG:HD2	2.23	0.53
1:C:318:GLY:N	1:C:323:ALA:HB2	2.23	0.53
1:D:313:GLN:HB3	1:D:334:LEU:HD23	1.90	0.53
1:F:242:LYS:O	1:F:246:GLU:HG3	2.08	0.53
1:C:369:ARG:CG	1:C:369:ARG:HH11	2.22	0.53
1:D:141:CYS:O	1:D:204:ARG:NH2	2.30	0.53
1:E:69:MET:CE	1:E:83:LEU:HD13	2.39	0.53
1:G:69:MET:CE	1:G:83:LEU:HD13	2.39	0.53
1:C:369:ARG:HG3	1:C:369:ARG:HH11	1.72	0.53
1:F:228:ASP:OD1	1:F:277:THR:CG2	2.57	0.53
1:G:228:ASP:OD1	1:G:277:THR:HG23	2.08	0.52
1:B:228:ASP:OD1	1:B:277:THR:HG23	2.09	0.52
1:B:112:ARG:O	1:B:113:SER:HB3	2.08	0.52
1:A:264:TRP:CD2	1:D:12:SER:CB	2.93	0.52
1:A:112:ARG:O	1:A:113:SER:HB3	2.09	0.52
1:F:69:MET:CE	1:F:83:LEU:HD13	2.39	0.52
1:C:228:ASP:OD1	1:C:277:THR:HG23	2.10	0.52
1:H:69:MET:CE	1:H:83:LEU:HD13	2.40	0.52
1:G:143:ARG:NH2	3:G:2014:HOH:O	2.43	0.52
1:H:143:ARG:NH2	3:H:2019:HOH:O	2.43	0.52
1:H:85:ASP:HB2	1:H:86:PRO:HD3	1.92	0.52
1:H:339:LYS:HE2	1:H:377:THR:OG1	2.10	0.52
1:C:3:SER:C	1:C:5:ARG:H	2.12	0.52
1:G:302:ARG:CB	1:G:370:ILE:HD11	2.34	0.52
1:D:112:ARG:O	1:D:113:SER:HB3	2.09	0.52
1:B:311:ARG:NH1	1:B:376:HIS:ND1	2.57	0.52
1:C:339:LYS:HE2	1:C:377:THR:HG1	1.75	0.52
1:G:5:ARG:NH1	1:G:5:ARG:HB3	2.25	0.52
1:B:179:GLN:O	1:B:183:ILE:HG13	2.11	0.52
1:A:303:PHE:N	1:A:304:PRO:HD2	2.25	0.51
1:F:316:GLY:HA2	1:F:324:ALA:CB	2.40	0.51
1:D:97:PRO:HB2	1:D:271:ARG:NH1	2.26	0.51
1:B:69:MET:CE	1:B:83:LEU:HD13	2.40	0.51
1:A:105:ASP:O	1:A:341:GLU:HG2	2.11	0.51
1:E:85:ASP:HB2	1:E:86:PRO:HD3	1.93	0.51
1:B:264:TRP:CD2	1:C:12:SER:CB	2.94	0.51
1:H:228:ASP:OD1	1:H:277:THR:HG23	2.11	0.51
1:D:242:LYS:O	1:D:246:GLU:HG3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:5:ARG:HG2	1:H:5:ARG:HH11	1.75	0.51
1:B:69:MET:HE2	1:B:84:PHE:CZ	2.46	0.51
1:D:323:ALA:O	1:D:324:ALA:HB3	2.11	0.51
1:H:311:ARG:HG3	1:H:374:VAL:CG2	2.41	0.51
1:F:5:ARG:NH1	1:F:5:ARG:CG	2.70	0.51
1:A:375:ILE:O	1:A:375:ILE:HG13	2.10	0.51
1:D:311:ARG:HG3	1:D:374:VAL:HG11	1.92	0.51
1:F:69:MET:HE1	1:F:83:LEU:HD13	1.92	0.51
1:A:97:PRO:HB2	1:A:271:ARG:NH1	2.26	0.51
1:D:69:MET:CE	1:D:83:LEU:HD13	2.40	0.51
1:C:105:ASP:O	1:C:341:GLU:HG2	2.11	0.50
1:D:64:ILE:HD12	1:D:64:ILE:N	2.25	0.50
1:A:256:GLU:O	1:A:260:GLN:HG3	2.12	0.50
1:B:287:ARG:HG2	1:B:336:ARG:NH2	2.26	0.50
1:E:105:ASP:O	1:E:341:GLU:HG2	2.11	0.50
1:A:61:HIS:ND1	1:A:64:ILE:HD11	2.26	0.50
1:C:61:HIS:ND1	1:C:62:PRO:HD2	2.27	0.50
1:G:85:ASP:HB2	1:G:86:PRO:HD3	1.92	0.50
1:H:287:ARG:HG2	1:H:336:ARG:NH2	2.27	0.50
1:E:242:LYS:O	1:E:246:GLU:HG3	2.12	0.50
1:C:339:LYS:HG2	1:C:377:THR:HG21	1.94	0.50
1:E:309:ASN:ND2	1:E:371:PRO:O	2.31	0.50
1:H:61:HIS:NE2	1:H:63:PHE:HB2	2.27	0.50
1:G:204:ARG:O	1:G:210:ARG:NH2	2.41	0.50
1:F:12:SER:HB2	1:G:264:TRP:CD2	2.47	0.50
1:D:228:ASP:OD1	1:D:277:THR:CG2	2.60	0.50
1:G:97:PRO:HB2	1:G:271:ARG:NH1	2.27	0.50
1:C:242:LYS:O	1:C:246:GLU:HG3	2.11	0.50
1:D:105:ASP:O	1:D:341:GLU:HG2	2.12	0.50
1:E:320:VAL:HG23	1:E:321:ASP:H	1.77	0.50
1:D:83:LEU:O	1:D:86:PRO:HD2	2.11	0.49
1:C:69:MET:CE	1:C:83:LEU:HD13	2.41	0.49
1:B:143:ARG:NH2	3:B:2014:HOH:O	2.43	0.49
1:E:294:LEU:N	1:E:327:GLY:O	2.41	0.49
1:C:325:THR:HG23	1:C:326:GLY:N	2.27	0.49
1:B:85:ASP:HB2	1:B:86:PRO:HD3	1.95	0.49
1:C:100:MET:HA	1:C:378:LYS:HE2	1.94	0.49
1:H:69:MET:HE3	1:H:83:LEU:HD13	1.94	0.49
1:E:2:ALA:O	1:E:3:SER:HB2	2.11	0.49
1:G:287:ARG:HG2	1:G:336:ARG:NH2	2.26	0.49
1:E:287:ARG:HG2	1:E:336:ARG:NH2	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:228:ASP:OD1	1:E:277:THR:HG23	2.13	0.49
1:D:85:ASP:HB2	1:D:86:PRO:HD3	1.94	0.49
1:E:311:ARG:HG3	1:E:374:VAL:HG22	1.92	0.49
1:B:97:PRO:HB2	1:B:271:ARG:NH1	2.28	0.49
1:D:270:GLU:HG2	3:D:2033:HOH:O	2.13	0.49
1:G:364:ARG:HB2	1:G:366:GLN:HG3	1.95	0.49
1:A:151:ARG:CD	1:H:151:ARG:HD3	2.41	0.49
