



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:38 PM GMT

PDB ID : 1PP9
Title : Bovine cytochrome bc1 complex with stigmatellin bound
Authors : Huang, L.S.; Cobessi, D.; Tung, E.Y.; Berry, E.A.
Deposited on : 2003-06-16
Resolution : 2.10 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

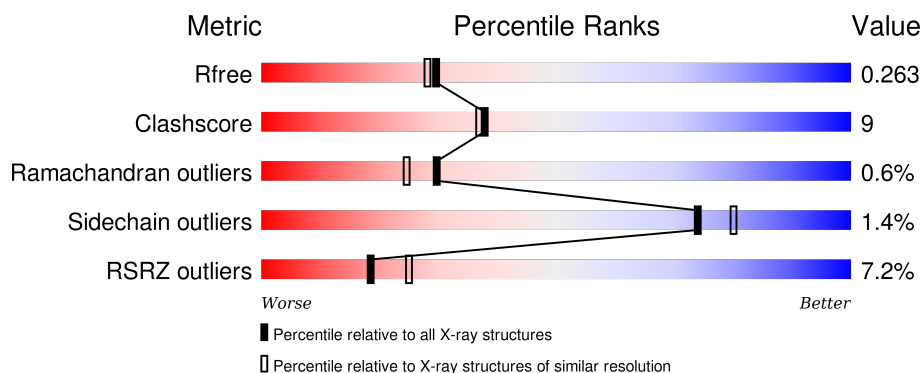
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	446	<div> <div>5%</div> <div>82%</div> <div>17%</div> <div>..</div> </div>
1	N	446	<div> <div>3%</div> <div>83%</div> <div>15%</div> <div>..</div> </div>
2	B	439	<div> <div>4%</div> <div>82%</div> <div>15%</div> <div>.</div> </div>
2	O	439	<div> <div>6%</div> <div>83%</div> <div>13%</div> <div>..</div> </div>
3	C	379	<div> <div>2%</div> <div>84%</div> <div>12%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
3	P	379	
4	D	241	
4	Q	241	
5	E	196	
5	R	196	
6	F	110	
6	S	110	
7	G	81	
7	T	81	
8	H	78	
8	U	78	
9	I	78	
9	V	78	
10	J	62	
10	W	62	

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
11	BHG	A	4002	X	-	-	X
11	BHG	C	2008	X	-	-	X
11	BHG	F	3011	X	-	-	X
11	BHG	F	4001	X	-	-	-
11	BHG	P	3008	X	-	-	X
11	BHG	S	2011	X	-	-	X
13	AZI	A	4005	-	-	-	X
13	AZI	C	2014	-	-	-	X
13	AZI	D	4004	-	-	-	X
13	AZI	P	3014	-	-	-	X
18	UQ	P	3002	-	-	-	X
19	CDL	G	2003	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
19	CDL	G	2004	-	-	-	X
20	PEE	C	2007	-	-	-	X
20	PEE	D	2006	-	-	-	X
20	PEE	G	2005	-	-	-	X
20	PEE	T	3005	-	-	-	X
21	GOL	B	2013	-	-	-	X
21	GOL	C	2009	-	-	-	X
21	GOL	O	3013	-	-	-	X
21	GOL	P	3009	-	-	-	X

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 33959 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 Ubiquinol-cytochrome C reductase complex core protein I, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	443	Total	C	N	O	S	10	0	1
			3403	2121	602	660	20			
1	N	443	Total	C	N	O	S	10	0	1
			3403	2121	602	660	20			

- Molecule 2 is a protein called Ubiquinol-cytochrome C reductase complex core protein 2, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	424	Total	C	N	O	S	0	0	1
			3177	1996	562	612	7			
2	O	424	Total	C	N	O	S	0	0	0
			3180	1998	562	613	7			

- Molecule 3 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	365	Total	C	N	O	S	0	0	0
			2892	1940	450	485	17			
3	P	370	Total	C	N	O	S	0	0	0
			2931	1968	455	490	18			

- Molecule 4 is a protein called Cytochrome c1, heme protein, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	241	Total	C	N	O	S	0	0	0
			1919	1225	330	349	15			
4	Q	241	Total	C	N	O	S	0	0	0
			1919	1225	330	349	15			

- Molecule 5 is a protein called Ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	196	Total	C	N	O	S	0	0	0
			1519	957	263	291	8			
5	R	196	Total	C	N	O	S	0	0	0
			1519	957	263	291	8			

- Molecule 6 is a protein called Ubiquinol-cytochrome C reductase complex 14 kDa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	99	Total	C	N	O	S	0	0	0
			861	545	155	159	2			
6	S	99	Total	C	N	O	S	0	0	0
			861	545	155	159	2			

- Molecule 7 is a protein called Ubiquinol-cytochrome C reductase complex ubiquinone-binding protein QP-C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	75	Total	C	N	O	S	0	0	2
			621	406	117	97	1			
7	T	76	Total	C	N	O	S	0	0	2
			626	409	118	98	1			

- Molecule 8 is a protein called Ubiquinol-cytochrome C reductase complex 11 kDa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	66	Total	C	N	O	S	0	0	0
			539	327	98	109	5			
8	U	66	Total	C	N	O	S	0	0	0
			539	327	98	109	5			

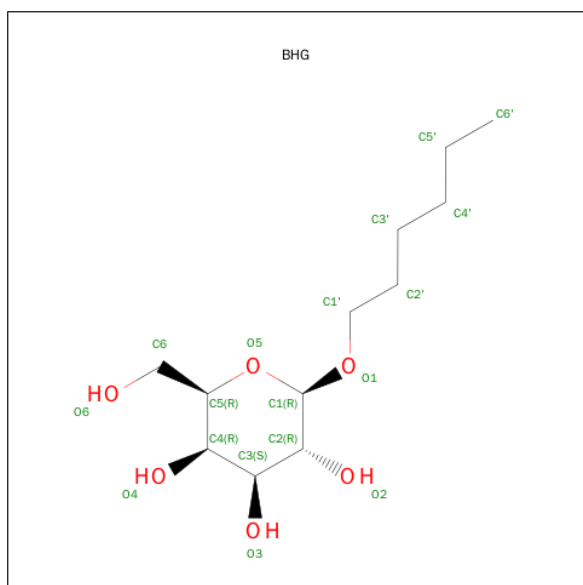
- Molecule 9 is a protein called Ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	42	Total	C	N	O	S	0	0	0
			285	174	55	55	1			
9	V	42	Total	C	N	O	S	0	0	0
			285	174	55	55	1			

- Molecule 10 is a protein called Ubiquinol-cytochrome C reductase complex 7.2 kDa protein.

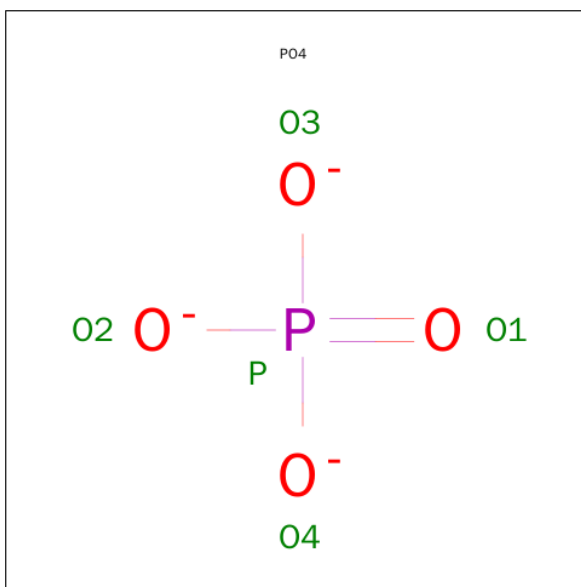
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	J	62	Total	C	N	O	0	0	0
			507	333	88	86			
10	W	62	Total	C	N	O	0	0	0
			507	333	88	86			

- Molecule 11 is SUGAR (2-HEXYLOXY-6-HYDROXYMETHYL-TETRAHYDRO-PYRAN-3,4,5-TRIOL) (three-letter code: BHG) (formula: C₁₂H₂₄O₆).



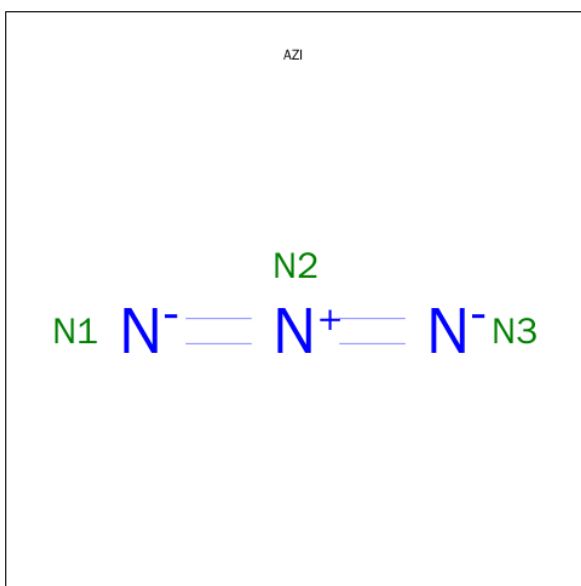
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	C	1	Total	C	O	0	0
			18	12	6		
11	S	1	Total	C	O	0	0
			18	12	6		
11	P	1	Total	C	O	0	0
			18	12	6		
11	F	1	Total	C	O	0	0
			18	12	6		
11	F	1	Total	C	O	0	0
			18	12	6		
11	A	1	Total	C	O	0	0
			18	12	6		

- Molecule 12 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	O	1	Total	O	P	0	0
			5	4	1		
12	B	1	Total	O	P	0	0
			5	4	1		

- Molecule 13 is AZIDE ION (three-letter code: AZI) (formula: N_3).



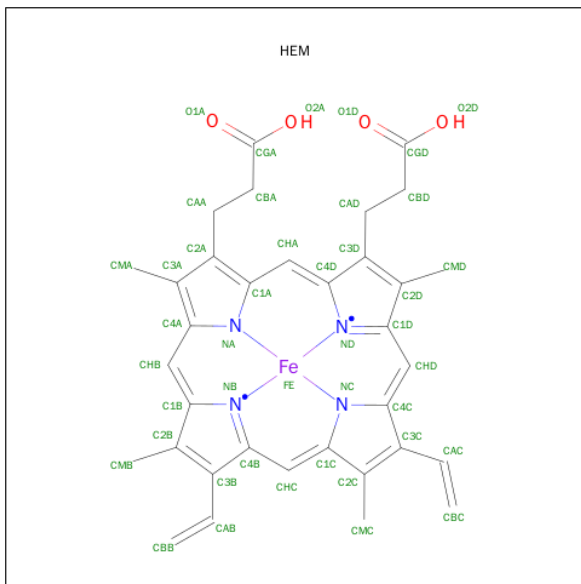
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	C	1	Total	N	0	0
			3	3		
13	P	1	Total	N	0	0
			3	3		

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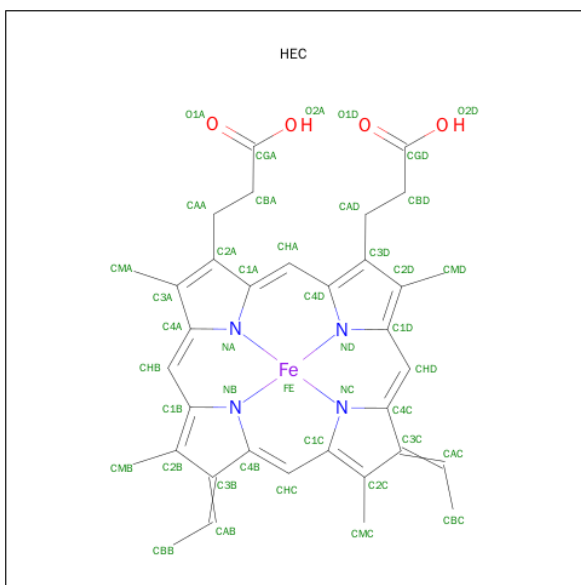
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	D	1	Total N 3 3	0	0
13	A	1	Total N 3 3	0	0

- Molecule 14 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



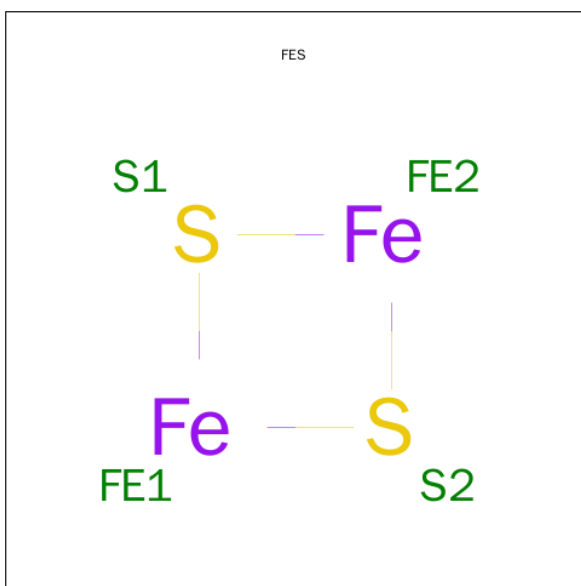
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
14	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
14	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
14	P	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
14	P	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 15 is HEME C (three-letter code: HEC) (formula: $\text{C}_{34}\text{H}_{34}\text{FeN}_4\text{O}_4$).



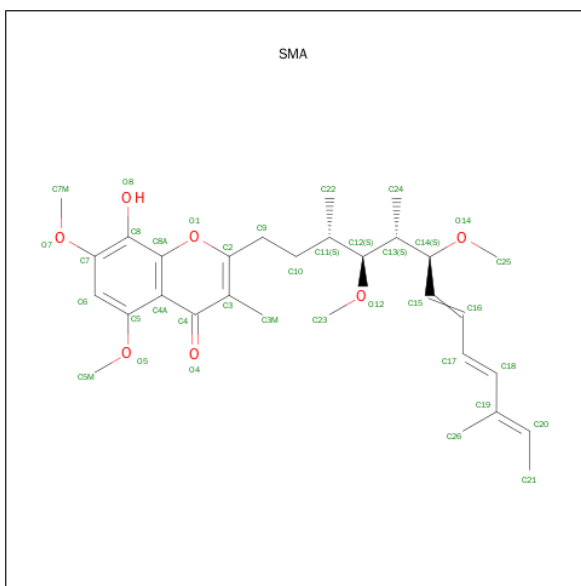
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
15	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
15	Q	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 16 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



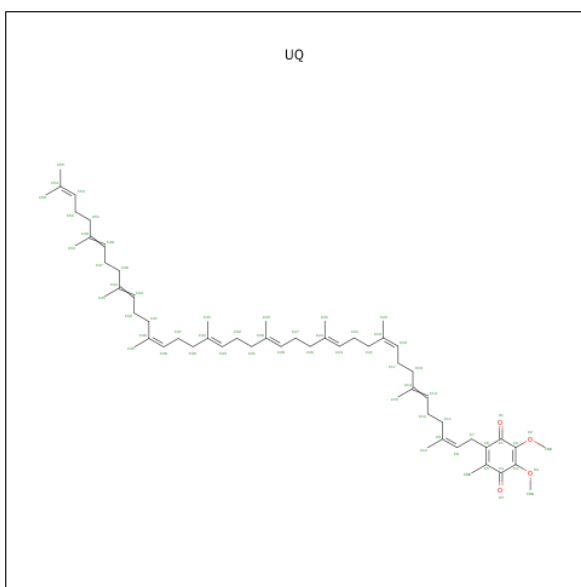
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
16	E	1	Total 4	Fe 2	S 2	0	0
16	R	1	Total 4	Fe 2	S 2	0	0

- Molecule 17 is STIGMATELLIN A (three-letter code: SMA) (formula: $\text{C}_{30}\text{H}_{42}\text{O}_7$).



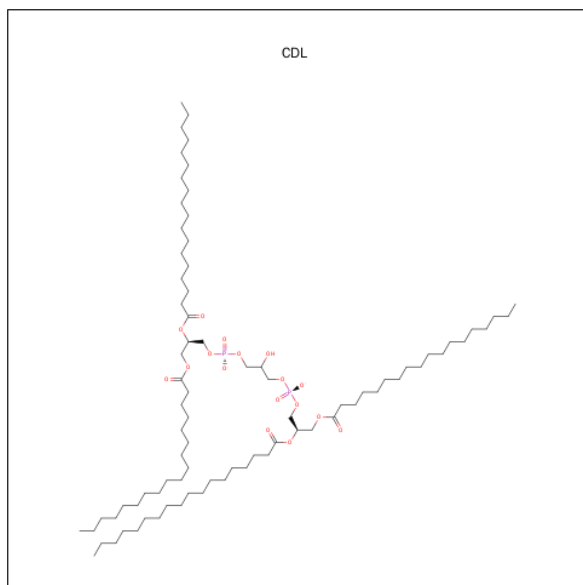
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
17	C	1	Total	C	O	0	0
			37	30	7		
17	P	1	Total	C	O	0	0
			37	30	7		

- Molecule 18 is COENZYME Q10, (2Z,6E,10Z,14E,18E,22E,26Z)-ISOMER (three-letter code: UQ) (formula: C₅₉H₉₀O₄).