1:G:61:HIS:HB3	1:G:64:ILE:HG13	1.95	0.49
1:E:204:ARG:O	1:E:210:ARG:NH2	2.40	0.49
1:E:97:PRO:HB2	1:E:271:ARG:NH1	2.27	0.49
1:A:85:ASP:HB2	1:A:86:PRO:HD3	1.95	0.49
1:A:61:HIS:CD2	1:A:62:PRO:HD2	2.40	0.49
1:B:141:CYS:O	1:B:204:ARG:NH2	2.29	0.48
1:H:97:PRO:HB2	1:H:271:ARG:NH1	2.28	0.48
1:H:138:PRO:HD2	1:H:277:THR:HG21	1.96	0.48
1:F:97:PRO:HB2	1:F:271:ARG:NH1	2.28	0.48
1:C:325:THR:CG2	1:C:328:VAL:HB	2.44	0.48
1:C:119:ARG:O	1:C:119:ARG:HG3	2.12	0.48
1:F:64:ILE:HG13	1:F:64:ILE:O	2.11	0.48
1:C:151:ARG:CZ	1:E:151:ARG:HD2	2.43	0.48
1:C:228:ASP:OD1	1:C:277:THR:CG2	2.61	0.48
1:C:287:ARG:HG2	1:C:336:ARG:NH2	2.28	0.48
1:C:64:ILE:O	1:C:64:ILE:HD12	2.14	0.48
1:A:264:TRP:CE3	1:D:12:SER:HB2	2.48	0.48
1:G:61:HIS:HD2	1:G:62:PRO:CD	2.27	0.48
1:H:204:ARG:O	1:H:210:ARG:NH2	2.41	0.48
1:A:242:LYS:O	1:A:246:GLU:HG3	2.13	0.48
1:A:228:ASP:OD1	1:A:277:THR:CG2	2.62	0.48
1:D:46:TRP:CZ3	1:D:140:ALA:HB2	2.49	0.48
1:C:317:THR:HG22	1:C:319:GLY:H	1.77	0.47
1:C:97:PRO:HB2	1:C:271:ARG:NH1	2.28	0.47
1:E:374:VAL:HG23	1:E:374:VAL:O	2.14	0.47
1:H:157:LEU:HD13	1:H:213:TRP:CG	2.50	0.47
1:B:242:LYS:O	1:B:246:GLU:HG3	2.14	0.47
1:B:46:TRP:CE3	1:B:140:ALA:HB2	2.50	0.47
1:G:293:LYS:O	1:G:294:LEU:HD23	2.14	0.47
1:F:339:LYS:HE2	1:F:376:HIS:CG	2.49	0.47
1:G:112:ARG:O	1:G:113:SER:HB3	2.14	0.47
1:F:85:ASP:HB2	1:F:86:PRO:HD3	1.96	0.47
1:B:46:TRP:CZ3	1:B:140:ALA:HB2	2.50	0.47
1:H:242:LYS:O	1:H:246:GLU:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:11:PRO:HD3	1:E:6:ARG:HH12	1.79	0.47
1:F:321:ASP:OD2	1:F:325:THR:HA	2.15	0.47
1:C:119:ARG:HG2	1:C:120:TYR:CE2	2.49	0.47
1:G:228:ASP:OD1	1:G:277:THR:CG2	2.63	0.47
1:A:264:TRP:CD2	1:D:12:SER:HB2	2.49	0.47
1:A:297:LEU:HG	1:A:303:PHE:CD1	2.50	0.47
1:G:125:ARG:NH2	2:G:400:PO4:O1	2.44	0.47
1:E:83:LEU:O	1:E:86:PRO:HD2	2.15	0.47
1:H:69:MET:HE2	1:H:84:PHE:CZ	2.49	0.47
1:G:293:LYS:HG2	1:G:328:VAL:HG22	1.97	0.47
1:E:323:ALA:O	1:E:324:ALA:HB2	2.15	0.47
1:A:138:PRO:HD2	1:A:277:THR:HG21	1.96	0.46
1:A:287:ARG:HG2	1:A:336:ARG:NH2	2.31	0.46
1:E:138:PRO:HD2	1:E:277:THR:HG21	1.98	0.46
1:A:69:MET:CE	1:A:83:LEU:HD13	2.45	0.46
1:B:246:GLU:HB3	3:B:2030:HOH:O	2.14	0.46
1:H:378:LYS:O	1:H:379:HIS:HB3	2.14	0.46
1:A:179:GLN:O	1:A:183:ILE:HG13	2.15	0.46
1:C:339:LYS:HG2	1:C:377:THR:CG2	2.45	0.46
1:B:204:ARG:O	1:B:210:ARG:NH2	2.41	0.46
1:B:264:TRP:CD2	1:C:12:SER:HB2	2.51	0.46
1:G:294:LEU:O	1:G:298:SER:HB3	2.15	0.46
1:A:294:LEU:HD23	1:A:359:GLU:HG3	1.98	0.46
1:A:217:GLU:HG2	3:A:2031:HOH:O	2.16	0.46
1:G:61:HIS:HB3	1:G:64:ILE:CG1	2.46	0.46
1:G:4:GLU:O	1:G:4:GLU:HG3	2.15	0.46
1:F:287:ARG:HG2	1:F:336:ARG:NH2	2.31	0.46
1:B:228:ASP:OD1	1:B:277:THR:CG2	2.64	0.46
1:H:361:ARG:NH1	1:H:367:ASP:O	2.49	0.46
1:G:157:LEU:HD13	1:G:213:TRP:CG	2.51	0.46
1:D:204:ARG:O	1:D:210:ARG:NH2	2.44	0.45
1:C:69:MET:HE2	1:C:84:PHE:CZ	2.50	0.45
1:E:119:ARG:CG	1:E:120:TYR:CE2	3.00	0.45
1:D:143:ARG:NH2	3:D:2019:HOH:O	2.49	0.45
1:A:204:ARG:O	1:A:210:ARG:NH2	2.39	0.45
1:B:210:ARG:HD2	1:B:225:ASN:O	2.16	0.45
1:C:61:HIS:HB3	1:C:64:ILE:CG1	2.46	0.45
1:G:69:MET:HE2	1:G:84:PHE:CZ	2.51	0.45
1:G:295:PRO:HD2	1:G:359:GLU:OE2	2.15	0.45
1:F:210:ARG:HD2	1:F:225:ASN:O	2.16	0.45
1:F:12:SER:HB3	1:G:264:TRP:CD2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:117:ASP:OD1	1:H:119:ARG:HD3	2.16	0.45
1:F:41:THR:HG23	1:F:42:THR:O	2.16	0.45
1:B:151:ARG:NH1	1:B:151:ARG:CG	2.78	0.45
1:B:361:ARG:NH1	1:B:367:ASP:O	2.50	0.45
1:H:355:LEU:HD12	1:H:355:LEU:HA	1.78	0.45
1:D:287:ARG:HG2	1:D:336:ARG:NH2	2.31	0.45
1:C:210:ARG:HD2	1:C:225:ASN:O	2.15	0.45
1:H:357:ASP:O	1:H:361:ARG:HG3	2.17	0.45
1:C:228:ASP:OD2	1:C:231:ARG:NH1	2.49	0.45
1:F:157:LEU:HD13	1:F:213:TRP:CG	2.52	0.45