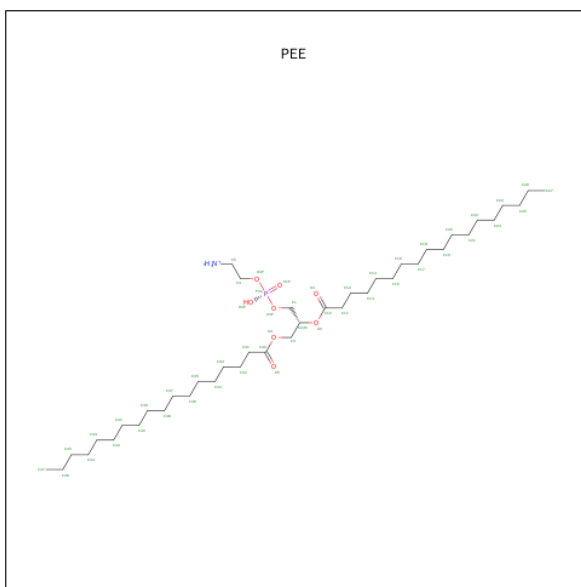
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
18	C	1	Total	C	O	0	0
			14	10	4		
18	P	1	Total	C	O	0	0
			14	10	4		

- Molecule 19 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
19	G	1	Total	C	O	P	0	0
			50	31	17	2		
19	G	1	Total	C	O	P	0	0
			44	25	17	2		
19	Q	1	Total	C	O	P	0	0
			50	31	17	2		
19	T	1	Total	C	O	P	0	0
			49	30	17	2		

- Molecule 20 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOETHANOLAMINE (three-letter code: PEE) (formula: $C_{41}H_{83}NO_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
20	G	1	Total	C	N	O	P	0	0
			49	39	1	8	1		
20	D	1	Total	C	N	O	P	0	0
			51	41	1	8	1		
20	C	1	Total	C	N	O	P	0	0
			49	39	1	8	1		
20	C	1	Total	O	P			0	0
			5	4	1				
20	T	1	Total	C	N	O	P	0	0
			49	39	1	8	1		
20	Q	1	Total	C	N	O	P	0	0
			51	41	1	8	1		
20	P	1	Total	C	N	O	P	0	0
			49	39	1	8	1		
20	N	1	Total	O	P			0	0
			5	4	1				
20	A	1	Total	C	O			0	0
			6	3	3				

- Molecule 21 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
21	C	1	Total	C	O	0	0
			6	3	3		
21	B	1	Total	C	O	0	0
			6	3	3		
21	P	1	Total	C	O	0	0
			6	3	3		
21	O	1	Total	C	O	0	0
			6	3	3		

- Molecule 22 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	A	187	Total	O	0	0
			187	187		
22	B	149	Total	O	0	0
			149	149		
22	C	125	Total	O	0	0
			125	125		
22	D	118	Total	O	0	0
			118	118		
22	E	54	Total	O	0	0
			54	54		
22	F	57	Total	O	0	0
			57	57		
22	G	24	Total	O	0	0
			24	24		
22	H	14	Total	O	0	0
			14	14		

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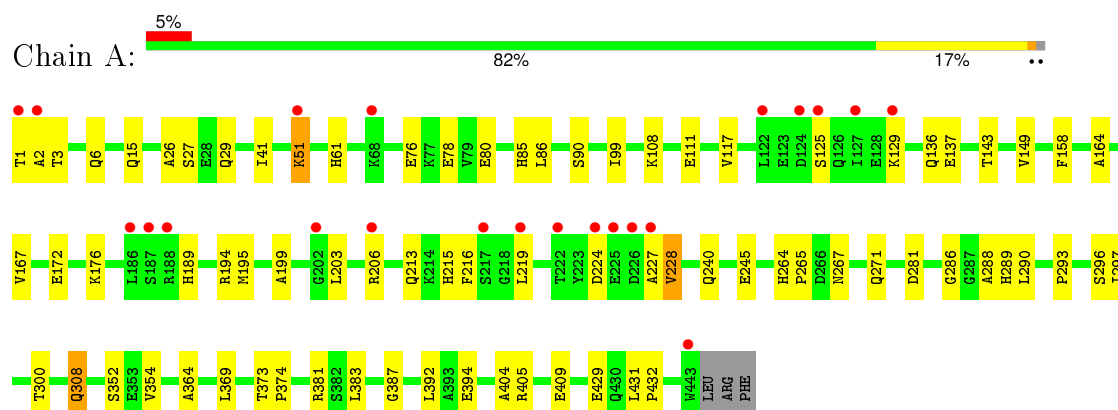
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	I	16	Total 16	O 16	0	0
22	J	5	Total 5	O 5	0	0
22	N	134	Total 134	O 134	0	0
22	O	130	Total 130	O 130	0	0
22	P	122	Total 122	O 122	0	0
22	Q	109	Total 109	O 109	0	0
22	R	64	Total 64	O 64	0	0
22	S	73	Total 73	O 73	0	0
22	T	21	Total 21	O 21	0	0
22	U	16	Total 16	O 16	0	0
22	V	10	Total 10	O 10	0	0
22	W	9	Total 9	O 9	0	0

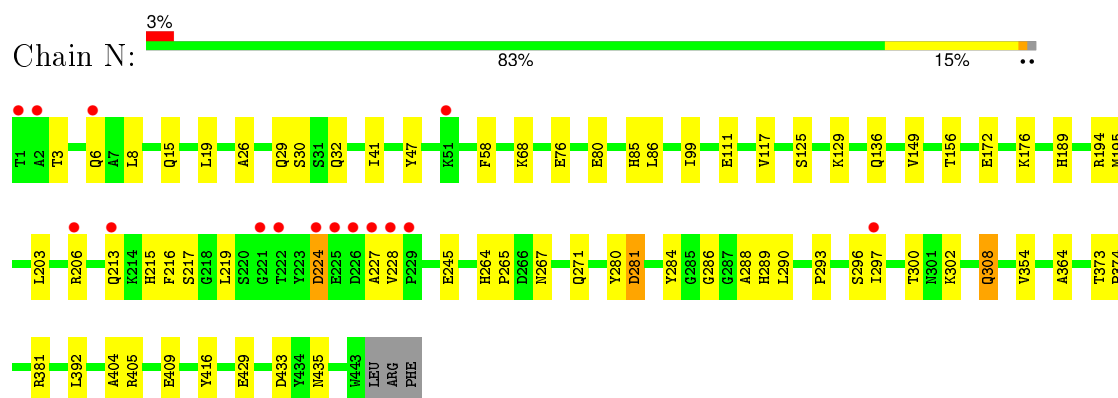
3 Residue-property plots [i](#)

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.

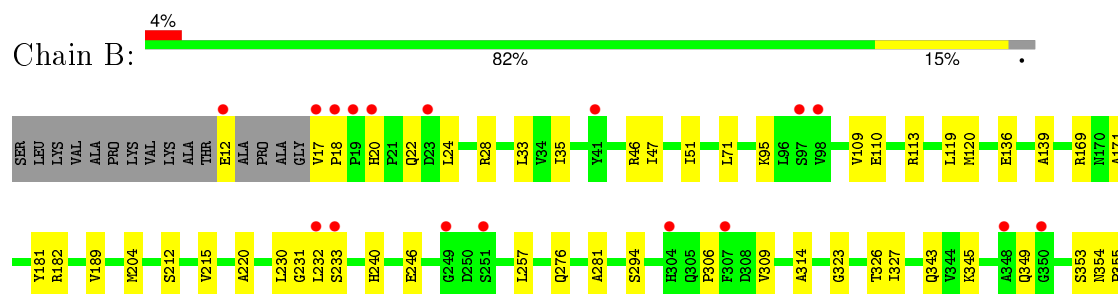
- Molecule 1: Ubiquinol-cytochrome C reductase complex core protein I, mitochondrial

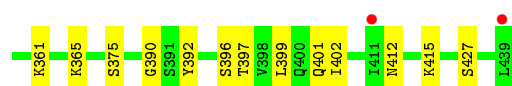


- Molecule 1: Ubiquinol-cytochrome C reductase complex core protein I, mitochondrial

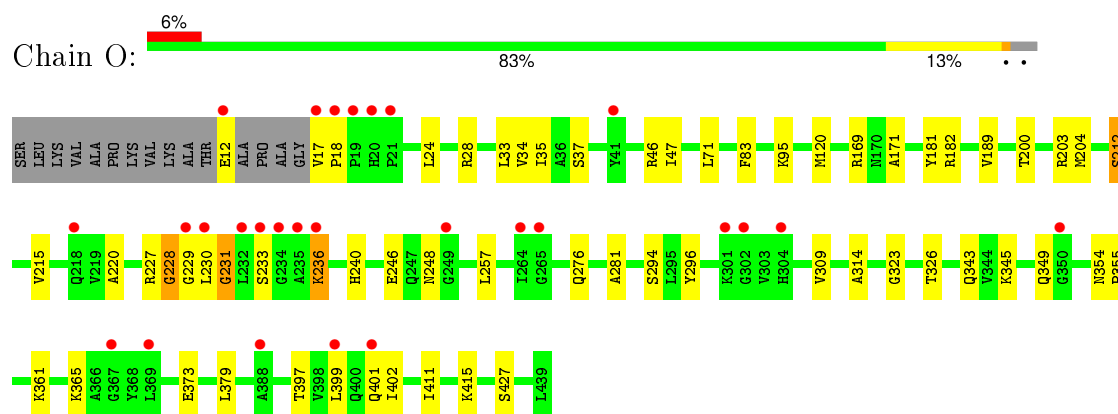


- Molecule 2: Ubiquinol-cytochrome C reductase complex core protein 2, mitochondrial

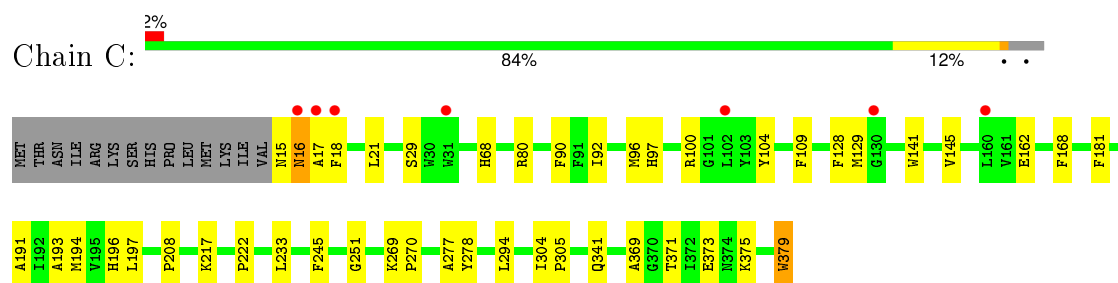




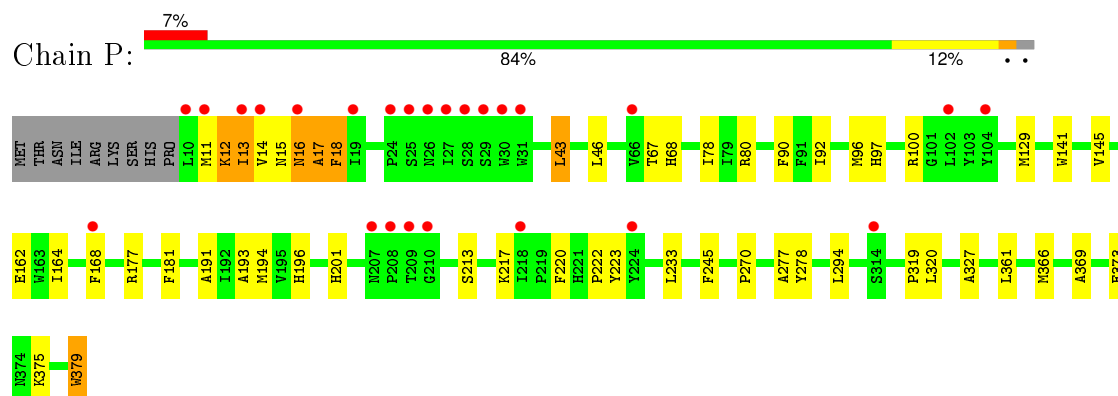
- Molecule 2: Ubiquinol-cytochrome C reductase complex core protein 2, mitochondrial



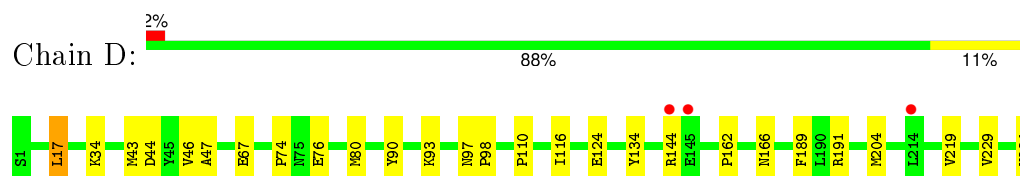
- Molecule 3: Cytochrome b



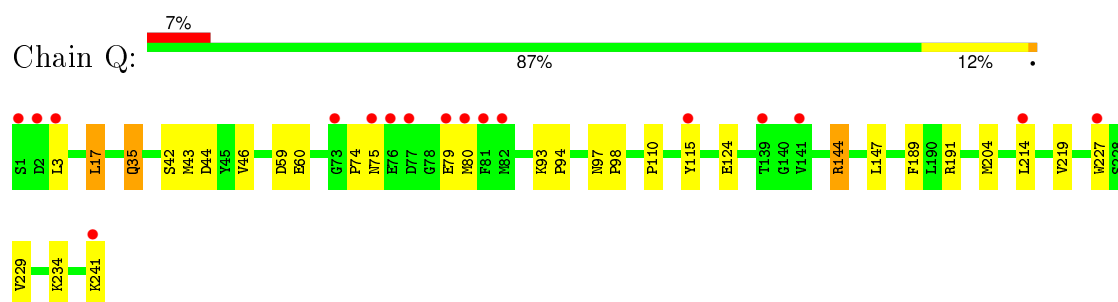
- Molecule 3: Cytochrome b



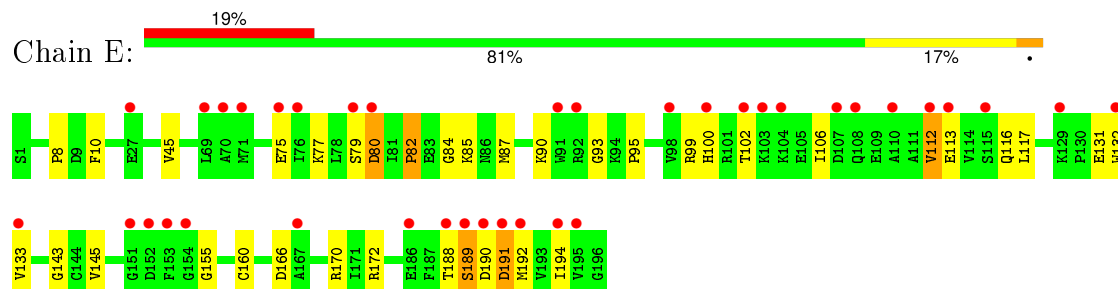
- Molecule 4: Cytochrome c1, heme protein, mitochondrial



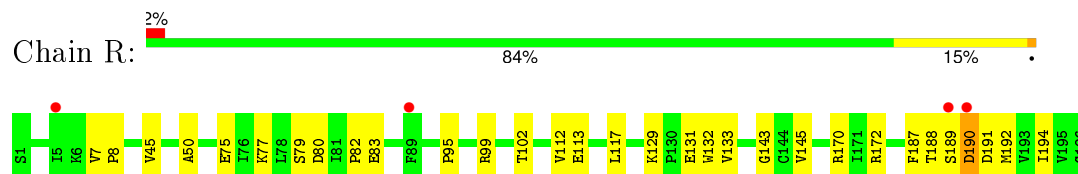
- Molecule 4: Cytochrome c1, heme protein, mitochondrial



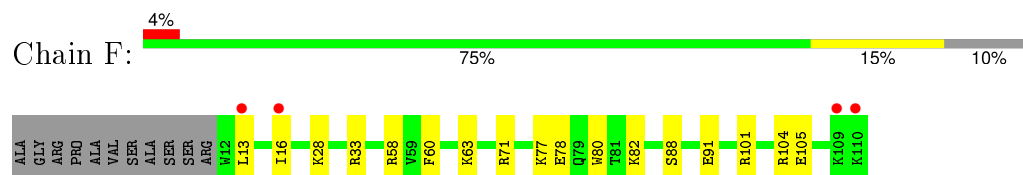
- Molecule 5: Ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial



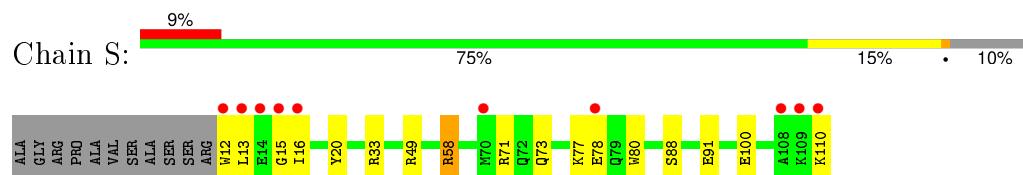
- Molecule 5: Ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial



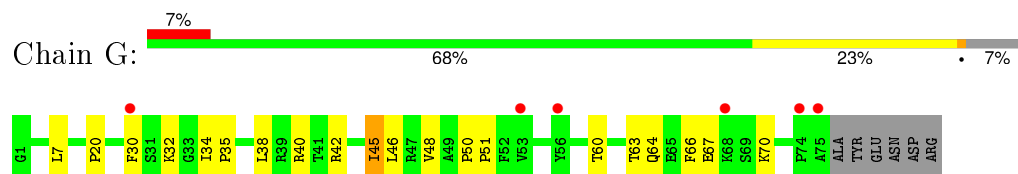
- Molecule 6: Ubiquinol-cytochrome C reductase complex 14 kDa protein



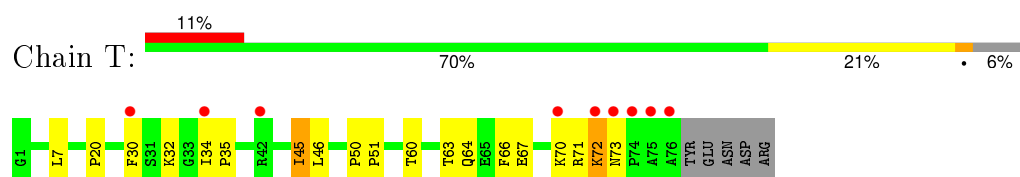
- Molecule 6: Ubiquinol-cytochrome C reductase complex 14 kDa protein



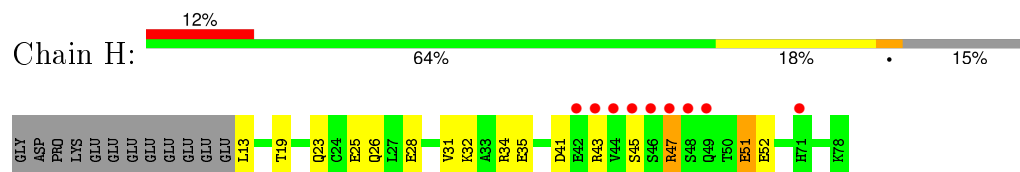
- Molecule 7: Ubiquinol-cytochrome C reductase complex ubiquinone-binding protein QP-C



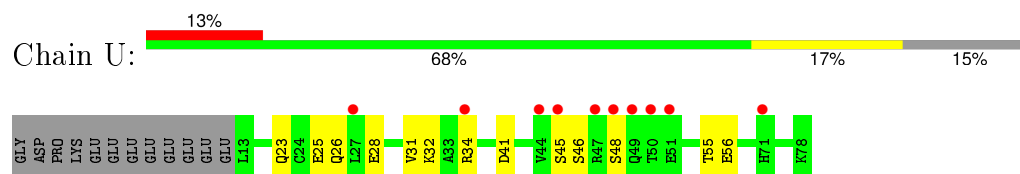
- Molecule 7: Ubiquinol-cytochrome C reductase complex ubiquinone-binding protein QP-C



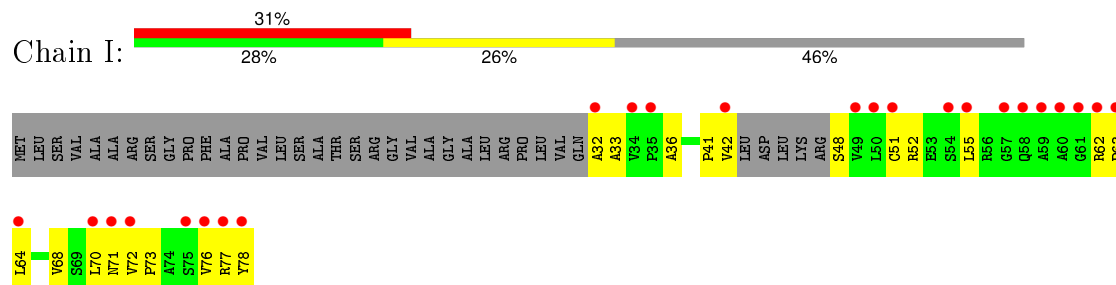
- Molecule 8: Ubiquinol-cytochrome C reductase complex 11 kDa protein



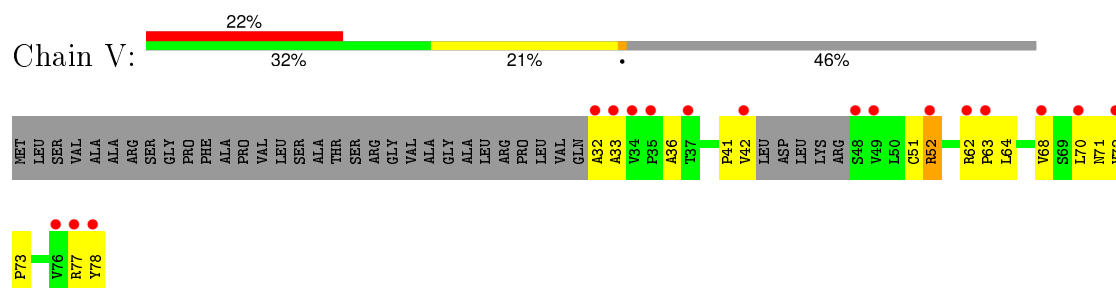
- Molecule 8: Ubiquinol-cytochrome C reductase complex 11 kDa protein



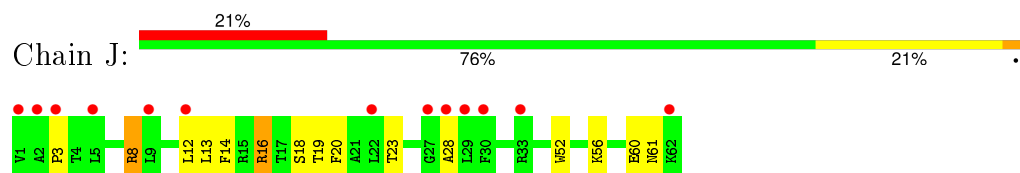
- Molecule 9: Ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial



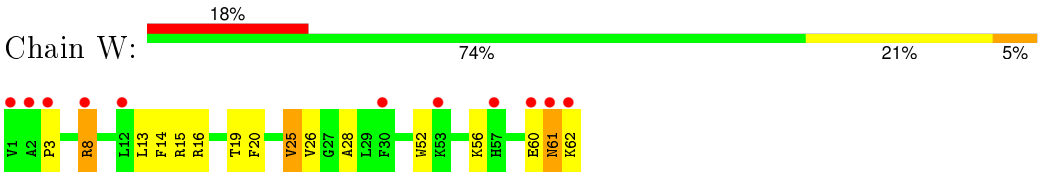
- Molecule 9: Ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial



- Molecule 10: Ubiquinol-cytochrome C reductase complex 7.2 kDa protein



- Molecule 10: Ubiquinol-cytochrome C reductase complex 7.2 kDa protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	139.12Å 171.06Å 227.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.98 – 2.10 40.02 – 2.08	Depositor EDS
% Data completeness (in resolution range)	97.3 (24.98-2.10) 96.1 (40.02-2.08)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.08Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.250 , 0.287 0.245 , 0.263	Depositor DCC
R_{free} test set	15200 reflections (5.23%)	DCC
Wilson B-factor (Å ²)	36.8	Xtriage
Anisotropy	0.517	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 60.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.39$	Xtriage
Outliers	2 of 308206 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	33959	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.53% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: AZI, GOL, CDL, PO4, UQ, BHG, FES, HEC, HEM, PEE, SMA

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	0.32	0/3472	0.66	0/4714
1	N	0.33	0/3472	0.67	0/4714
2	B	0.32	0/3235	0.65	0/4387
2	O	0.31	0/3239	0.65	1/4393 (0.0%)
3	C	0.36	0/2986	0.65	1/4089 (0.0%)
3	P	0.35	0/3024	0.64	0/4137
4	D	0.34	0/1978	0.65	0/2684
4	Q	0.34	0/1978	0.65	0/2684
5	E	0.31	0/1553	0.67	1/2100 (0.0%)
5	R	0.35	0/1553	0.69	1/2100 (0.0%)
6	F	0.32	0/878	0.64	0/1175
6	S	0.32	0/878	0.65	0/1175
7	G	0.32	0/642	0.65	0/869
7	T	0.34	0/647	0.68	0/876
8	H	0.30	0/544	0.60	0/729
8	U	0.31	0/544	0.56	0/729
9	I	0.32	0/285	0.66	0/384
9	V	0.32	0/285	0.69	0/384
10	J	0.36	0/520	0.65	0/699
10	W	0.36	0/520	0.65	0/699
All	All	0.33	0/32233	0.65	4/43721 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	228	GLY	N-CA-C	-6.96	95.71	113.10
5	R	143	GLY	N-CA-C	5.70	127.36	113.10
5	E	143	GLY	N-CA-C	5.38	126.54	113.10
3	C	109	PHE	N-CA-C	-5.22	96.91	111.00

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	3403	0	3302	63	0
1	N	3403	0	3302	53	0
2	B	3177	0	3152	64	0
2	O	3180	0	3156	56	0
3	C	2892	0	2938	39	0
3	P	2931	0	2989	59	0
4	D	1919	0	1868	25	0
4	Q	1919	0	1868	36	0
5	E	1519	0	1503	30	0
5	R	1519	0	1503	25	0
6	F	861	0	854	14	0
6	S	861	0	854	20	0
7	G	621	0	626	17	0
7	T	626	0	631	23	0
8	H	539	0	524	14	0
8	U	539	0	524	10	0
9	I	285	0	288	37	0
9	V	285	0	288	31	0
10	J	507	0	513	24	0
10	W	507	0	513	27	0
11	A	18	0	24	1	0
11	C	18	0	24	0	0
11	F	36	0	48	3	0
11	P	18	0	24	0	0
11	S	18	0	24	8	0
12	B	5	0	0	0	0
12	O	5	0	0	0	0
13	A	3	0	0	0	0
13	C	3	0	0	0	0
13	D	3	0	0	0	0
13	P	3	0	0	0	0
14	C	86	0	60	5	0
14	P	86	0	60	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	D	43	0	30	3	0
15	Q	43	0	30	2	0
16	E	4	0	0	0	0
16	R	4	0	0	0	0
17	C	37	0	42	1	0
17	P	37	0	42	2	0
18	C	14	0	9	3	0
18	P	14	0	9	5	0
19	G	94	0	76	5	0
19	Q	50	0	44	0	0
19	T	49	0	42	0	0
20	A	6	0	5	0	0
20	C	54	0	72	2	0
20	D	51	0	82	1	0
20	G	49	0	72	0	0
20	N	5	0	0	0	0
20	P	49	0	72	2	0
20	Q	51	0	82	9	0
20	T	49	0	72	1	0
21	B	6	0	8	0	0
21	C	6	0	8	0	0
21	O	6	0	8	0	0
21	P	6	0	8	0	0
22	A	187	0	0	8	0
22	B	149	0	0	2	0
22	C	125	0	0	4	0
22	D	118	0	0	2	0
22	E	54	0	0	2	0
22	F	57	0	0	3	0
22	G	24	0	0	1	0
22	H	14	0	0	0	0
22	I	16	0	0	1	0
22	J	5	0	0	0	0
22	N	134	0	0	1	0
22	O	130	0	0	1	0
22	P	122	0	0	6	0
22	Q	109	0	0	1	0
22	R	64	0	0	0	0
22	S	73	0	0	2	0
22	T	21	0	0	1	0
22	U	16	0	0	0	0
22	V	10	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	W	9	0	0	0	0
All	All	33959	0	32273	593	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 9.