1:G:64:ILE:O	1:G:64:ILE:HG13	2.17	0.45
1:D:374:VAL:CG1	1:D:375:ILE:N	2.79	0.45
1:E:31:PRO:HB3	1:H:263:GLY:O	2.17	0.45
1:E:167:ARG:NH1	1:E:167:ARG:HG3	2.32	0.45
1:B:83:LEU:O	1:B:86:PRO:HD2	2.17	0.45
1:F:83:LEU:O	1:F:86:PRO:HD2	2.18	0.44
1:E:69:MET:HE2	1:E:84:PHE:CZ	2.53	0.44
1:H:83:LEU:O	1:H:86:PRO:HD2	2.18	0.44
1:E:228:ASP:OD1	1:E:277:THR:CG2	2.65	0.44
1:C:151:ARG:NE	1:E:151:ARG:HD2	2.33	0.44
1:F:167:ARG:NH1	1:F:167:ARG:HG3	2.29	0.44
1:B:61:HIS:HD2	1:B:62:PRO:CD	2.30	0.44
1:E:3:SER:C	1:E:5:ARG:H	2.20	0.44
1:C:157:LEU:HD13	1:C:213:TRP:CG	2.52	0.44
1:H:210:ARG:HD2	1:H:225:ASN:O	2.17	0.44
1:H:228:ASP:OD1	1:H:277:THR:CG2	2.65	0.44
1:D:46:TRP:CE3	1:D:140:ALA:HB2	2.52	0.44
1:F:354:TYR:CE1	1:F:371:PRO:HD3	2.52	0.44
1:E:316:GLY:HA3	1:E:322:THR:HB	2.00	0.44
1:D:167:ARG:NH1	1:D:167:ARG:HG3	2.31	0.44
1:F:12:SER:HB2	1:G:264:TRP:CE3	2.52	0.44
1:H:320:VAL:HG23	1:H:321:ASP:H	1.82	0.44
1:C:61:HIS:HB3	1:C:64:ILE:CD1	2.47	0.44
1:C:204:ARG:O	1:C:210:ARG:NH2	2.42	0.44
1:D:306:ILE:HG12	1:D:371:PRO:HD2	2.00	0.44
1:C:61:HIS:CE1	1:C:63:PHE:HB2	2.53	0.44
1:F:46:TRP:CZ3	1:F:140:ALA:HB2	2.53	0.44
1:H:175:THR:OG1	1:H:178:GLU:HG3	2.18	0.44
1:A:19:ARG:HD3	1:C:261:GLU:HG2	2.00	0.44
1:A:151:ARG:NH1	1:H:151:ARG:HD3	2.33	0.44
1:G:360:ARG:HA	1:G:363:GLU:OE1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:157:LEU:HD13	1:E:213:TRP:CG	2.52	0.44
1:A:41:THR:HG23	1:A:42:THR:O	2.17	0.44
1:D:41:THR:HG23	1:D:42:THR:O	2.18	0.44
1:E:317:THR:HG23	1:E:318:GLY:N	2.33	0.44
1:H:46:TRP:CZ3	1:H:140:ALA:HB2	2.52	0.44
1:H:6:ARG:HH11	1:H:6:ARG:HG3	1.81	0.43
1:B:61:HIS:CD2	1:B:62:PRO:CD	3.01	0.43
1:B:167:ARG:HG3	1:B:167:ARG:NH1	2.32	0.43
1:D:376:HIS:N	1:D:376:HIS:ND1	2.66	0.43
1:A:167:ARG:HG3	1:A:167:ARG:NH1	2.32	0.43
1:B:375:ILE:HG22	1:B:376:HIS:N	2.33	0.43
1:F:46:TRP:CE3	1:F:140:ALA:HB2	2.53	0.43
1:D:157:LEU:HD13	1:D:213:TRP:CG	2.53	0.43
1:C:175:THR:OG1	1:C:178:GLU:HG3	2.19	0.43
1:F:167:ARG:CG	1:F:167:ARG:HH11	2.31	0.43
1:G:138:PRO:HD2	1:G:277:THR:HG21	2.00	0.43
1:A:185:ASP:O	1:A:186:HIS:HB2	2.18	0.43
1:B:175:THR:OG1	1:B:178:GLU:HG3	2.19	0.43
1:G:46:TRP:CZ3	1:G:140:ALA:HB2	2.54	0.43
1:F:360:ARG:HH11	1:F:360:ARG:HG2	1.83	0.43
1:B:263:GLY:O	1:C:31:PRO:HB3	2.18	0.43
1:B:302:ARG:O	1:B:306:ILE:HG13	2.19	0.43
1:G:210:ARG:HD2	1:G:225:ASN:O	2.18	0.43
1:G:309:ASN:ND2	1:G:373:PRO:HG3	2.33	0.43
1:F:138:PRO:HD2	1:F:277:THR:HG21	2.01	0.43
1:A:69:MET:HE2	1:A:84:PHE:CZ	2.54	0.43
1:H:376:HIS:CD2	1:H:378:LYS:HD3	2.54	0.43
1:C:111:ILE:HD13	1:C:111:ILE:HA	1.82	0.43
1:D:228:ASP:OD2	1:D:231:ARG:NH1	2.52	0.43
1:D:69:MET:HE1	1:D:83:LEU:HD13	2.01	0.43
1:E:179:GLN:O	1:E:183:ILE:HG13	2.19	0.43
1:E:293:LYS:HA	1:E:327:GLY:O	2.19	0.42
1:A:112:ARG:O	1:A:113:SER:CB	2.67	0.42
1:H:46:TRP:CE3	1:H:140:ALA:HB2	2.54	0.42
1:D:347:LEU:HD23	1:D:347:LEU:C	2.39	0.42
1:C:339:LYS:CE	1:C:377:THR:OG1	2.67	0.42
1:E:298:SER:HB2	1:E:329:PHE:CE1	2.53	0.42
1:D:217:GLU:HG2	3:D:2026:HOH:O	2.19	0.42
1:F:236:GLU:HG3	1:F:247:ARG:HH22	1.84	0.42
1:E:307:LEU:HD11	1:E:355:LEU:HD21	2.00	0.42
1:C:364:ARG:HG3	1:C:366:GLN:HG3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:138:PRO:HD2	1:C:277:THR:HG21	2.02	0.42
1:H:179:GLN:O	1:H:183:ILE:HG13	2.19	0.42
1:A:210:ARG:HD2	1:A:225:ASN:O	2.19	0.42
1:H:112:ARG:O	1:H:113:SER:CB	2.67	0.42
1:B:143:ARG:O	1:B:147:ARG:HG3	2.19	0.42
1:E:119:ARG:HG2	1:E:120:TYR:CE2	2.55	0.42
1:G:307:LEU:HD12	1:G:307:LEU:HA	1.89	0.42
1:E:303:PHE:CE2	1:E:314:LYS:HD3	2.54	0.42
1:A:151:ARG:HD2	1:H:151:ARG:CD	2.46	0.42
1:A:151:ARG:HH11	1:H:151:ARG:CD	2.31	0.42
1:D:210:ARG:HD2	1:D:225:ASN:O	2.19	0.42
1:B:185:ASP:O	1:B:186:HIS:HB2	2.20	0.42
1:F:175:THR:OG1	1:F:178:GLU:HG3	2.20	0.42