All (593) 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)
2:O:95:LYS:HB2	9:V:32:ALA:HB2	1.20	1.12
2:B:12:GLU:HG2	2:B:17:VAL:H	1.15	1.09
7:T:45:ILE:HG22	7:T:46:LEU:HD22	1.31	1.04
2:O:200:THR:HB	2:O:229:GLY:HA2	1.36	1.04
3:P:43:LEU:HD21	20:Q:3006:PEE:H30	1.40	1.01
5:E:166:ASP:HA	22:E:541:HOH:O	1.59	1.01
4:Q:59:ASP:OD2	10:W:62:LYS:HB3	1.71	0.91
1:A:136:GLN:HE21	9:I:51:CYS:HB3	1.34	0.91
6:S:13:LEU:HD12	6:S:16:ILE:HD11	1.52	0.91
6:F:104:ARG:HH11	11:F:3011:BHG:H61	1.36	0.91
1:A:293:PRO:O	1:A:297:ILE:HG12	1.71	0.90
1:N:136:GLN:HE21	9:V:51:CYS:HB3	1.37	0.89
2:O:229:GLY:C	2:O:231:GLY:H	1.76	0.89
9:V:64:LEU:HD12	9:V:77:ARG:O	1.73	0.88
9:I:32:ALA:N	9:I:72:VAL:HG23	1.88	0.88
10:W:16:ARG:HB2	10:W:19:THR:HG22	1.56	0.87
1:A:1:THR:HG21	2:B:212:SER:HB3	1.55	0.86
9:V:52:ARG:HH11	9:V:52:ARG:HB3	1.40	0.86
3:C:129:MET:HE1	3:C:181:PHE:HD2	1.41	0.85
2:B:12:GLU:HG2	2:B:17:VAL:N	1.90	0.85
2:O:236:LYS:H	2:O:236:LYS:HD2	1.42	0.84
2:O:95:LYS:CB	9:V:32:ALA:HB2	2.06	0.84
1:N:293:PRO:O	1:N:297:ILE:HG12	1.78	0.83
4:D:74:PRO:HG3	4:D:80:MET:HE1	1.59	0.83
2:B:95:LYS:HB2	9:I:32:ALA:HB2	1.57	0.83
9:I:36:ALA:HB2	9:I:73:PRO:HD2	1.61	0.83
3:P:12:LYS:HE2	3:P:16:ASN:H	1.42	0.82
9:V:52:ARG:HB3	9:V:52:ARG:NH1	1.94	0.82
10:J:16:ARG:HB2	10:J:19:THR:HG22	1.58	0.82
9:I:64:LEU:HD12	9:I:77:ARG:O	1.78	0.81
1:N:29:GLN:HB3	2:O:12:GLU:O	1.80	0.80
7:T:72:LYS:HG3	8:U:56:GLU:OE2	1.81	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:12:LYS:HA	3:P:12:LYS:HE3	1.62	0.80
2:O:200:THR:CB	2:O:229:GLY:HA2	2.11	0.79
1:A:1:THR:HG21	2:B:212:SER:CB	2.13	0.78
10:J:16:ARG:NH1	10:J:19:THR:HG21	1.99	0.78
9:I:32:ALA:N	9:I:71:ASN:HB3	1.99	0.77
4:Q:110:PRO:HG3	15:Q:501:HEC:HMD3	1.66	0.77
10:W:13:LEU:O	10:W:19:THR:HG23	1.84	0.76
1:A:2:ALA:HB1	1:A:6:GLN:HB2	1.65	0.76
10:W:3:PRO:HB2	10:W:8:ARG:NH1	2.01	0.76
3:P:43:LEU:HD21	20:Q:3006:PEE:C19	2.17	0.75
4:Q:74:PRO:HG3	4:Q:80:MET:HE1	1.69	0.74
3:P:379:TRP:CZ3	6:S:33:ARG:HD3	2.22	0.74
3:P:129:MET:HE1	3:P:181:PHE:HD2	1.52	0.74
9:I:32:ALA:N	9:I:71:ASN:CB	2.51	0.74
2:O:71:LEU:HD23	9:V:68:VAL:HG21	1.69	0.74
10:W:16:ARG:HH11	10:W:19:THR:HG21	1.54	0.73
1:A:3:THR:OG1	1:A:6:GLN:HG3	1.88	0.73
8:U:28:GLU:O	8:U:31:VAL:HG22	1.89	0.73
1:A:352:SER:HB3	6:S:110:LYS:HD2	1.71	0.72
8:H:43:ARG:O	8:H:47:ARG:HD2	1.89	0.72
6:F:13:LEU:O	6:F:16:ILE:HG12	1.89	0.72
2:B:71:LEU:HD23	9:I:68:VAL:HG21	1.70	0.72
10:J:16:ARG:HB2	10:J:16:ARG:HH11	1.55	0.72
3:C:129:MET:CE	3:C:181:PHE:HD2	2.02	0.71
5:E:113:GLU:HB3	5:E:116:GLN:NE2	2.05	0.71
5:E:113:GLU:HB3	5:E:116:GLN:HE21	1.55	0.71
10:J:13:LEU:O	10:J:19:THR:HG23	1.90	0.71
4:Q:35:GLN:HG3	22:Q:3086:HOH:O	1.91	0.71
1:A:51:LYS:H	1:A:51:LYS:HZ1	1.39	0.70
4:Q:74:PRO:HG3	4:Q:80:MET:CE	2.22	0.70
3:P:96:MET:HE2	20:P:3007:PEE:H27	1.74	0.70
3:C:129:MET:HE1	3:C:181:PHE:CD2	2.26	0.70
2:B:47:ILE:HG21	2:B:120:MET:HE3	1.73	0.69
8:H:28:GLU:O	8:H:31:VAL:HG22	1.92	0.69
1:A:352:SER:HB3	6:S:110:LYS:CD	2.23	0.69
3:P:68:HIS:HD2	22:P:3131:HOH:O	1.75	0.69
2:B:231:GLY:N	2:B:233:SER:H	1.90	0.69
4:Q:75:ASN:HD21	4:Q:79:GLU:HG2	1.58	0.69
3:C:379:TRP:CZ3	6:F:33:ARG:HD3	2.28	0.69
1:A:136:GLN:HE21	9:I:51:CYS:CB	2.04	0.68
22:A:4185:HOH:O	9:I:73:PRO:HG3	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:29:GLN:HG3	1:N:203:LEU:O	1.94	0.68
2:B:353:SER:HB3	2:B:355:PRO:HD2	1.76	0.68
9:I:36:ALA:CB	9:I:73:PRO:HD2	2.23	0.68
5:R:79:SER:HB3	5:R:191:ASP:OD1	1.93	0.68
2:B:95:LYS:HD3	2:B:110:GLU:OE2	1.94	0.68
1:A:86:LEU:HD13	1:A:99:ILE:HG12	1.76	0.67
6:S:100:GLU:HB3	11:S:2011:BHG:H62	1.76	0.67
2:O:169:ARG:HG3	2:O:240:HIS:HB2	1.76	0.67
10:W:16:ARG:NH1	10:W:19:THR:HG21	2.10	0.67
1:N:32:GLN:OE1	2:O:373:GLU:HB2	1.94	0.67
3:P:129:MET:CE	3:P:181:PHE:HD2	2.08	0.66
1:A:2:ALA:O	2:B:113:ARG:NE	2.28	0.66
10:W:8:ARG:HG2	10:W:8:ARG:HH11	1.60	0.65
5:R:190:ASP:HB2	5:R:192:MET:HG2	1.79	0.65
10:J:16:ARG:HB2	10:J:19:THR:CG2	2.26	0.65
7:G:60:THR:O	7:G:64:GLN:HG3	1.95	0.65
2:O:365:LYS:HG2	2:O:399:LEU:HD22	1.78	0.65
6:S:13:LEU:HA	6:S:16:ILE:HG12	1.78	0.65
4:D:74:PRO:HG3	4:D:80:MET:CE	2.27	0.64
3:P:96:MET:CE	20:P:3007:PEE:H27	2.27	0.64
2:B:95:LYS:HD2	9:I:32:ALA:HB2	1.79	0.64
3:P:129:MET:HE1	3:P:181:PHE:CD2	2.32	0.64
9:I:36:ALA:HB3	9:I:73:PRO:HG2	1.78	0.64
1:N:136:GLN:NE2	9:V:51:CYS:HB3	2.11	0.64
2:B:231:GLY:N	2:B:232:LEU:N	2.46	0.64
7:T:60:THR:O	7:T:64:GLN:HG3	1.98	0.64
10:J:16:ARG:HH11	10:J:16:ARG:CB	2.10	0.64
8:H:25:GLU:HG2	8:H:34:ARG:HH22	1.62	0.64
2:O:95:LYS:HB2	9:V:32:ALA:CB	2.12	0.63
2:O:236:LYS:H	2:O:236:LYS:CD	2.07	0.63
2:B:95:LYS:CB	9:I:32:ALA:HB2	2.26	0.63
2:O:47:ILE:HG21	2:O:120:MET:HE3	1.81	0.63
7:T:71:ARG:HH11	7:T:72:LYS:HZ2	1.45	0.63
4:Q:75:ASN:ND2	4:Q:79:GLU:HG2	2.13	0.63
6:F:28:LYS:HE3	22:F:4052:HOH:O	1.98	0.63
5:E:113:GLU:CB	5:E:116:GLN:HE21	2.12	0.62
5:E:45:VAL:HG13	10:J:28:ALA:HA	1.80	0.62
10:J:14:PHE:HA	10:J:20:PHE:HD2	1.64	0.62
10:J:16:ARG:CG	10:J:16:ARG:HH11	2.12	0.62
9:V:32:ALA:N	9:V:71:ASN:CB	2.63	0.62
2:B:397:THR:O	2:B:401:GLN:HG3	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:296:TYR:OH	9:V:52:ARG:NE	2.33	0.62
3:C:29:SER:HB2	19:G:2004:CDL:HA31	1.82	0.62
2:B:47:ILE:HG21	2:B:120:MET:CE	2.30	0.61
3:C:96:MET:HE2	20:C:2007:PEE:H27	1.80	0.61
2:B:412:ASN:HA	2:B:415:LYS:HD2	1.80	0.61
1:N:41:ILE:HG12	1:N:195:MET:HG2	1.83	0.61
10:J:3:PRO:HD2	10:J:8:ARG:CZ	2.30	0.61
2:O:397:THR:O	2:O:401:GLN:HG3	2.01	0.61
2:O:227:ARG:C	2:O:229:GLY:N	2.50	0.61
4:Q:60:GLU:HG3	10:W:62:LYS:NZ	2.15	0.61
9:V:32:ALA:N	9:V:71:ASN:HB2	2.15	0.61
1:A:29:GLN:HG3	1:A:203:LEU:O	2.00	0.61
2:O:35:ILE:N	2:O:35:ILE:HD12	2.16	0.60
2:O:203:ARG:HH12	2:O:233:SER:HA	1.65	0.60
1:N:172:GLU:OE2	1:N:176:LYS:HE3	2.01	0.60
4:D:116:ILE:HG12	15:D:501:HEC:HMA3	1.83	0.60
3:P:145:VAL:HG21	17:P:3001:SMA:H6	1.84	0.60
4:Q:43:MET:HE2	4:Q:46:VAL:HG21	1.84	0.60
9:I:36:ALA:HB3	9:I:73:PRO:CG	2.31	0.60
3:P:14:VAL:O	3:P:18:PHE:HB3	2.01	0.60
7:T:71:ARG:HH11	7:T:72:LYS:NZ	1.99	0.60
1:N:308:GLN:HG2	22:N:3026:HOH:O	2.01	0.60
2:O:47:ILE:HG21	2:O:120:MET:CE	2.32	0.60
1:N:86:LEU:HD13	1:N:99:ILE:HG12	1.82	0.60
5:E:85:LYS:NZ	5:E:87:MET:SD	2.75	0.60
1:N:216:PHE:HD2	1:N:219:LEU:HD22	1.67	0.59
5:E:99:ARG:HB3	5:E:133:VAL:CG1	2.33	0.59
2:B:412:ASN:HD22	2:B:415:LYS:HD2	1.67	0.59
9:V:36:ALA:HB2	9:V:73:PRO:HD2	1.84	0.59
3:P:43:LEU:HD21	20:Q:3006:PEE:C20	2.33	0.59
2:O:227:ARG:C	2:O:229:GLY:H	2.02	0.59
4:D:43:MET:HE1	4:D:189:PHE:CZ	2.37	0.59
7:G:40:ARG:HB3	19:G:2004:CDL:HB32	1.85	0.59
10:J:3:PRO:HD2	10:J:8:ARG:NH2	2.18	0.59
1:A:296:SER:O	1:A:300:THR:HG23	2.02	0.59
7:G:45:ILE:HG22	7:G:46:LEU:HD12	1.85	0.59
2:B:354:ASN:N	2:B:355:PRO:CD	2.66	0.59
2:B:169:ARG:HG3	2:B:240:HIS:HB2	1.84	0.59
7:T:66:PHE:CZ	7:T:70:LYS:HD2	2.38	0.58
3:C:96:MET:CE	20:C:2007:PEE:H27	2.34	0.58
2:B:189:VAL:HG23	22:B:3089:HOH:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:77:LYS:HE3	5:E:79:SER:OG	2.03	0.58
1:N:8:LEU:HD22	1:N:392:LEU:HB3	1.84	0.58
2:B:309:VAL:HG23	2:B:326:THR:HG22	1.85	0.58
1:A:289:HIS:HE1	11:S:2011:BHG:H1'2	1.69	0.58
9:V:32:ALA:N	9:V:72:VAL:HG23	2.18	0.58
10:J:12:LEU:O	10:J:13:LEU:HD23	2.04	0.58
2:B:20:HIS:HB2	2:B:22:GLN:HG3	1.84	0.58
2:B:365:LYS:HG2	2:B:399:LEU:HD22	1.86	0.58
1:N:30:SER:HA	2:O:18:PRO:HG3	1.85	0.58
1:N:286:GLY:HA3	1:N:290:LEU:HD21	1.85	0.58
2:O:229:GLY:C	2:O:231:GLY:N	2.47	0.57
2:B:139:ALA:HB3	11:S:2011:BHG:H5'1	1.86	0.57
10:W:8:ARG:HH11	10:W:8:ARG:CG	2.18	0.57
1:A:136:GLN:NE2	9:I:51:CYS:CB	2.67	0.57
7:T:71:ARG:HD3	7:T:72:LYS:HZ3	1.70	0.57
3:C:145:VAL:HG21	17:C:2001:SMA:H6	1.84	0.57
6:F:82:LYS:HE3	22:F:4032:HOH:O	2.04	0.57
1:N:373:THR:HB	1:N:374:PRO:HD3	1.86	0.57
9:V:62:ARG:O	9:V:78:TYR:HB3	2.05	0.57
3:P:129:MET:HE2	3:P:181:PHE:HB2	1.87	0.56
10:J:3:PRO:HB2	10:J:8:ARG:HD3	1.86	0.56
10:W:25:VAL:HG12	10:W:26:VAL:N	2.20	0.56
2:B:95:LYS:CG	9:I:32:ALA:HB2	2.35	0.56
4:D:43:MET:HE1	4:D:189:PHE:HZ	1.69	0.56
2:B:20:HIS:HB2	2:B:22:GLN:CG	2.36	0.56
9:I:32:ALA:N	9:I:71:ASN:HB2	2.19	0.56
8:H:25:GLU:CG	8:H:34:ARG:HH22	2.19	0.56
7:T:30:PHE:O	7:T:34:ILE:HG12	2.06	0.56
8:U:25:GLU:HG2	8:U:34:ARG:HH22	1.71	0.56
5:E:190:ASP:O	5:E:192:MET:HG2	2.05	0.56
3:P:319:PRO:HD2	22:P:3113:HOH:O	2.05	0.55
7:G:63:THR:O	7:G:67:GLU:HG2	2.06	0.55
7:G:30:PHE:O	7:G:34:ILE:HG12	2.06	0.55
5:E:90:LYS:HE2	5:E:93:GLY:HA2	1.87	0.55
11:F:3011:BHG:H62	2:O:83:PHE:HB2	1.89	0.55
7:T:34:ILE:HB	7:T:35:PRO:HD3	1.89	0.55
3:P:201:HIS:NE2	18:P:3002:UQ:O4	2.28	0.55
3:C:217:LYS:HG3	7:G:7:LEU:HD13	1.89	0.55
4:Q:241:LYS:OXT	4:Q:241:LYS:HD3	2.06	0.55
9:I:62:ARG:O	9:I:78:TYR:HB3	2.07	0.55
1:A:51:LYS:NZ	1:A:51:LYS:H	2.03	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:12:GLU:CG	2:B:17:VAL:H	2.04	0.55
1:N:136:GLN:HE21	9:V:51:CYS:CB	2.15	0.55
2:B:95:LYS:HD2	9:I:32:ALA:CB	2.37	0.55
1:N:364:ALA:HB2	9:V:33:ALA:HB1	1.89	0.55
5:R:77:LYS:HE3	5:R:79:SER:OG	2.07	0.54
3:C:341:GLN:NE2	22:C:2099:HOH:O	2.39	0.54
3:C:245:PHE:CD1	4:D:17:LEU:HD13	2.41	0.54
9:V:36:ALA:HB3	9:V:73:PRO:HG2	1.89	0.54
6:F:63:LYS:HE2	22:G:1280:HOH:O	2.06	0.54
7:T:63:THR:O	7:T:67:GLU:HG2	2.07	0.54
3:P:12:LYS:HA	3:P:12:LYS:CE	2.37	0.54
1:A:216:PHE:HD2	1:A:219:LEU:HD22	1.71	0.54
7:T:45:ILE:HG22	7:T:46:LEU:CD2	2.22	0.54
1:A:172:GLU:OE2	1:A:176:LYS:HE3	2.06	0.54
1:A:76:GLU:HG2	1:A:80:GLU:OE2	2.07	0.54
2:B:12:GLU:O	2:B:18:PRO:HD3	2.08	0.54
5:R:191:ASP:N	5:R:191:ASP:OD2	2.40	0.54
2:O:411:ILE:O	2:O:415:LYS:HG3	2.08	0.54
10:W:56:LYS:HG2	10:W:60:GLU:CD	2.28	0.54
1:A:41:ILE:HG12	1:A:195:MET:HG2	1.89	0.53
3:P:100:ARG:C	3:P:100:ARG:HD2	2.28	0.53
2:B:306:PRO:HA	9:I:52:ARG:HE	1.74	0.53
3:P:43:LEU:HD21	20:Q:3006:PEE:H31	1.89	0.53
4:Q:59:ASP:OD2	10:W:62:LYS:CB	2.52	0.53
5:R:188:THR:HG21	5:R:194:ILE:CD1	2.37	0.53
4:Q:60:GLU:HG3	10:W:62:LYS:HZ3	1.74	0.53
2:O:229:GLY:O	2:O:230:LEU:HB2	2.07	0.53
3:P:220:PHE:HE1	18:P:3002:UQ:CM2	2.22	0.53
10:W:56:LYS:O	10:W:60:GLU:HG3	2.09	0.53
2:B:294:SER:OG	2:B:343:GLN:NE2	2.42	0.53
4:D:166:ASN:HB3	8:H:13:LEU:HD23	1.91	0.53
9:V:32:ALA:N	9:V:71:ASN:HB3	2.24	0.53
2:B:353:SER:CB	2:B:355:PRO:HD2	2.38	0.52
4:D:34:LYS:NZ	4:D:67:GLU:OE1	2.31	0.52
2:O:95:LYS:HG3	9:V:32:ALA:N	2.24	0.52
9:I:72:VAL:HG13	9:I:73:PRO:HD2	1.92	0.52
5:E:99:ARG:HB3	5:E:133:VAL:HG12	1.91	0.52
5:E:90:LYS:CE	5:E:93:GLY:HA2	2.40	0.52
4:Q:229:VAL:CG2	7:T:20:PRO:HD3	2.40	0.52
8:H:41:ASP:O	8:H:45:SER:HB2	2.09	0.52
10:J:13:LEU:HB3	10:J:23:THR:OG1	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:314:ALA:HA	9:I:63:PRO:HD3	1.90	0.52
4:D:234:LYS:HD3	5:E:8:PRO:HB2	1.91	0.52
2:O:276:GLN:HG2	2:O:281:ALA:HB2	1.91	0.52
1:N:76:GLU:HG2	1:N:80:GLU:OE2	2.09	0.52
2:O:189:VAL:HG23	22:O:3052:HOH:O	2.10	0.52
2:O:46:ARG:HG2	2:O:379:LEU:HD22	1.92	0.52
1:A:289:HIS:HE1	11:S:2011:BHG:C1'	2.23	0.52
1:N:30:SER:CA	2:O:18:PRO:HG3	2.39	0.52
2:O:181:TYR:CE1	2:O:182:ARG:HG2	2.44	0.52
9:V:72:VAL:HG13	9:V:73:PRO:HD2	1.91	0.52
4:D:34:LYS:HE3	22:D:4097:HOH:O	2.09	0.52
3:P:12:LYS:CE	3:P:15:ASN:HB3	2.39	0.52
5:E:102:THR:O	5:E:106:ILE:HG13	2.09	0.52
2:B:276:GLN:HG2	2:B:281:ALA:HB2	1.91	0.52
3:P:220:PHE:HE1	18:P:3002:UQ:HM22	1.74	0.52
3:C:129:MET:HE2	3:C:181:PHE:HB2	1.91	0.51
3:P:162:GLU:OE2	3:P:168:PHE:HD1	1.93	0.51
6:S:88:SER:OG	6:S:91:GLU:HB2	2.09	0.51
3:P:379:TRP:CE3	6:S:33:ARG:HD3	2.44	0.51
6:S:71:ARG:O	6:S:73:GLN:HG3	2.10	0.51
3:P:12:LYS:CA	3:P:12:LYS:HE3	2.36	0.51
10:W:52:TRP:O	10:W:56:LYS:HB2	2.11	0.51
5:R:77:LYS:HD3	5:R:80:ASP:OD2	2.10	0.51
1:N:206:ARG:HH11	1:N:206:ARG:HG3	1.75	0.51
4:D:234:LYS:HE2	5:E:10:PHE:CE1	2.46	0.51
14:C:502:HEM:HBA1	18:C:2002:UQ:O2	2.11	0.51
2:O:294:SER:OG	2:O:343:GLN:NE2	2.44	0.51
2:B:33:LEU:CD2	2:B:220:ALA:HB1	2.41	0.51
1:A:227:ALA:O	1:A:228:VAL:C	2.49	0.51
2:O:309:VAL:HG23	2:O:326:THR:HG22	1.93	0.51
6:S:12:TRP:O	6:S:16:ILE:N	2.36	0.51
10:W:16:ARG:HB2	10:W:19:THR:CG2	2.33	0.51
7:G:40:ARG:CB	19:G:2004:CDL:HB32	2.41	0.51
1:A:189:HIS:ND1	1:A:194:ARG:NH2	2.59	0.51
1:N:68:LYS:HA	1:N:68:LYS:HE3	1.93	0.51
1:A:206:ARG:HG3	1:A:206:ARG:HH11	1.76	0.51
8:U:25:GLU:CG	8:U:34:ARG:HH22	2.24	0.51
1:N:381:ARG:HH11	1:N:381:ARG:HG2	1.75	0.51
5:E:189:SER:C	5:E:190:ASP:OD1	2.49	0.50
5:R:188:THR:HG21	5:R:194:ILE:HD12	1.91	0.50
3:C:369:ALA:O	3:C:373:GLU:HG3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:T:71:ARG:HB2	7:T:72:LYS:HD3	1.93	0.50
1:A:308:GLN:HG2	22:A:4140:HOH:O	2.10	0.50
1:N:136:GLN:NE2	9:V:51:CYS:CB	2.72	0.50
5:R:99:ARG:HB3	5:R:133:VAL:CG1	2.42	0.50
3:C:68:HIS:HD2	22:C:2126:HOH:O	1.95	0.50
3:P:245:PHE:CG	4:Q:17:LEU:HD13	2.47	0.50
2:B:35:ILE:HD12	2:B:35:ILE:N	2.27	0.50
5:R:129:LYS:HG3	5:R:187:PHE:CE1	2.47	0.50
11:F:3011:BHG:H4	1:N:289:HIS:CE1	2.47	0.50
6:F:88:SER:OG	6:F:91:GLU:HB2	2.12	0.50
2:O:229:GLY:O	2:O:231:GLY:N	2.44	0.50
3:P:15:ASN:O	3:P:17:ALA:N	2.44	0.50
4:Q:124:GLU:OE2	4:Q:191:ARG:CD	2.60	0.50
1:A:373:THR:HB	1:A:374:PRO:HD3	1.92	0.50
2:O:200:THR:O	2:O:204:MET:HG3	2.12	0.50
2:B:95:LYS:CD	9:I:32:ALA:HB2	2.42	0.50
5:R:80:ASP:O	5:R:82:PRO:HD3	2.12	0.50
1:A:90:SER:HB3	22:A:4116:HOH:O	2.11	0.50
1:A:289:HIS:CE1	11:S:2011:BHG:H1'2	2.47	0.50
3:C:191:ALA:HA	3:C:194:MET:HE2	1.94	0.50
7:G:66:PHE:CZ	7:G:70:LYS:HD2	2.47	0.50
1:N:125:SER:O	1:N:129:LYS:HG3	2.11	0.50
1:A:125:SER:O	1:A:129:LYS:HG3	2.12	0.49
9:V:32:ALA:HA	9:V:71:ASN:HD22	1.77	0.49
20:Q:3006:PEE:H56	5:R:50:ALA:CB	2.42	0.49
2:O:354:ASN:N	2:O:355:PRO:CD	2.75	0.49
3:P:164:ILE:O	3:P:177:ARG:HD2	2.12	0.49
3:C:96:MET:HA	3:C:96:MET:HE2	1.93	0.49
10:W:3:PRO:HB2	10:W:8:ARG:HH11	1.74	0.49
15:D:501:HEC:HMC1	15:D:501:HEC:HBC3	1.94	0.49
5:E:82:PRO:O	5:E:100:HIS:HB3	2.12	0.49
5:R:99:ARG:HB3	5:R:133:VAL:HG12	1.94	0.49
1:A:364:ALA:HB2	9:I:33:ALA:HB1	1.95	0.49
1:N:405:ARG:O	1:N:409:GLU:HG3	2.13	0.49
8:H:28:GLU:O	8:H:32:LYS:HG2	2.13	0.49
1:A:172:GLU:HG3	1:A:176:LYS:HE3	1.95	0.49
1:N:227:ALA:O	1:N:228:VAL:HB	2.13	0.49
1:N:264:HIS:ND1	1:N:265:PRO:HD2	2.28	0.49
3:C:15:ASN:O	3:C:16:ASN:C	2.50	0.49
6:S:78:GLU:CD	6:S:78:GLU:H	2.16	0.48
6:S:100:GLU:OE1	11:S:2011:BHG:H4	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:191:ALA:HA	3:C:194:MET:CE	2.43	0.48
3:P:191:ALA:HA	3:P:194:MET:CE	2.43	0.48
3:C:21:LEU:HD21	18:C:2002:UQ:HM32	1.95	0.48
3:C:371:THR:O	3:C:375:LYS:HG2	2.13	0.48
2:B:109:VAL:HB	2:B:119:LEU:HD12	1.94	0.48
3:C:251:GLY:HA3	22:C:2091:HOH:O	2.13	0.48
6:S:13:LEU:HB3	22:S:2070:HOH:O	2.13	0.48
10:J:16:ARG:CG	10:J:16:ARG:NH1	2.75	0.48
5:R:79:SER:CB	5:R:191:ASP:OD1	2.61	0.48
4:D:110:PRO:HG3	15:D:501:HEC:HMD3	1.95	0.48
3:C:97:HIS:CD2	14:C:502:HEM:NC	2.81	0.48
3:P:245:PHE:CD1	4:Q:17:LEU:HD13	2.48	0.48
1:A:143:THR:OG1	9:I:48:SER:HB3	2.13	0.48
1:A:15:GLN:NE2	2:B:12:GLU:HB2	2.29	0.48
1:A:431:LEU:HD12	1:A:432:PRO:HD2	1.96	0.48
2:B:24:LEU:HD13	2:B:392:TYR:CD2	2.49	0.48
5:R:83:GLU:HG2	5:R:102:THR:HG22	1.96	0.48
3:C:379:TRP:CE3	6:F:33:ARG:HD3	2.47	0.48
2:O:365:LYS:HG2	2:O:399:LEU:CD2	2.42	0.48
1:A:117:VAL:HG11	1:A:195:MET:HE1	1.96	0.48
5:E:131:GLU:HG2	5:E:132:TRP:CD1	2.49	0.48
4:D:124:GLU:OE2	4:D:191:ARG:HD2	2.14	0.48
5:R:131:GLU:HG2	5:R:132:TRP:CD1	2.49	0.48
10:W:61:ASN:C	10:W:62:LYS:HG3	2.35	0.48
4:Q:43:MET:HE1	4:Q:189:PHE:HZ	1.79	0.48
4:Q:3:LEU:HD12	8:U:55:THR:HG22	1.96	0.48
3:C:141:TRP:CH2	5:R:145:VAL:HG23	2.49	0.48
5:E:155:GLY:N	22:E:541:HOH:O	2.46	0.47
2:O:354:ASN:HB3	2:O:355:PRO:HD3	1.96	0.47
6:F:78:GLU:H	6:F:78:GLU:CD	2.16	0.47
10:J:16:ARG:O	10:J:19:THR:HG22	2.14	0.47
10:J:16:ARG:CB	10:J:19:THR:HG22	2.38	0.47
10:W:8:ARG:CG	10:W:8:ARG:NH1	2.75	0.47
2:B:51:ILE:HG12	2:B:204:MET:HG2	1.95	0.47
2:B:212:SER:OG	2:B:215:VAL:HG23	2.15	0.47
3:P:14:VAL:O	3:P:15:ASN:O	2.32	0.47
1:A:213:GLN:HG2	22:A:4055:HOH:O	2.15	0.47
3:C:277:ALA:HB1	3:C:294:LEU:CD1	2.44	0.47
1:A:429:GLU:OE2	7:G:7:LEU:HB2	2.14	0.47
4:Q:97:ASN:HB2	4:Q:98:PRO:HD2	1.96	0.47
1:N:296:SER:O	1:N:300:THR:HG23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:52:TRP:O	10:J:56:LYS:HB2	2.13	0.47
3:P:14:VAL:C	3:P:15:ASN:CA	2.83	0.47
3:C:100:ARG:C	3:C:100:ARG:HD2	2.35	0.47
2:O:361:LYS:HE2	2:O:402:ILE:O	2.14	0.47
1:A:167:VAL:HG13	22:A:4111:HOH:O	2.15	0.47
2:B:246:GLU:O	2:B:427:SER:HA	2.15	0.47
2:B:345:LYS:O	2:B:349:GLN:HG3	2.14	0.47
3:P:193:ALA:O	3:P:196:HIS:HB3	2.15	0.47
7:T:46:LEU:HD23	22:T:3018:HOH:O	2.13	0.47
8:U:28:GLU:O	8:U:32:LYS:HG2	2.15	0.47
4:Q:43:MET:HE1	4:Q:189:PHE:CZ	2.50	0.47
2:B:396:SER:HB3	22:B:3031:HOH:O	2.14	0.47
1:N:111:GLU:HG3	1:N:215:HIS:CE1	2.50	0.47
2:O:17:VAL:HG13	2:O:18:PRO:HD2	1.96	0.47
4:Q:234:LYS:HD3	5:R:8:PRO:HB2	1.95	0.47
3:C:162:GLU:OE2	3:C:168:PHE:HD1	1.98	0.47
1:A:394:GLU:HA	11:A:4002:BHG:H2	1.96	0.47
7:T:46:LEU:HD22	7:T:46:LEU:N	2.30	0.47
2:B:95:LYS:HE3	9:I:72:VAL:HG21	1.97	0.47
1:N:172:GLU:HG3	1:N:176:LYS:HE3	1.96	0.47
5:E:79:SER:HB3	5:E:191:ASP:OD2	2.15	0.47
3:P:97:HIS:CD2	14:P:502:HEM:NC	2.83	0.47
2:B:257:LEU:O	2:B:323:GLY:HA3	2.15	0.47
5:R:45:VAL:HG13	10:W:28:ALA:HA	1.97	0.47
1:A:286:GLY:HA3	1:A:290:LEU:HD21	1.95	0.47
14:P:502:HEM:HBA1	18:P:3002:UQ:O2	2.15	0.46
4:D:124:GLU:OE2	4:D:191:ARG:CD	2.63	0.46
3:P:361:LEU:O	3:P:366:MET:HG3	2.15	0.46
5:E:85:LYS:HZ3	5:E:87:MET:HA	1.80	0.46
4:D:44:ASP:OD1	4:D:93:LYS:HE2	2.15	0.46
2:O:33:LEU:CD2	2:O:220:ALA:HB1	2.45	0.46
3:P:375:LYS:HD2	3:P:375:LYS:N	2.29	0.46
3:C:104:TYR:CD1	3:C:208:PRO:HA	2.51	0.46
1:A:15:GLN:HE21	2:B:12:GLU:HB2	1.81	0.46
3:P:92:ILE:O	3:P:96:MET:HG2	2.16	0.46
2:B:46:ARG:HD2	2:B:375:SER:OG	2.14	0.46
3:C:245:PHE:CG	4:D:17:LEU:HD13	2.50	0.46
10:J:16:ARG:HH12	10:J:19:THR:HG21	1.76	0.46
8:H:31:VAL:HG23	8:H:32:LYS:N	2.30	0.46
7:G:34:ILE:HB	7:G:35:PRO:HD3	1.95	0.46
22:P:3113:HOH:O	6:S:20:TYR:HE1	1.99	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:369:LEU:HD12	1:A:392:LEU:HD21	1.98	0.46
1:N:47:TYR:HB3	1:N:189:HIS:CE1	2.51	0.46
3:P:277:ALA:HB1	3:P:294:LEU:CD1	2.45	0.46
15:Q:501:HEC:HBC3	15:Q:501:HEC:HMC1	1.98	0.46
22:A:4072:HOH:O	6:S:110:LYS:HD2	2.15	0.46
2:O:24:LEU:HD12	2:O:37:SER:O	2.15	0.46
3:P:129:MET:CE	3:P:181:PHE:CD2	2.94	0.46
3:C:233:LEU:HD11	4:D:219:VAL:HG21	1.98	0.46
1:N:354:VAL:HG21	1:N:404:ALA:HA	1.96	0.46
20:Q:3006:PEE:H56	5:R:50:ALA:HB1	1.98	0.46
10:W:56:LYS:HG2	10:W:60:GLU:CG	2.46	0.46
1:A:29:GLN:HB3	2:B:12:GLU:O	2.16	0.46
4:Q:124:GLU:OE2	4:Q:191:ARG:HD2	2.16	0.46
9:I:70:LEU:HB3	22:I:1016:HOH:O	2.16	0.46
1:A:15:GLN:O	1:A:26:ALA:HA	2.16	0.46
9:I:36:ALA:CB	9:I:73:PRO:HB2	2.46	0.46
4:D:134:TYR:CG	4:D:162:PRO:HG3	2.51	0.46
9:V:36:ALA:CB	9:V:73:PRO:HB2	2.46	0.45
8:U:31:VAL:HG23	8:U:32:LYS:N	2.30	0.45
2:B:365:LYS:HG2	2:B:399:LEU:CD2	2.45	0.45
3:C:193:ALA:O	3:C:196:HIS:HB3	2.16	0.45
3:P:327:ALA:HA	7:T:51:PRO:HB3	1.98	0.45
3:P:43:LEU:CD2	20:Q:3006:PEE:H30	2.29	0.45
7:G:40:ARG:NH2	19:G:2004:CDL:HB31	2.32	0.45
1:A:264:HIS:HA	1:A:265:PRO:HD3	1.82	0.45
8:U:41:ASP:O	8:U:45:SER:HB2	2.15	0.45
2:O:71:LEU:CD2	9:V:68:VAL:HG21	2.43	0.45
10:W:16:ARG:O	10:W:19:THR:HG22	2.17	0.45
9:V:62:ARG:HB3	9:V:63:PRO:HD2	1.99	0.45
5:E:95:PRO:HG2	5:E:145:VAL:HG22	1.98	0.45
3:P:96:MET:HE2	3:P:96:MET:HA	1.99	0.45
1:N:117:VAL:HG11	1:N:195:MET:HE1	1.99	0.45
5:E:145:VAL:HG23	3:P:141:TRP:CH2	2.52	0.45
1:A:85:HIS:O	1:A:99:ILE:HA	2.16	0.45
1:N:195:MET:HE1	1:N:219:LEU:HD21	1.99	0.45
3:P:217:LYS:HG3	7:T:7:LEU:HD13	1.99	0.45
9:V:36:ALA:HB3	9:V:73:PRO:CG	2.46	0.45
10:J:16:ARG:HG3	10:J:16:ARG:NH1	2.32	0.45
3:P:12:LYS:HE2	3:P:16:ASN:HB2	1.99	0.44
3:C:92:ILE:O	3:C:96:MET:HG2	2.17	0.44
3:P:213:SER:OG	3:P:217:LYS:NZ	2.42	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:13:ILE:O	3:P:13:ILE:HG22	2.17	0.44
1:N:19:LEU:HD22	1:N:213:GLN:HG3	1.99	0.44
5:R:112:VAL:CG2	5:R:172:ARG:NH2	2.80	0.44
9:V:36:ALA:CB	9:V:73:PRO:HD2	2.47	0.44
7:G:38:LEU:HB3	7:G:42:ARG:NH1	2.32	0.44
2:B:28:ARG:HH21	2:B:390:GLY:HA3	1.81	0.44
8:H:51:GLU:HG3	8:H:52:GLU:N	2.32	0.44
1:A:354:VAL:HG21	1:A:404:ALA:HA	1.98	0.44
3:C:304:ILE:HB	3:C:305:PRO:HD3	1.99	0.44
7:T:71:ARG:NH1	7:T:72:LYS:HD2	2.31	0.44
8:H:31:VAL:O	8:H:35:GLU:HG3	2.17	0.44
1:N:213:GLN:O	1:N:217:SER:OG	2.25	0.44
4:Q:144:ARG:HG3	4:Q:147:LEU:HD12	1.98	0.44
9:I:76:VAL:O	9:I:76:VAL:HG13	2.16	0.44
4:Q:44:ASP:OD1	4:Q:93:LYS:HE2	2.18	0.44
6:S:110:LYS:O	6:S:110:LYS:HG3	2.17	0.44
3:P:270:PRO:HG2	3:P:278:TYR:CG	2.53	0.44
2:B:327:ILE:HG21	9:I:55:LEU:HD11	1.98	0.44
7:G:40:ARG:CZ	19:G:2004:CDL:HB31	2.47	0.44
5:R:75:GLU:HG2	5:R:194:ILE:HG12	2.00	0.44
2:B:230:LEU:HB3	2:B:233:SER:OG	2.18	0.44
18:P:3002:UQ:HM31	22:P:3116:HOH:O	2.17	0.44
3:C:197:LEU:HD21	14:C:502:HEM:HMA1	2.00	0.44
6:S:58:ARG:HD3	22:S:2031:HOH:O	2.18	0.44
6:S:49:ARG:HH22	11:S:2011:BHG:H4	1.83	0.43
14:C:501:HEM:HBC2	14:C:501:HEM:HMC1	2.00	0.43
5:R:117:LEU:HD13	5:R:170:ARG:HD2	2.00	0.43
4:Q:42:SER:HB3	4:Q:94:PRO:HD2	2.00	0.43
1:A:86:LEU:HD13	1:A:99:ILE:CG1	2.45	0.43
2:O:314:ALA:HA	9:V:63:PRO:HD3	2.00	0.43
10:J:56:LYS:HG2	10:J:60:GLU:CD	2.39	0.43
5:R:112:VAL:HG22	5:R:172:ARG:NH2	2.33	0.43
6:S:77:LYS:HA	6:S:80:TRP:CE2	2.54	0.43
2:B:361:LYS:HE2	2:B:402:ILE:O	2.18	0.43
3:C:129:MET:CE	3:C:181:PHE:CD2	2.90	0.43
1:N:288:ALA:HB2	1:N:300:THR:HG22	2.01	0.43
1:N:433:ASP:OD2	1:N:435:ASN:HB2	2.17	0.43
8:H:19:THR:O	8:H:23:GLN:HG3	2.19	0.43
4:D:204:MET:HE3	20:D:2006:PEE:O4	2.18	0.43
3:P:78:ILE:HD12	4:Q:204:MET:CE	2.49	0.43
1:A:27:SER:HA	1:A:199:ALA:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:15:GLN:O	1:N:26:ALA:HA	2.18	0.43
3:P:369:ALA:O	3:P:373:GLU:HG3	2.19	0.43
3:C:68:HIS:HE1	22:C:2049:HOH:O	2.01	0.43
7:G:50:PRO:HB2	7:G:51:PRO:HD3	2.01	0.43
2:O:228:GLY:O	2:O:231:GLY:HA2	2.18	0.43
2:B:136:GLU:HG2	11:S:2011:BHG:H2'1	2.00	0.43
5:E:112:VAL:HG22	5:E:172:ARG:NH2	2.34	0.43
2:B:181:TYR:CD2	2:O:248:ASN:HA	2.54	0.43
22:D:4077:HOH:O	6:F:71:ARG:HD3	2.18	0.43
9:I:36:ALA:HB2	9:I:73:PRO:CD	2.40	0.43
7:T:72:LYS:CG	8:U:56:GLU:OE2	2.62	0.43
14:C:501:HEM:O2D	14:C:501:HEM:O2A	2.37	0.43
4:D:47:ALA:HA	4:D:90:TYR:HA	2.01	0.43
4:Q:204:MET:HE3	4:Q:204:MET:HB3	1.83	0.43
4:Q:74:PRO:HG3	4:Q:80:MET:HE2	1.99	0.43
1:N:224:ASP:OD1	1:N:227:ALA:HB2	2.18	0.43
2:O:345:LYS:O	2:O:349:GLN:HG3	2.19	0.43
1:A:383:LEU:O	1:A:387:GLY:HA2	2.18	0.43
1:A:61:HIS:CE1	1:A:137:GLU:OE1	2.72	0.43
7:G:32:LYS:C	7:G:35:PRO:HD2	2.39	0.43
5:E:75:GLU:HG2	5:E:194:ILE:HG12	2.00	0.43
1:N:416:TYR:HB3	10:W:15:ARG:NH2	2.33	0.43
7:G:48:VAL:O	7:G:51:PRO:HD2	2.19	0.42
2:B:181:TYR:CE1	2:B:182:ARG:HG2	2.54	0.42
1:A:381:ARG:HG2	22:A:4120:HOH:O	2.19	0.42
1:N:3:THR:OG1	1:N:6:GLN:HG3	2.19	0.42
9:I:77:ARG:O	9:I:78:TYR:HB2	2.19	0.42
1:N:280:TYR:HA	1:N:284:TYR:CE2	2.54	0.42
1:A:111:GLU:HG3	1:A:215:HIS:CE1	2.54	0.42
3:C:269:LYS:HA	3:C:270:PRO:HD3	1.81	0.42
3:P:68:HIS:HE1	22:P:3053:HOH:O	2.03	0.42
1:A:117:VAL:HG11	1:A:195:MET:CE	2.49	0.42
1:A:240:GLN:NE2	22:A:4184:HOH:O	2.51	0.42
3:P:67:THR:HB	4:Q:115:TYR:OH	2.20	0.42
1:A:381:ARG:HH11	1:A:381:ARG:HG2	1.84	0.42
8:U:23:GLN:O	8:U:26:GLN:HG2	2.20	0.42
2:O:28:ARG:HB2	2:O:28:ARG:NH1	2.35	0.42
4:D:43:MET:CE	4:D:46:VAL:HG21	2.50	0.42
1:N:286:GLY:HA3	1:N:290:LEU:CD2	2.47	0.42
3:C:270:PRO:HG2	3:C:278:TYR:CG	2.54	0.42
1:A:158:PHE:O	1:A:164:ALA:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:GLU:OE2	1:A:108:LYS:HD2	2.20	0.42
4:D:97:ASN:HB2	4:D:98:PRO:HD2	2.01	0.42
7:T:71:ARG:HB2	7:T:72:LYS:H	1.66	0.42
3:P:320:LEU:HG	22:P:3113:HOH:O	2.19	0.42
1:A:267:ASN:O	1:A:271:GLN:HG2	2.20	0.42
3:P:46:LEU:HD11	20:Q:3006:PEE:H81	2.01	0.42
4:Q:75:ASN:HD21	4:Q:79:GLU:CG	2.30	0.42
4:Q:43:MET:HE2	4:Q:46:VAL:CG2	2.48	0.42
5:R:95:PRO:HG2	5:R:145:VAL:HG22	2.02	0.42
2:O:17:VAL:HA	2:O:18:PRO:HD3	1.85	0.42
2:O:257:LEU:O	2:O:323:GLY:HA3	2.19	0.42
1:N:267:ASN:O	1:N:271:GLN:HG2	2.19	0.42
1:N:281:ASP:OD1	1:N:281:ASP:C	2.58	0.42
7:T:32:LYS:C	7:T:35:PRO:HD2	2.40	0.42
10:W:14:PHE:HA	10:W:20:PHE:HD2	1.85	0.41
2:O:203:ARG:HH12	2:O:233:SER:CA	2.32	0.41
1:N:156:THR:HA	5:R:7:VAL:HG21	2.01	0.41
4:D:229:VAL:CG2	7:G:20:PRO:HD3	2.49	0.41
4:D:237:TYR:HB2	6:F:60:PHE:CD1	2.56	0.41
2:O:212:SER:OG	2:O:215:VAL:HG23	2.20	0.41
1:N:189:HIS:ND1	1:N:194:ARG:NH2	2.68	0.41
2:O:246:GLU:O	2:O:427:SER:HA	2.19	0.41
6:F:77:LYS:HA	6:F:80:TRP:CE2	2.55	0.41
5:E:117:LEU:HD13	5:E:170:ARG:HD2	2.03	0.41
9:I:36:ALA:HB3	9:I:73:PRO:HB2	2.02	0.41
2:B:46:ARG:O	2:B:47:ILE:HD13	2.21	0.41
1:N:302:LYS:HD3	1:N:302:LYS:HA	1.93	0.41
8:H:31:VAL:CG2	8:H:32:LYS:N	2.83	0.41
2:B:412:ASN:HD22	2:B:412:ASN:HA	1.67	0.41
1:N:429:GLU:OE2	7:T:7:LEU:HB2	2.21	0.41
5:E:160:CYS:HB3	17:P:3001:SMA:H4	2.03	0.41
5:E:84:GLY:N	5:E:100:HIS:O	2.54	0.41
7:T:50:PRO:HB2	7:T:51:PRO:HD3	2.03	0.41
6:S:12:TRP:O	6:S:15:GLY:N	2.53	0.41
10:W:16:ARG:HG3	10:W:16:ARG:NH1	2.36	0.41
6:F:63:LYS:HG3	22:F:4045:HOH:O	2.20	0.41
4:Q:124:GLU:OE2	4:Q:191:ARG:HD3	2.21	0.41
1:A:264:HIS:ND1	1:A:265:PRO:HD2	2.36	0.41
8:H:51:GLU:HG3	8:H:52:GLU:H	1.86	0.41
1:N:85:HIS:O	1:N:99:ILE:HA	2.20	0.41
8:H:23:GLN:O	8:H:26:GLN:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:101:ARG:O	6:F:105:GLU:HG3	2.21	0.41
2:B:71:LEU:CD2	9:I:68:VAL:HG21	2.44	0.41
2:O:47:ILE:HG13	2:O:120:MET:CE	2.51	0.41
10:J:14:PHE:CD1	10:J:14:PHE:N	2.87	0.41
2:O:34:VAL:C	2:O:35:ILE:HD12	2.41	0.41
9:I:62:ARG:HB3	9:I:63:PRO:HD2	2.02	0.41
1:A:288:ALA:HB2	1:A:300:THR:HG22	2.02	0.41
3:P:162:GLU:OE2	3:P:168:PHE:CD1	2.73	0.41
1:A:405:ARG:O	1:A:409:GLU:HG3	2.20	0.41
2:B:95:LYS:HB2	9:I:32:ALA:CB	2.41	0.40
5:E:80:ASP:O	5:E:82:PRO:HD3	2.21	0.40
1:N:19:LEU:CD2	1:N:213:GLN:HG3	2.51	0.40
4:Q:204:MET:HE3	20:Q:3006:PEE:O4	2.21	0.40
4:D:43:MET:HE2	4:D:46:VAL:HG21	2.01	0.40
10:J:56:LYS:HE2	10:J:56:LYS:HB3	1.76	0.40
10:J:18:SER:OG	10:J:19:THR:N	2.55	0.40
9:V:62:ARG:HB2	9:V:78:TYR:CG	2.56	0.40
3:P:223:TYR:HB3	4:Q:227:TRP:CZ2	2.56	0.40
4:Q:214:LEU:HA	20:T:3005:PEE:H58	2.03	0.40
2:B:47:ILE:HG13	2:B:120:MET:CE	2.52	0.40
10:W:56:LYS:HE2	10:W:56:LYS:HB3	1.75	0.40
3:P:191:ALA:HA	3:P:194:MET:HE2	2.03	0.40
9:V:70:LEU:HB3	22:V:1017:HOH:O	2.22	0.40
3:P:233:LEU:HD11	4:Q:219:VAL:HG21	2.03	0.40
5:E:188:THR:C	5:E:189:SER:O	2.60	0.40
3:C:21:LEU:HD21	18:C:2002:UQ:CM3	2.52	0.40
10:W:14:PHE:N	10:W:14:PHE:CD1	2.89	0.40
14:P:501:HEM:HMC1	14:P:501:HEM:HBC2	2.02	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	441/446 (99%)	425 (96%)	14 (3%)	2 (0%)	34	30
1	N	441/446 (99%)	425 (96%)	15 (3%)	1 (0%)	52	53
2	B	418/439 (95%)	409 (98%)	8 (2%)	1 (0%)	52	53
2	O	420/439 (96%)	406 (97%)	12 (3%)	2 (0%)	34	30
3	C	363/379 (96%)	354 (98%)	6 (2%)	3 (1%)	24	17
3	P	366/379 (97%)	353 (96%)	8 (2%)	5 (1%)	14	7
4	D	239/241 (99%)	234 (98%)	5 (2%)	0	100	100
4	Q	239/241 (99%)	235 (98%)	4 (2%)	0	100	100
5	E	194/196 (99%)	183 (94%)	7 (4%)	4 (2%)	9	3
5	R	194/196 (99%)	184 (95%)	9 (5%)	1 (0%)	34	30
6	F	97/110 (88%)	96 (99%)	1 (1%)	0	100	100
6	S	97/110 (88%)	96 (99%)	1 (1%)	0	100	100
7	G	73/81 (90%)	72 (99%)	1 (1%)	0	100	100
7	T	74/81 (91%)	69 (93%)	4 (5%)	1 (1%)	14	7
8	H	64/78 (82%)	61 (95%)	3 (5%)	0	100	100
8	U	64/78 (82%)	62 (97%)	1 (2%)	1 (2%)	12	6
9	I	38/78 (49%)	36 (95%)	1 (3%)	1 (3%)	7	2
9	V	38/78 (49%)	36 (95%)	1 (3%)	1 (3%)	7	2
10	J	60/62 (97%)	57 (95%)	2 (3%)	1 (2%)	11	5
10	W	60/62 (97%)	58 (97%)	1 (2%)	1 (2%)	11	5
All	All	3980/4220 (94%)	3851 (97%)	104 (3%)	25 (1%)	30	24