1:H:228:ASP:OD2	1:H:231:ARG:NH1	2.52	0.42
1:F:354:TYR:OH	1:F:369:ARG:O	2.31	0.42
1:A:157:LEU:HD13	1:A:213:TRP:CG	2.55	0.42
1:B:316:GLY:C	1:B:318:GLY:H	2.23	0.42
1:F:316:GLY:HA2	1:F:324:ALA:HB1	2.00	0.42
1:D:138:PRO:HD2	1:D:277:THR:HG21	2.00	0.42
1:H:376:HIS:HD2	1:H:378:LYS:HD3	1.84	0.42
1:G:61:HIS:CD2	1:G:62:PRO:CD	3.03	0.42
1:B:21:HIS:CD2	1:B:59:PRO:HA	2.55	0.42
1:H:61:HIS:HB3	1:H:64:ILE:HD12	2.02	0.42
1:C:3:SER:C	1:C:5:ARG:N	2.73	0.42
1:H:117:ASP:OD1	1:H:119:ARG:HD2	2.20	0.42
1:A:228:ASP:OD2	1:A:231:ARG:NH1	2.53	0.42
1:A:300:ASP:OD1	1:A:301:SER:N	2.53	0.42
1:E:41:THR:HG23	1:E:42:THR:O	2.20	0.42
1:C:100:MET:CA	1:C:378:LYS:HE2	2.50	0.42
1:E:111:ILE:O	1:E:242:LYS:HE2	2.20	0.42
1:A:374:VAL:O	1:A:376:HIS:N	2.45	0.42
1:F:361:ARG:NH2	1:F:367:ASP:O	2.50	0.42
1:C:317:THR:HB	1:C:323:ALA:N	2.34	0.41
1:B:316:GLY:O	1:B:318:GLY:N	2.51	0.41
1:F:12:SER:HB3	1:G:264:TRP:CE2	2.55	0.41
1:F:228:ASP:OD2	1:F:231:ARG:NH1	2.53	0.41
1:A:236:GLU:HG3	1:A:247:ARG:HH22	1.85	0.41
1:E:210:ARG:HD2	1:E:225:ASN:O	2.21	0.41
1:H:311:ARG:HG3	1:H:374:VAL:HG22	2.00	0.41
1:D:63:PHE:C	1:D:64:ILE:HG13	2.40	0.41
1:A:175:THR:OG1	1:A:178:GLU:HG3	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:37:LEU:HB2	1:G:48:LEU:HD22	2.02	0.41
1:G:167:ARG:HG3	1:G:167:ARG:NH1	2.32	0.41
1:B:157:LEU:HD13	1:B:213:TRP:CG	2.56	0.41
1:G:41:THR:HG23	1:G:42:THR:O	2.19	0.41
1:A:119:ARG:O	1:A:119:ARG:HG2	2.19	0.41
1:H:119:ARG:HG2	1:H:120:TYR:CD2	2.55	0.41
1:H:41:THR:HG23	1:H:42:THR:O	2.20	0.41
1:E:296:LEU:N	1:E:296:LEU:HD12	2.35	0.41
1:C:210:ARG:NH1	3:C:2023:HOH:O	2.54	0.41
1:H:117:ASP:OD2	1:H:360:ARG:NH2	2.54	0.41
1:C:46:TRP:CZ3	1:C:140:ALA:HB2	2.55	0.41
1:E:364:ARG:HG2	1:E:364:ARG:HH11	1.86	0.41
1:C:101:LYS:H	1:C:378:LYS:CE	2.33	0.41
1:G:297:LEU:HD22	1:G:358:CYS:HB3	2.02	0.41
1:C:41:THR:HG23	1:C:42:THR:O	2.21	0.41
1:A:347:LEU:C	1:A:347:LEU:HD23	2.41	0.41
1:H:37:LEU:HB2	1:H:48:LEU:HD22	2.03	0.41
1:D:95:TYR:CD2	1:D:337:LEU:HD13	2.56	0.41
1:E:175:THR:OG1	1:E:178:GLU:HG3	2.20	0.41
1:A:46:TRP:CZ3	1:A:140:ALA:HB2	2.56	0.41
1:C:61:HIS:HE1	1:C:63:PHE:CD2	2.38	0.41
1:C:167:ARG:HG3	1:C:167:ARG:NH1	2.32	0.41
1:G:83:LEU:O	1:G:86:PRO:HD2	2.21	0.41
1:H:339:LYS:HE2	1:H:377:THR:CG2	2.50	0.41
1:G:46:TRP:CE3	1:G:140:ALA:HB2	2.56	0.41
1:F:179:GLN:O	1:F:183:ILE:HG13	2.21	0.41
1:A:83:LEU:O	1:A:86:PRO:HD2	2.21	0.41
1:H:254:GLU:OE2	1:H:257:ARG:NH2	2.23	0.41
1:C:37:LEU:HB2	1:C:48:LEU:HD22	2.03	0.41
1:F:309:ASN:ND2	1:F:373:PRO:HG3	2.36	0.41
1:E:228:ASP:OD2	1:E:231:ARG:NH1	2.53	0.40
1:H:21:HIS:CD2	1:H:59:PRO:HA	2.57	0.40
1:B:307:LEU:HA	1:B:307:LEU:HD12	1.88	0.40
1:F:122:LEU:HD21	1:F:293:LYS:HE2	2.03	0.40
1:E:74:GLU:HB2	1:E:267:MET:SD	2.61	0.40
1:A:64:ILE:N	1:A:64:ILE:HD13	2.31	0.40
1:G:175:THR:OG1	1:G:178:GLU:HG3	2.20	0.40
1:E:12:SER:HB3	1:H:264:TRP:CD2	2.56	0.40
1:F:324:ALA:O	1:F:325:THR:CB	2.68	0.40
1:F:12:SER:CB	1:G:264:TRP:CE2	3.05	0.40
1:G:228:ASP:OD2	1:G:231:ARG:NH1	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:163:ASP:OD2	1:C:250:ARG:NH2	2.55	0.40
1:D:37:LEU:HB2	1:D:48:LEU:HD22	2.03	0.40
1:E:46:TRP:CE3	1:E:140:ALA:HB2	2.57	0.40
1:B:293:LYS:HG2	1:B:328:VAL:HG22	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	377/379 (100%)	360 (96%)	13 (3%)	4 (1%)	17	42
1	B	377/379 (100%)	358 (95%)	15 (4%)	4 (1%)	17	42
1	C	377/379 (100%)	354 (94%)	14 (4%)	9 (2%)	7	19
1	D	377/379 (100%)	355 (94%)	15 (4%)	7 (2%)	10	25
1	E	377/379 (100%)	354 (94%)	15 (4%)	8 (2%)	9	23
1	F	377/379 (100%)	357 (95%)	15 (4%)	5 (1%)	15	37
1	G	377/379 (100%)	358 (95%)	17 (4%)	2 (0%)	34	63
1	H	377/379 (100%)	357 (95%)	12 (3%)	8 (2%)	9	23
All	All	3016/3032 (100%)	2853 (95%)	116 (4%)	47 (2%)	12	30