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	224	ASP
3	C	16	ASN
3	C	17	ALA
9	I	41	PRO
10	J	61	ASN
1	N	224	ASP
3	P	17	ALA
7	T	72	LYS
9	V	41	PRO
10	W	61	ASN
2	B	171	ALA

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Mol	Chain	Res	Type
5	E	112	VAL
2	O	171	ALA
2	O	231	GLY
3	P	16	ASN
8	U	48	SER
5	R	189	SER
1	A	228	VAL
3	C	18	PHE
5	E	189	SER
5	E	191	ASP
3	P	11	MET
3	P	18	PHE
5	E	82	PRO
3	P	13	ILE

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	364/370 (98%)	359 (99%)	5 (1%)	74	80
1	N	364/370 (98%)	359 (99%)	5 (1%)	74	80
2	B	332/343 (97%)	332 (100%)	0	100	100
2	O	332/343 (97%)	330 (99%)	2 (1%)	90	94
3	C	312/327 (95%)	307 (98%)	5 (2%)	70	76
3	P	316/327 (97%)	310 (98%)	6 (2%)	65	70
4	D	206/206 (100%)	203 (98%)	3 (2%)	72	78
4	Q	206/206 (100%)	203 (98%)	3 (2%)	72	78
5	E	168/168 (100%)	167 (99%)	1 (1%)	90	94
5	R	168/168 (100%)	166 (99%)	2 (1%)	78	84
6	F	90/98 (92%)	89 (99%)	1 (1%)	80	85
6	S	90/98 (92%)	89 (99%)	1 (1%)	80	85
7	G	66/71 (93%)	65 (98%)	1 (2%)	72	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	T	66/71 (93%)	64 (97%)	2 (3%)	48	51
8	H	63/74 (85%)	61 (97%)	2 (3%)	46	48
8	U	63/74 (85%)	62 (98%)	1 (2%)	70	76
9	I	28/60 (47%)	27 (96%)	1 (4%)	42	43
9	V	28/60 (47%)	26 (93%)	2 (7%)	18	14
10	J	51/52 (98%)	49 (96%)	2 (4%)	39	39
10	W	51/52 (98%)	49 (96%)	2 (4%)	39	39
All	All	3364/3538 (95%)	3317 (99%)	47 (1%)	74	80

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	LYS
1	A	149	VAL
1	A	245	GLU
1	A	281	ASP
1	A	308	GLN
3	C	80	ARG
3	C	90	PHE
3	C	128	PHE
3	C	222	PRO
3	C	379	TRP
4	D	17	LEU
4	D	76	GLU
4	D	144	ARG
5	E	80	ASP
6	F	58	ARG
7	G	45	ILE
8	H	47	ARG
8	H	51	GLU
9	I	42	VAL
10	J	8	ARG
10	J	16	ARG
1	N	58	PHE
1	N	149	VAL
1	N	245	GLU
1	N	281	ASP
1	N	308	GLN
2	O	212	SER
2	O	236	LYS

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Mol	Chain	Res	Type
3	P	12	LYS
3	P	43	LEU
3	P	80	ARG
3	P	90	PHE
3	P	222	PRO
3	P	379	TRP
4	Q	17	LEU
4	Q	35	GLN
4	Q	144	ARG
5	R	113	GLU
5	R	190	ASP
6	S	58	ARG
7	T	45	ILE
7	T	73	ASN
8	U	46	SER
9	V	42	VAL
9	V	52	ARG
10	W	8	ARG
10	W	25	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	GLN
1	A	61	HIS
1	A	136	GLN
1	A	213	GLN
1	A	271	GLN
1	A	289	HIS
2	B	22	GLN
2	B	104	ASN
2	B	343	GLN
2	B	412	ASN
3	C	68	HIS
3	C	159	ASN
4	D	106	ASN
5	E	57	GLN
5	E	116	GLN
7	G	73	ASN
1	N	15	GLN
1	N	61	HIS
1	N	136	GLN

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Mol	Chain	Res	Type
1	N	165	GLN
1	N	213	GLN
1	N	271	GLN
2	O	104	ASN
2	O	240	HIS
2	O	343	GLN
2	O	412	ASN
3	P	68	HIS
3	P	159	ASN
4	Q	106	ASN
4	Q	121	HIS
5	R	57	GLN
6	S	73	GLN
7	T	28	HIS
9	V	71	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

41 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
11	BHG	A	4002	-	18,18,18	1.84	4 (22%)	23,23,23	0.77	1 (4%)
20	PEE	A	4003	-	5,5,50	1.26	0	5,5,55	0.68	0
13	AZI	A	4005	-	0,2,2	0.00	-	0,1,1	0.00	-
21	GOL	B	2013	-	5,5,5	1.25	0	5,5,5	0.68	0
12	PO4	B	3010	-	4,4,4	0.78	0	6,6,6	0.89	0
17	SMA	C	2001	-	35,38,38	1.81	6 (17%)	40,52,52	1.91	3 (7%)
18	UQ	C	2002	-	14,14,63	2.18	8 (57%)	18,20,79	0.52	0
20	PEE	C	2007	-	48,48,50	1.18	5 (10%)	49,53,55	0.85	4 (8%)
11	BHG	C	2008	-	18,18,18	1.76	4 (22%)	23,23,23	0.72	0
21	GOL	C	2009	-	5,5,5	1.28	0	5,5,5	0.66	0
20	PEE	C	2012	-	4,4,50	3.40	3 (75%)	6,6,55	0.52	0
13	AZI	C	2014	-	0,2,2	0.00	-	0,1,1	0.00	-
14	HEM	C	501	3	30,50,50	2.80	7 (23%)	24,82,82	2.37	10 (41%)
14	HEM	C	502	3	30,50,50	2.58	10 (33%)	24,82,82	2.61	10 (41%)
20	PEE	D	2006	-	50,50,50	1.25	7 (14%)	51,55,55	0.87	4 (7%)
13	AZI	D	4004	-	0,2,2	0.00	-	0,1,1	0.00	-
15	HEC	D	501	4	24,50,50	1.96	6 (25%)	19,82,82	3.03	5 (26%)
16	FES	E	501	5	0,4,4	0.00	-	0,4,4	0.00	-
11	BHG	F	3011	-	18,18,18	1.84	4 (22%)	23,23,23	0.75	0
11	BHG	F	4001	-	18,18,18	1.74	5 (27%)	23,23,23	0.71	0
19	CDL	G	2003	-	49,49,99	1.08	3 (6%)	51,61,111	1.11	4 (7%)
19	CDL	G	2004	-	43,43,99	1.10	2 (4%)	45,55,111	1.24	4 (8%)
20	PEE	G	2005	-	48,48,50	1.26	7 (14%)	49,53,55	0.84	4 (8%)
20	PEE	N	3012	-	4,4,50	3.20	3 (75%)	6,6,55	0.52	0
12	PO4	O	2010	-	4,4,4	0.82	0	6,6,6	0.89	0
21	GOL	O	3013	-	5,5,5	1.25	0	5,5,5	0.74	0
17	SMA	P	3001	-	35,38,38	2.01	8 (22%)	40,52,52	1.95	3 (7%)
18	UQ	P	3002	-	14,14,63	1.98	8 (57%)	18,20,79	0.36	0
20	PEE	P	3007	-	48,48,50	1.21	5 (10%)	49,53,55	0.84	4 (8%)
11	BHG	P	3008	-	18,18,18	1.77	4 (22%)	23,23,23	0.70	0
21	GOL	P	3009	-	5,5,5	1.31	0	5,5,5	0.65	0
13	AZI	P	3014	-	0,2,2	0.00	-	0,1,1	0.00	-
14	HEM	P	501	3	30,50,50	3.25	9 (30%)	24,82,82	2.39	8 (33%)
14	HEM	P	502	3	30,50,50	3.13	10 (33%)	24,82,82	2.60	11 (45%)
19	CDL	Q	3003	-	49,49,99	1.07	4 (8%)	51,61,111	1.18	4 (7%)
20	PEE	Q	3006	-	50,50,50	1.24	6 (12%)	51,55,55	0.88	4 (7%)
15	HEC	Q	501	4	24,50,50	1.92	4 (16%)	19,82,82	2.57	3 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
16	FES	R	501	5	0,4,4	0.00	-	0,4,4	0.00	-
11	BHG	S	2011	-	18,18,18	1.77	3 (16%)	23,23,23	0.77	0
19	CDL	T	3004	-	48,48,99	1.13	4 (8%)	50,60,111	1.14	2 (4%)
20	PEE	T	3005	-	48,48,50	1.28	8 (16%)	49,53,55	0.85	5 (10%)

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
11	BHG	A	4002	-	1/1/5/5	0/9/29/29	0/1/1/1
20	PEE	A	4003	-	-	0/4/4/54	0/0/0/0
13	AZI	A	4005	-	-	0/0/0/0	0/0/0/0
21	GOL	B	2013	-	-	0/4/4/4	0/0/0/0
12	PO4	B	3010	-	-	0/0/0/0	0/0/0/0
17	SMA	C	2001	-	-	0/33/34/34	0/2/2/2
18	UQ	C	2002	-	-	0/4/28/87	0/1/1/1
20	PEE	C	2007	-	-	0/52/52/54	0/0/0/0
11	BHG	C	2008	-	1/1/5/5	0/9/29/29	0/1/1/1
21	GOL	C	2009	-	-	0/4/4/4	0/0/0/0
20	PEE	C	2012	-	-	0/0/0/54	0/0/0/0
13	AZI	C	2014	-	-	0/0/0/0	0/0/0/0
14	HEM	C	501	3	-	0/10/54/54	0/0/8/8
14	HEM	C	502	3	-	0/10/54/54	0/0/8/8
20	PEE	D	2006	-	-	0/54/54/54	0/0/0/0
13	AZI	D	4004	-	-	0/0/0/0	0/0/0/0
15	HEC	D	501	4	-	0/6/54/54	0/0/8/8
16	FES	E	501	5	-	0/0/4/4	0/1/1/1
11	BHG	F	3011	-	1/1/5/5	0/9/29/29	0/1/1/1
11	BHG	F	4001	-	1/1/5/5	0/9/29/29	0/1/1/1
19	CDL	G	2003	-	-	0/58/58/110	0/0/0/0
19	CDL	G	2004	-	-	0/52/52/110	0/0/0/0
20	PEE	G	2005	-	-	0/52/52/54	0/0/0/0
20	PEE	N	3012	-	-	0/0/0/54	0/0/0/0
12	PO4	O	2010	-	-	0/0/0/0	0/0/0/0
21	GOL	O	3013	-	-	0/4/4/4	0/0/0/0
17	SMA	P	3001	-	-	0/33/34/34	0/2/2/2
18	UQ	P	3002	-	-	0/4/28/87	0/1/1/1
20	PEE	P	3007	-	-	0/52/52/54	0/0/0/0
11	BHG	P	3008	-	1/1/5/5	0/9/29/29	0/1/1/1
21	GOL	P	3009	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	AZI	P	3014	-	-	0/0/0/0	0/0/0/0
14	HEM	P	501	3	-	0/10/54/54	0/0/8/8
14	HEM	P	502	3	-	0/10/54/54	0/0/8/8
19	CDL	Q	3003	-	-	0/58/58/110	0/0/0/0
20	PEE	Q	3006	-	-	0/54/54/54	0/0/0/0
15	HEC	Q	501	4	-	0/6/54/54	0/0/8/8
16	FES	R	501	5	-	0/0/4/4	0/1/1/1
11	BHG	S	2011	-	1/1/5/5	0/9/29/29	0/1/1/1
19	CDL	T	3004	-	-	0/57/57/110	0/0/0/0
20	PEE	T	3005	-	-	0/52/52/54	0/0/0/0

All (157) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	P	501	HEM	C3B-CAB	-8.00	1.36	1.51
14	C	501	HEM	C3C-CAC	-8.00	1.36	1.51
14	P	501	HEM	C3C-CAC	-7.44	1.37	1.51
14	C	502	HEM	C3C-CAC	-7.43	1.37	1.51
14	P	502	HEM	C3B-CAB	-7.33	1.37	1.51
14	P	502	HEM	C3C-CAC	-7.33	1.37	1.51
14	P	501	HEM	C3B-C4B	-7.19	1.45	1.51
14	C	501	HEM	C3B-CAB	-7.05	1.38	1.51
14	P	501	HEM	C2D-C3D	-6.77	1.34	1.54
14	P	502	HEM	C2D-C3D	-6.37	1.35	1.54
14	C	501	HEM	C2D-C3D	-6.23	1.35	1.54
15	Q	501	HEC	C3C-C2C	-6.06	1.34	1.40
15	D	501	HEC	C3B-C2B	-5.97	1.34	1.40
14	C	502	HEM	C2D-C3D	-5.77	1.37	1.54
15	D	501	HEC	C3C-C2C	-4.88	1.35	1.40
14	C	501	HEM	C3B-C4B	-4.70	1.47	1.51
14	C	502	HEM	C3B-CAB	-4.62	1.42	1.51
14	P	502	HEM	C2C-C1C	-4.08	1.44	1.52
14	P	502	HEM	C3B-C4B	-3.66	1.48	1.51
15	Q	501	HEC	C3B-C2B	-3.46	1.37	1.40
20	Q	3006	PEE	C19-C18	-3.07	1.33	1.51
14	P	502	HEM	C3D-C4D	-3.05	1.47	1.51
20	G	2005	PEE	C22-C21	-2.97	1.34	1.51
20	T	3005	PEE	C22-C21	-2.96	1.34	1.51
20	Q	3006	PEE	C22-C21	-2.95	1.34	1.51
20	D	2006	PEE	C19-C18	-2.94	1.34	1.51
20	C	2007	PEE	C19-C18	-2.93	1.34	1.51
20	G	2005	PEE	C19-C18	-2.91	1.34	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	D	2006	PEE	C22-C21	-2.89	1.34	1.51
20	P	3007	PEE	C19-C18	-2.87	1.34	1.51
20	P	3007	PEE	C22-C21	-2.87	1.34	1.51
20	T	3005	PEE	C19-C18	-2.83	1.35	1.51
20	C	2007	PEE	C22-C21	-2.80	1.35	1.51
14	P	501	HEM	C2C-C1C	-2.75	1.47	1.52
19	T	3004	CDL	OB8-CB6	-2.45	1.39	1.45
19	T	3004	CDL	OA8-CA6	-2.37	1.39	1.45
14	C	502	HEM	C3B-C4B	-2.30	1.49	1.51
14	C	502	HEM	C2C-C1C	-2.23	1.48	1.52
17	P	3001	SMA	C9-C2	-2.20	1.48	1.50
19	Q	3003	CDL	OA8-CA6	-2.09	1.40	1.45
19	G	2004	CDL	OA8-CA6	-2.07	1.40	1.45
19	Q	3003	CDL	OB8-CB6	-2.06	1.40	1.45
14	C	502	HEM	C3D-C4D	-2.04	1.49	1.51
19	G	2003	CDL	OB8-CB6	-2.01	1.40	1.45
15	D	501	HEC	C4A-NA	2.00	1.39	1.36
20	T	3005	PEE	C31-C30	2.01	1.56	1.50
11	F	4001	BHG	C1-C2	2.02	1.58	1.52
11	F	4001	BHG	O5-C5	2.05	1.49	1.44
11	P	3008	BHG	O5-C5	2.05	1.49	1.44
20	D	2006	PEE	C31-C30	2.07	1.56	1.50
11	C	2008	BHG	O5-C5	2.07	1.49	1.44
15	D	501	HEC	C4C-NC	2.13	1.39	1.36
15	D	501	HEC	C3B-C4B	2.14	1.47	1.42
20	T	3005	PEE	C1-C2	2.15	1.56	1.50
18	C	2002	UQ	C5-C4	2.17	1.55	1.47
20	D	2006	PEE	C3-C2	2.17	1.56	1.50
19	Q	3003	CDL	CA3-CA4	2.18	1.56	1.50
19	G	2003	CDL	O1-C1	2.18	1.50	1.43
18	P	3002	UQ	C5-C4	2.20	1.55	1.47
20	Q	3006	PEE	C3-C2	2.21	1.57	1.50
18	C	2002	UQ	C6-C1	2.23	1.55	1.47
19	G	2003	CDL	CA3-CA4	2.24	1.57	1.50
17	P	3001	SMA	C6-C5	2.24	1.45	1.37
11	F	3011	BHG	O5-C5	2.24	1.50	1.44
20	G	2005	PEE	C1-C2	2.25	1.57	1.50
20	T	3005	PEE	C3-C2	2.25	1.57	1.50
19	Q	3003	CDL	O1-C1	2.26	1.50	1.43
14	C	502	HEM	C4C-NC	2.28	1.38	1.36
20	G	2005	PEE	C3-C2	2.29	1.57	1.50
11	A	4002	BHG	O5-C5	2.30	1.50	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	F	3011	BHG	C4-C5	2.30	1.58	1.53
18	P	3002	UQ	O3-C3	2.31	1.43	1.37
18	P	3002	UQ	O2-C2	2.33	1.43	1.37
20	N	3012	PEE	P-O3P	2.34	1.63	1.54
18	P	3002	UQ	C6-C1	2.34	1.56	1.47
14	C	501	HEM	C1C-NC	2.35	1.38	1.36
11	F	4001	BHG	C4-C5	2.37	1.58	1.53
20	C	2012	PEE	P-O3P	2.39	1.63	1.54
15	Q	501	HEC	C3C-C4C	2.39	1.48	1.42
18	P	3002	UQ	C3-C4	2.39	1.55	1.48
19	T	3004	CDL	O1-C1	2.40	1.50	1.43
20	N	3012	PEE	P-O4P	2.44	1.63	1.54
11	S	2011	BHG	O5-C5	2.44	1.50	1.44
17	C	2001	SMA	C4A-C8A	2.44	1.44	1.41
11	C	2008	BHG	C4-C5	2.48	1.58	1.53
19	T	3004	CDL	CB3-CB4	2.52	1.57	1.50
11	A	4002	BHG	C4-C5	2.54	1.58	1.53
19	G	2004	CDL	O1-C1	2.54	1.51	1.43
20	C	2007	PEE	O2-C10	2.54	1.41	1.34
20	C	2012	PEE	P-O4P	2.55	1.63	1.54
20	P	3007	PEE	O2-C10	2.57	1.42	1.34
11	P	3008	BHG	C4-C5	2.61	1.58	1.53
20	T	3005	PEE	O2-C10	2.62	1.42	1.34
20	Q	3006	PEE	O2-C10	2.63	1.42	1.34
18	P	3002	UQ	C2-C1	2.63	1.56	1.48
18	C	2002	UQ	O2-C2	2.64	1.44	1.37
20	D	2006	PEE	O2-C10	2.64	1.42	1.34
20	G	2005	PEE	O2-C10	2.66	1.42	1.34
20	G	2005	PEE	O3-C30	2.67	1.41	1.33
20	C	2007	PEE	P-O1P	2.73	1.61	1.51
17	P	3001	SMA	C7-C8	2.73	1.44	1.40
15	D	501	HEC	C3C-C4C	2.74	1.49	1.42
18	P	3002	UQ	CM5-C5	2.76	1.56	1.50
20	G	2005	PEE	P-O1P	2.80	1.61	1.51
18	C	2002	UQ	CM5-C5	2.81	1.56	1.50
20	T	3005	PEE	O3-C30	2.85	1.41	1.33
20	T	3005	PEE	P-O1P	2.89	1.61	1.51
20	D	2006	PEE	P-O1P	2.89	1.61	1.51
20	Q	3006	PEE	P-O1P	2.91	1.61	1.51
17	C	2001	SMA	C7-C8	2.92	1.44	1.40
18	C	2002	UQ	O3-C3	2.93	1.44	1.37
20	Q	3006	PEE	O3-C30	2.94	1.42	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	C	2001	SMA	C6-C7	2.95	1.44	1.38
14	P	501	HEM	C1C-NC	2.96	1.39	1.36
18	C	2002	UQ	C7-C6	2.98	1.57	1.50
20	C	2007	PEE	O3-C30	2.99	1.42	1.33
18	P	3002	UQ	C7-C6	2.99	1.57	1.50
20	P	3007	PEE	P-O1P	3.05	1.62	1.51
18	C	2002	UQ	C2-C1	3.05	1.57	1.48
17	P	3001	SMA	C4A-C8A	3.06	1.45	1.41
18	C	2002	UQ	C3-C4	3.06	1.57	1.48
20	P	3007	PEE	O3-C30	3.10	1.42	1.33
17	P	3001	SMA	C6-C7	3.11	1.44	1.38
11	P	3008	BHG	O5-C1	3.15	1.49	1.41
11	C	2008	BHG	O5-C1	3.16	1.49	1.41
11	F	4001	BHG	O5-C1	3.19	1.50	1.41
20	D	2006	PEE	O3-C30	3.26	1.43	1.33
11	A	4002	BHG	O5-C1	3.31	1.50	1.41
17	C	2001	SMA	O1-C2	3.33	1.39	1.35
17	P	3001	SMA	C4-C3	3.43	1.51	1.41
11	F	3011	BHG	O5-C1	3.49	1.50	1.41
17	C	2001	SMA	C4-C3	3.49	1.51	1.41
11	S	2011	BHG	O5-C1	3.65	1.51	1.41
15	Q	501	HEC	C3B-C4B	3.80	1.51	1.42
14	P	501	HEM	CBC-CAC	3.93	1.52	1.29
14	P	502	HEM	CBC-CAC	4.01	1.52	1.29
14	C	502	HEM	CBC-CAC	4.18	1.53	1.29
14	C	502	HEM	CBB-CAB	4.25	1.53	1.29
17	P	3001	SMA	O1-C2	4.26	1.40	1.35
14	C	501	HEM	CBC-CAC	4.28	1.54	1.29
11	F	4001	BHG	O1-C1	4.33	1.48	1.40
14	C	501	HEM	CBB-CAB	4.36	1.54	1.29
11	C	2008	BHG	O1-C1	4.38	1.48	1.40
11	P	3008	BHG	O1-C1	4.40	1.48	1.40
14	C	502	HEM	C1C-NC	4.56	1.41	1.36
11	A	4002	BHG	O1-C1	4.67	1.48	1.40
11	S	2011	BHG	O1-C1	4.69	1.48	1.40
14	P	501	HEM	CBB-CAB	4.73	1.56	1.29
11	F	3011	BHG	O1-C1	4.79	1.48	1.40
14	P	502	HEM	CBB-CAB	4.79	1.57	1.29
14	P	501	HEM	C4C-NC	4.97	1.42	1.36
14	P	502	HEM	C1C-NC	5.11	1.42	1.36
20	N	3012	PEE	P-O1P	5.17	1.60	1.50
14	P	502	HEM	C4C-NC	5.37	1.42	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	C	2012	PEE	P-O1P	5.53	1.61	1.50
17	C	2001	SMA	C4-C4A	6.77	1.50	1.41
17	P	3001	SMA	C4-C4A	7.65	1.52	1.41