All (47) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	375	ILE
1	B	4	GLU
1	B	317	THR
1	B	375	ILE
1	C	325	THR
1	C	376	HIS

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Mol	Chain	Res	Type
1	C	377	THR
1	E	324	ALA
1	F	325	THR
1	G	324	ALA
1	H	376	HIS
1	A	93	ASN
1	B	93	ASN
1	C	93	ASN
1	C	323	ALA
1	D	93	ASN
1	D	378	LYS
1	E	3	SER
1	E	93	ASN
1	E	318	GLY
1	E	377	THR
1	E	378	LYS
1	F	93	ASN
1	F	326	GLY
1	G	93	ASN
1	H	93	ASN
1	A	366	GLN
1	C	321	ASP
1	D	2	ALA
1	D	375	ILE
1	F	318	GLY
1	H	113	SER
1	H	320	VAL
1	H	365	GLY
1	C	4	GLU
1	C	319	GLY
1	C	375	ILE
1	H	318	GLY
1	A	113	SER
1	D	113	SER
1	D	324	ALA
1	E	113	SER
1	H	63	PHE
1	D	373	PRO
1	H	326	GLY
1	F	320	VAL
1	E	295	PRO

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	328/328 (100%)	304 (93%)	24 (7%)	17	39
1	B	328/328 (100%)	307 (94%)	21 (6%)	22	47
1	C	328/328 (100%)	303 (92%)	25 (8%)	16	37
1	D	328/328 (100%)	303 (92%)	25 (8%)	16	37
1	E	328/328 (100%)	304 (93%)	24 (7%)	17	39
1	F	328/328 (100%)	303 (92%)	25 (8%)	16	37
1	G	328/328 (100%)	306 (93%)	22 (7%)	20	44
1	H	328/328 (100%)	306 (93%)	22 (7%)	20	44
All	All	2624/2624 (100%)	2436 (93%)	188 (7%)	18	41

All (188) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	THR
1	A	64	ILE
1	A	83	LEU
1	A	103	THR
1	A	115	TYR
1	A	127	ARG
1	A	190	ASP
1	A	197	LEU
1	A	207	PRO
1	A	210	ARG
1	A	221	LEU
1	A	240	ASN
1	A	277	THR
1	A	282	LEU
1	A	286	LEU
1	A	287	ARG
1	A	307	LEU
1	A	336	ARG
1	A	337	LEU

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Mol	Chain	Res	Type
1	A	355	LEU
1	A	357	ASP
1	A	367	ASP
1	A	369	ARG
1	A	376	HIS
1	B	41	THR
1	B	83	LEU
1	B	103	THR
1	B	115	TYR
1	B	127	ARG
1	B	190	ASP
1	B	197	LEU
1	B	207	PRO
1	B	210	ARG
1	B	221	LEU
1	B	240	ASN
1	B	277	THR
1	B	282	LEU
1	B	286	LEU
1	B	287	ARG
1	B	307	LEU
1	B	336	ARG
1	B	337	LEU
1	B	355	LEU
1	B	372	THR
1	B	377	THR
1	C	41	THR
1	C	83	LEU
1	C	103	THR
1	C	115	TYR
1	C	119	ARG
1	C	127	ARG
1	C	151	ARG
1	C	190	ASP
1	C	197	LEU
1	C	207	PRO
1	C	210	ARG
1	C	221	LEU
1	C	240	ASN
1	C	277	THR
1	C	282	LEU
1	C	287	ARG

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Mol	Chain	Res	Type
1	C	299	LYS
1	C	307	LEU
1	C	336	ARG
1	C	337	LEU
1	C	355	LEU
1	C	357	ASP
1	C	360	ARG
1	C	369	ARG
1	C	375	ILE
1	D	4	GLU
1	D	41	THR
1	D	64	ILE
1	D	83	LEU
1	D	103	THR
1	D	115	TYR
1	D	127	ARG
1	D	151	ARG
1	D	190	ASP
1	D	197	LEU
1	D	207	PRO
1	D	210	ARG
1	D	221	LEU
1	D	240	ASN
1	D	277	THR
1	D	282	LEU
1	D	287	ARG
1	D	307	LEU
1	D	336	ARG
1	D	337	LEU
1	D	355	LEU
1	D	364	ARG
1	D	369	ARG
1	D	373	PRO
1	D	376	HIS
1	E	41	THR
1	E	61	HIS
1	E	83	LEU
1	E	103	THR
1	E	115	TYR
1	E	119	ARG
1	E	127	ARG
1	E	190	ASP

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Mol	Chain	Res	Type
1	E	197	LEU
1	E	207	PRO
1	E	210	ARG
1	E	221	LEU
1	E	240	ASN
1	E	277	THR
1	E	282	LEU
1	E	287	ARG
1	E	299	LYS
1	E	307	LEU
1	E	336	ARG
1	E	337	LEU
1	E	355	LEU
1	E	369	ARG
1	E	372	THR
1	E	377	THR
1	F	5	ARG
1	F	41	THR
1	F	83	LEU
1	F	103	THR
1	F	115	TYR
1	F	125	ARG
1	F	127	ARG
1	F	151	ARG
1	F	190	ASP
1	F	197	LEU
1	F	207	PRO
1	F	210	ARG
1	F	221	LEU
1	F	240	ASN
1	F	277	THR
1	F	282	LEU
1	F	286	LEU
1	F	287	ARG
1	F	307	LEU
1	F	322	THR
1	F	336	ARG
1	F	337	LEU
1	F	355	LEU
1	F	362	LEU
1	F	369	ARG
1	G	41	THR

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Mol	Chain	Res	Type
1	G	83	LEU
1	G	103	THR
1	G	115	TYR
1	G	119	ARG
1	G	127	ARG
1	G	190	ASP
1	G	197	LEU
1	G	207	PRO
1	G	210	ARG
1	G	221	LEU
1	G	240	ASN
1	G	277	THR
1	G	282	LEU
1	G	287	ARG
1	G	307	LEU
1	G	321	ASP
1	G	336	ARG
1	G	337	LEU
1	G	357	ASP
1	G	369	ARG
1	G	378	LYS
1	H	41	THR
1	H	83	LEU
1	H	103	THR
1	H	115	TYR
1	H	119	ARG
1	H	125	ARG
1	H	127	ARG
1	H	190	ASP
1	H	197	LEU
1	H	207	PRO
1	H	221	LEU
1	H	240	ASN
1	H	277	THR
1	H	282	LEU
1	H	287	ARG
1	H	307	LEU
1	H	336	ARG
1	H	337	LEU
1	H	355	LEU
1	H	357	ASP
1	H	360	ARG

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Mol	Chain	Res	Type
1	H	374	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	HIS
1	A	179	GLN
1	A	240	ASN
1	A	376	HIS
1	B	61	HIS
1	B	179	GLN
1	B	240	ASN
1	C	186	HIS
1	C	240	ASN
1	D	179	GLN
1	D	240	ASN
1	E	179	GLN
1	E	240	ASN
1	E	366	GLN
1	F	179	GLN
1	F	240	ASN
1	F	291	HIS
1	G	61	HIS
1	G	179	GLN
1	G	240	ASN
1	G	366	GLN
1	H	179	GLN
1	H	240	ASN
1	H	291	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

8 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	PO4	A	400	-	4,4,4	1.15	0	6,6,6	0.27	0
2	PO4	B	400	-	4,4,4	1.06	0	6,6,6	0.27	0
2	PO4	C	400	-	4,4,4	1.08	0	6,6,6	0.27	0
2	PO4	D	400	-	4,4,4	1.18	0	6,6,6	0.27	0
2	PO4	E	400	-	4,4,4	1.05	0	6,6,6	0.27	0
2	PO4	F	400	-	4,4,4	1.13	0	6,6,6	0.27	0
2	PO4	G	400	-	4,4,4	1.09	0	6,6,6	0.27	0
2	PO4	H	400	-	4,4,4	1.05	0	6,6,6	0.27	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PO4	A	400	-	-	0/0/0/0	0/0/0/0
2	PO4	B	400	-	-	0/0/0/0	0/0/0/0
2	PO4	C	400	-	-	0/0/0/0	0/0/0/0
2	PO4	D	400	-	-	0/0/0/0	0/0/0/0
2	PO4	E	400	-	-	0/0/0/0	0/0/0/0
2	PO4	F	400	-	-	0/0/0/0	0/0/0/0
2	PO4	G	400	-	-	0/0/0/0	0/0/0/0
2	PO4	H	400	-	-	0/0/0/0	0/0/0/0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	400	PO4	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	379/379 (100%)	-0.18	19 (5%)	32	31	23, 41, 84, 100	0
1	B	379/379 (100%)	-0.11	19 (5%)	32	31	23, 40, 87, 100	0
1	C	379/379 (100%)	-0.18	18 (4%)	35	34	23, 40, 84, 100	0
1	D	379/379 (100%)	-0.25	16 (4%)	40	39	22, 41, 89, 100	0
1	E	379/379 (100%)	-0.17	17 (4%)	37	36	23, 41, 88, 100	0
1	F	379/379 (100%)	-0.16	19 (5%)	32	31	23, 40, 90, 100	0
1	G	379/379 (100%)	-0.06	27 (7%)	19	17	24, 44, 97, 100	0
1	H	379/379 (100%)	-0.17	18 (4%)	35	34	23, 40, 85, 100	0
All	All	3032/3032 (100%)	-0.16	153 (5%)	32	31	22, 41, 91, 100	0

All (153) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2	ALA	15.4
1	F	1	ALA	14.3
1	E	377	THR	13.7
1	F	2	ALA	13.6
1	F	320	VAL	12.8
1	B	379	HIS	12.2
1	D	1	ALA	12.2
1	H	379	HIS	12.1
1	E	320	VAL	12.0
1	C	379	HIS	11.3
1	H	1	ALA	11.3
1	A	322	THR	11.1
1	B	322	THR	11.1
1	H	319	GLY	11.1
1	H	377	THR	10.9
1	B	377	THR	10.6

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Mol	Chain	Res	Type	RSRZ
1	F	379	HIS	10.4
1	B	321	ASP	10.3
1	E	379	HIS	10.3
1	C	1	ALA	10.2
1	H	323	ALA	10.1
1	E	378	LYS	10.1
1	H	376	HIS	10.1
1	F	322	THR	10.1
1	A	1	ALA	9.9
1	E	319	GLY	9.6
1	A	323	ALA	9.5
1	D	375	ILE	9.5
1	H	320	VAL	9.4
1	C	378	LYS	9.4
1	D	320	VAL	9.4
1	G	379	HIS	9.3
1	B	1	ALA	9.2
1	G	378	LYS	9.1
1	C	376	HIS	9.1
1	F	319	GLY	9.1
1	E	321	ASP	9.0
1	B	320	VAL	8.9
1	D	377	THR	8.9
1	G	377	THR	8.9
1	D	322	THR	8.8
1	G	323	ALA	8.7
1	G	324	ALA	8.7
1	B	323	ALA	8.6
1	H	2	ALA	8.5
1	A	320	VAL	8.3
1	C	322	THR	8.3
1	A	324	ALA	8.3
1	C	321	ASP	8.2
1	A	377	THR	8.2
1	C	323	ALA	8.2
1	H	321	ASP	8.2
1	H	322	THR	8.2
1	C	377	THR	8.1
1	D	378	LYS	8.1
1	F	376	HIS	7.9
1	C	2	ALA	7.9
1	D	379	HIS	7.8

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Mol	Chain	Res	Type	RSRZ
1	A	379	HIS	7.8
1	G	1	ALA	7.7
1	G	321	ASP	7.7
1	H	324	ALA	7.7
1	A	319	GLY	7.6
1	A	321	ASP	7.6
1	B	319	GLY	7.5
1	G	319	GLY	7.4
1	H	318	GLY	7.4
1	D	2	ALA	7.3
1	C	320	VAL	7.3
1	F	323	ALA	7.3
1	H	325	THR	7.2
1	D	3	SER	7.1
1	D	324	ALA	7.0
1	D	376	HIS	6.9
1	B	376	HIS	6.9
1	E	376	HIS	6.9
1	G	376	HIS	6.8
1	A	378	LYS	6.8
1	F	321	ASP	6.8
1	D	323	ALA	6.6
1	G	320	VAL	6.5
1	H	378	LYS	6.5
1	B	324	ALA	6.5
1	F	324	ALA	6.3
1	F	377	THR	6.2
1	B	378	LYS	6.1
1	D	321	ASP	6.1
1	C	319	GLY	6.0
1	G	325	THR	5.9
1	G	322	THR	5.9
1	F	318	GLY	5.6
1	A	318	GLY	5.6
1	F	325	THR	5.3
1	G	2	ALA	5.2
1	E	322	THR	5.2
1	A	376	HIS	5.1
1	B	325	THR	5.1
1	E	1	ALA	5.1
1	E	318	GLY	4.8
1	C	325	THR	4.7

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Mol	Chain	Res	Type	RSRZ
1	G	318	GLY	4.7
1	F	3	SER	4.7
1	B	375	ILE	4.6
1	D	325	THR	4.6
1	E	375	ILE	4.6
1	D	319	GLY	4.5
1	H	3	SER	4.5
1	C	324	ALA	4.5
1	B	318	GLY	4.5
1	F	378	LYS	4.4
1	F	63	PHE	4.4
1	A	325	THR	4.1
1	B	317	THR	4.0
1	A	375	ILE	3.9
1	C	61	HIS	3.5
1	H	112	ARG	3.4
1	F	4	GLU	3.4
1	A	63	PHE	3.3
1	D	318	GLY	3.3
1	E	2	ALA	3.3
1	E	112	ARG	3.3
1	E	63	PHE	3.3
1	G	4	GLU	3.2
1	G	326	GLY	3.2
1	C	318	GLY	3.2
1	E	374	VAL	3.1
1	A	2	ALA	3.1
1	B	63	PHE	3.0
1	G	120	TYR	2.9
1	F	317	THR	2.9
1	G	61	HIS	2.8
1	G	115	TYR	2.8
1	G	317	THR	2.8
1	A	317	THR	2.8
1	G	295	PRO	2.8
1	E	323	ALA	2.7
1	A	326	GLY	2.6
1	E	324	ALA	2.6
1	G	299	LYS	2.6
1	F	61	HIS	2.6
1	A	61	HIS	2.5
1	C	375	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	63	PHE	2.5
1	C	3	SER	2.5
1	H	63	PHE	2.5
1	G	375	ILE	2.4
1	B	3	SER	2.3
1	G	3	SER	2.2
1	G	327	GLY	2.1
1	G	329	PHE	2.1
1	G	181	GLN	2.1
1	B	369	ARG	2.1
1	H	61	HIS	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	PO4	D	400	5/5	0.98	0.13	-0.96	58,59,60,61	0
2	PO4	G	400	5/5	0.96	0.16	-	76,77,77,78	0
2	PO4	E	400	5/5	0.99	0.08	-	52,52,53,53	0
2	PO4	C	400	5/5	0.98	0.09	-	67,68,69,69	0
2	PO4	A	400	5/5	0.98	0.13	-	52,54,54,56	0
2	PO4	B	400	5/5	0.98	0.12	-	49,50,53,53	0
2	PO4	H	400	5/5	0.97	0.16	-	60,62,62,63	0
2	PO4	F	400	5/5	0.98	0.10	-	56,58,58,59	0

6.5 Other polymers

There are no such residues in this entry.