All (93) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	D	501	HEC	CBB-CAB-C3B	-8.77	107.87	127.35
15	Q	501	HEC	CBB-CAB-C3B	-8.63	108.16	127.35
15	D	501	HEC	CBC-CAC-C3C	-7.90	109.80	127.35
17	P	3001	SMA	C9-C10-C11	-7.48	105.94	114.75
17	C	2001	SMA	C9-C10-C11	-6.79	106.74	114.75
15	Q	501	HEC	CBC-CAC-C3C	-5.62	114.85	127.35
17	P	3001	SMA	C3-C4-C4A	-4.85	114.62	121.35
17	C	2001	SMA	C3-C4-C4A	-4.67	114.88	121.35
19	G	2004	CDL	CB4-OB6-CB5	-4.29	109.83	117.92
14	P	502	HEM	CMA-C3A-C4A	-4.16	121.48	128.36
19	Q	3003	CDL	CA4-OA6-CA5	-3.76	110.83	117.92
19	T	3004	CDL	CB4-OB6-CB5	-3.75	110.84	117.92
14	P	501	HEM	CAA-C2A-C1A	-3.73	122.96	127.01
19	G	2003	CDL	CA4-OA6-CA5	-3.52	111.28	117.92
14	C	502	HEM	CBD-CAD-C3D	-3.19	104.27	113.55
19	T	3004	CDL	CA4-OA6-CA5	-3.12	110.42	117.89
19	Q	3003	CDL	CB6-CB4-CB3	-3.08	104.86	112.07
15	D	501	HEC	CMD-C2D-C1D	-3.07	123.28	128.36
14	C	501	HEM	CBA-CAA-C2A	-3.01	107.13	112.53
19	G	2004	CDL	CA6-CA4-CA3	-2.86	105.37	112.07
19	G	2003	CDL	CB4-OB6-CB5	-2.80	111.16	117.89
19	Q	3003	CDL	CB4-OB6-CB5	-2.70	111.41	117.89
19	G	2003	CDL	CB6-CB4-CB3	-2.50	106.23	112.07
14	C	502	HEM	CMA-C3A-C4A	-2.42	124.35	128.36
14	C	501	HEM	CAA-C2A-C3A	-2.28	122.48	129.00
19	G	2004	CDL	CA4-OA6-CA5	-2.28	112.42	117.89
19	G	2004	CDL	CB6-CB4-CB3	-2.22	106.88	112.07
19	Q	3003	CDL	CA6-OA8-CA7	-2.20	111.59	117.14
15	Q	501	HEC	CMC-C2C-C1C	-2.17	124.77	128.36
19	G	2003	CDL	CA6-OA8-CA7	-2.09	111.85	117.14
14	P	501	HEM	CMA-C3A-C2A	2.01	129.43	125.24
11	A	4002	BHG	C1'-O1-C1	2.04	117.51	113.94
14	P	502	HEM	C2C-C1C-CHC	2.10	126.88	123.68
20	Q	3006	PEE	C23-C22-C21	2.14	125.58	114.53
20	D	2006	PEE	C23-C22-C21	2.15	125.63	114.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	T	3005	PEE	O3-C3-C2	2.15	114.49	108.69
15	D	501	HEC	CMA-C3A-C2A	2.20	129.83	125.24
20	T	3005	PEE	C23-C22-C21	2.22	126.00	114.53
20	G	2005	PEE	C23-C22-C21	2.25	126.14	114.53
20	Q	3006	PEE	C22-C21-C20	2.29	126.36	114.53
14	C	502	HEM	CMA-C3A-C2A	2.32	130.09	125.24
15	D	501	HEC	C4B-C3B-C2B	2.34	108.88	106.35
20	T	3005	PEE	C22-C21-C20	2.37	126.77	114.53
20	G	2005	PEE	C22-C21-C20	2.37	126.78	114.53
20	P	3007	PEE	C23-C22-C21	2.38	126.80	114.53
20	C	2007	PEE	C23-C22-C21	2.39	126.88	114.53
20	C	2007	PEE	C22-C21-C20	2.41	126.95	114.53
14	C	501	HEM	C2C-C1C-CHC	2.41	127.35	123.68
20	P	3007	PEE	C22-C21-C20	2.41	126.99	114.53
20	D	2006	PEE	C22-C21-C20	2.44	127.13	114.53
14	P	502	HEM	CMD-C2D-C3D	2.45	125.17	114.35
14	P	502	HEM	C1D-CHD-C4C	2.45	129.91	125.82
14	P	501	HEM	CMD-C2D-C3D	2.46	125.23	114.35
20	D	2006	PEE	C19-C18-C17	2.48	127.32	114.53
20	G	2005	PEE	C19-C18-C17	2.51	127.50	114.53
20	C	2007	PEE	C19-C18-C17	2.54	127.63	114.53
20	Q	3006	PEE	C20-C19-C18	2.54	127.67	114.53
14	P	502	HEM	CMA-C3A-C2A	2.55	130.56	125.24
20	Q	3006	PEE	C19-C18-C17	2.59	127.91	114.53
20	T	3005	PEE	C19-C18-C17	2.61	128.00	114.53
20	D	2006	PEE	C20-C19-C18	2.61	128.00	114.53
20	P	3007	PEE	C19-C18-C17	2.64	128.15	114.53
20	G	2005	PEE	C20-C19-C18	2.68	128.39	114.53
20	C	2007	PEE	C20-C19-C18	2.72	128.58	114.53
20	T	3005	PEE	C20-C19-C18	2.74	128.66	114.53
20	P	3007	PEE	C20-C19-C18	2.74	128.70	114.53
14	P	502	HEM	C2D-C3D-C4D	2.95	106.51	101.50
14	C	502	HEM	C2D-C3D-C4D	3.07	106.70	101.50
14	C	502	HEM	CMD-C2D-C3D	3.12	128.15	114.35
14	C	501	HEM	C3B-CAB-CBB	3.21	129.37	124.46
14	P	501	HEM	C2D-C3D-C4D	3.23	106.97	101.50
14	C	501	HEM	CMD-C2D-C3D	3.44	129.58	114.35
14	C	501	HEM	CAD-C3D-C4D	3.45	124.64	112.47
14	C	501	HEM	C2D-C3D-C4D	3.47	107.38	101.50
14	C	501	HEM	CMB-C2B-C3B	3.56	125.42	116.53
14	P	502	HEM	CMB-C2B-C3B	3.56	125.42	116.53
14	C	502	HEM	C3B-CAB-CBB	3.73	130.17	124.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	C	502	HEM	CAD-C3D-C4D	3.74	125.66	112.47
14	P	501	HEM	CAD-C3D-C2D	3.90	124.42	113.22
14	C	501	HEM	CMC-C2C-C3C	4.05	126.65	116.53
14	P	502	HEM	C3B-CAB-CBB	4.08	130.71	124.46
14	P	502	HEM	CAD-C3D-C2D	4.09	124.98	113.22
14	P	501	HEM	CMB-C2B-C3B	4.44	127.61	116.53
14	P	502	HEM	CAD-C3D-C4D	4.49	128.30	112.47
14	P	501	HEM	CAD-C3D-C4D	4.57	128.59	112.47
14	C	502	HEM	CMB-C2B-C3B	4.59	127.98	116.53
14	C	502	HEM	CAD-C3D-C2D	4.93	127.39	113.22
14	C	501	HEM	CAD-C3D-C2D	5.05	127.74	113.22
14	P	501	HEM	CMC-C2C-C3C	5.50	130.25	116.53
14	C	502	HEM	CMC-C2C-C3C	5.60	130.50	116.53
14	P	502	HEM	CMC-C2C-C3C	6.02	131.57	116.53
17	C	2001	SMA	C9-C2-C3	7.22	130.09	120.56
17	P	3001	SMA	C9-C2-C3	7.23	130.10	120.56

All (6) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
11	F	3011	BHG	C4
11	S	2011	BHG	C4
11	P	3008	BHG	C4
11	C	2008	BHG	C4
11	F	4001	BHG	C4
11	A	4002	BHG	C4

There are no torsion outliers.

There are no ring outliers.

19 monomers are involved in 54 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	A	4002	BHG	1	0
17	C	2001	SMA	1	0
18	C	2002	UQ	3	0
20	C	2007	PEE	2	0
14	C	501	HEM	2	0
14	C	502	HEM	3	0
20	D	2006	PEE	1	0
15	D	501	HEC	3	0
11	F	3011	BHG	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	G	2004	CDL	5	0
17	P	3001	SMA	2	0
18	P	3002	UQ	5	0
20	P	3007	PEE	2	0
14	P	501	HEM	1	0
14	P	502	HEM	2	0
20	Q	3006	PEE	9	0
15	Q	501	HEC	2	0
11	S	2011	BHG	8	0
20	T	3005	PEE	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	442/446 (99%)	0.15	22 (4%) 32 41	27, 43, 65, 115	1 (0%)
1	N	442/446 (99%)	0.20	15 (3%) 49 58	28, 43, 63, 128	1 (0%)
2	B	424/439 (96%)	0.20	19 (4%) 37 46	29, 45, 67, 132	0
2	O	424/439 (96%)	0.31	27 (6%) 23 30	33, 47, 73, 162	0
3	C	365/379 (96%)	0.27	7 (1%) 70 75	25, 34, 47, 106	0
3	P	370/379 (97%)	0.34	25 (6%) 20 28	26, 34, 52, 165	0
4	D	241/241 (100%)	0.05	4 (1%) 73 78	28, 39, 59, 80	0
4	Q	241/241 (100%)	0.12	17 (7%) 19 26	28, 38, 59, 81	0
5	E	196/196 (100%)	0.80	37 (18%) 2 2	29, 54, 96, 117	0
5	R	196/196 (100%)	0.05	4 (2%) 68 73	29, 43, 61, 85	0
6	F	99/110 (90%)	0.28	4 (4%) 42 51	29, 44, 70, 80	0
6	S	99/110 (90%)	0.42	10 (10%) 9 12	28, 39, 79, 109	0
7	G	75/81 (92%)	0.51	6 (8%) 15 21	31, 50, 72, 80	0
7	T	76/81 (93%)	1.00	9 (11%) 6 8	30, 50, 97, 117	0
8	H	66/78 (84%)	0.88	9 (13%) 4 6	40, 55, 87, 101	0
8	U	66/78 (84%)	0.77	10 (15%) 3 4	40, 54, 79, 89	0
9	I	42/78 (53%)	2.64	24 (57%) 0 0	40, 75, 88, 93	0
9	V	42/78 (53%)	2.06	17 (40%) 0 0	45, 72, 92, 97	0
10	J	62/62 (100%)	1.18	13 (20%) 1 1	35, 60, 85, 116	0
10	W	62/62 (100%)	1.01	11 (17%) 2 3	34, 51, 80, 111	0
All	All	4030/4220 (95%)	0.35	290 (7%) 18 25	25, 42, 76, 165	2 (0%)

All (290) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	T	76	ALA	34.0
10	J	1	VAL	17.1
1	N	1	THR	11.6
2	O	19	PRO	10.6
3	P	13	ILE	9.9
10	W	2	ALA	9.8
1	A	222	THR	9.7
2	O	233	SER	8.8
6	S	12	TRP	8.7
2	O	232	LEU	8.3
10	W	62	LYS	7.9
7	T	73	ASN	7.9
3	C	17	ALA	7.8
2	O	18	PRO	7.3
1	A	1	THR	7.2
2	O	17	VAL	7.1
2	O	229	GLY	7.1
5	E	71	MET	7.0
2	B	41	TYR	6.9
2	O	230	LEU	6.9
10	W	1	VAL	6.8
10	W	61	ASN	6.7
9	I	78	TYR	6.7
7	T	75	ALA	6.4
2	O	234	GLY	6.4
1	N	2	ALA	6.3
5	E	191	ASP	6.3
4	Q	241	LYS	6.1
5	E	103	LYS	6.1
1	N	229	PRO	6.0
2	B	233	SER	5.9
6	S	110	LYS	5.9
9	V	32	ALA	5.8
5	E	194	ILE	5.8
9	I	49	VAL	5.7
9	I	63	PRO	5.7
1	A	2	ALA	5.6
9	V	78	TYR	5.6
2	B	19	PRO	5.4
6	F	13	LEU	5.3
3	P	16	ASN	5.3
9	V	63	PRO	5.2
1	A	226	ASP	5.2

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Mol	Chain	Res	Type	RSRZ
5	E	190	ASP	5.2
1	N	227	ALA	5.2
10	J	2	ALA	5.0
1	N	222	THR	4.9
9	I	62	ARG	4.9
10	J	62	LYS	4.9
5	E	70	ALA	4.9
2	B	304	HIS	4.7
2	O	12	GLU	4.7
9	I	59	ALA	4.7
10	J	30	PHE	4.7
7	G	30	PHE	4.6
7	T	74	PRO	4.6
3	P	168	PHE	4.6
5	E	108	GLN	4.6
8	H	46	SER	4.5
9	I	77	ARG	4.4
2	B	18	PRO	4.4
1	N	226	ASP	4.4
8	H	47	ARG	4.3
5	E	76	ILE	4.3
6	S	13	LEU	4.3
8	U	48	SER	4.2
5	E	112	VAL	4.2
8	U	45	SER	4.2
2	B	12	GLU	4.2
8	U	47	ARG	4.1
3	P	10	LEU	4.1
5	E	132	TRP	4.1
3	P	11	MET	4.0
5	E	110	ALA	4.0
1	A	443	TRP	3.9
9	I	76	VAL	3.9
5	E	80	ASP	3.9
7	T	72	LYS	3.9
1	A	51	LYS	3.9
1	A	227	ALA	3.9
2	B	249	GLY	3.9
10	J	27	GLY	3.8
10	J	29	LEU	3.8
5	E	92	ARG	3.8
10	J	33	ARG	3.8

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Mol	Chain	Res	Type	RSRZ
7	G	74	PRO	3.8
9	I	51	CYS	3.8
7	G	56	TYR	3.7
9	V	33	ALA	3.7
9	I	50	LEU	3.7
9	V	42	VAL	3.7
10	J	3	PRO	3.7
9	V	70	LEU	3.7
2	B	20	HIS	3.7
9	I	57	GLY	3.6
9	I	61	GLY	3.6
9	V	62	ARG	3.6
9	I	32	ALA	3.6
2	O	41	TYR	3.6
9	I	35	PRO	3.5
10	W	12	LEU	3.5
9	I	70	LEU	3.5
3	P	14	VAL	3.4
8	H	49	GLN	3.3
2	O	21	PRO	3.3
2	O	20	HIS	3.3
5	E	189	SER	3.3
5	E	69	LEU	3.3
6	S	16	ILE	3.2
9	I	60	ALA	3.2
5	R	189	SER	3.2
5	E	107	ASP	3.2
9	V	34	VAL	3.2
8	U	27	LEU	3.2
6	S	108	ALA	3.2
1	N	206	ARG	3.2
8	U	44	VAL	3.2
9	V	49	VAL	3.2
9	I	55	LEU	3.2
4	Q	73	GLY	3.1
3	C	16	ASN	3.1
4	Q	141	VAL	3.1
3	P	218	ILE	3.1
6	S	14	GLU	3.1
4	D	241	LYS	3.0
1	N	228	VAL	3.0
5	E	133	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
9	I	72	VAL	3.0
9	V	48	SER	3.0
2	O	235	ALA	3.0
1	A	122	LEU	3.0
5	E	154	GLY	3.0
5	E	104	LYS	3.0
1	N	225	GLU	3.0
8	H	44	VAL	3.0
1	N	297	ILE	3.0
2	B	17	VAL	3.0
1	A	219	LEU	2.9
4	Q	81	PHE	2.9
2	O	265	GLY	2.9
5	E	129	LYS	2.9
3	P	31	TRP	2.9
8	H	42	GLU	2.9
4	D	145	GLU	2.9
1	A	68	LYS	2.9
6	F	109	LYS	2.9
1	N	224	ASP	2.9
2	O	218	GLN	2.9
1	A	217	SER	2.9
2	O	369	LEU	2.9
3	P	208	PRO	2.9
8	U	50	THR	2.8
10	J	5	LEU	2.8
5	E	195	VAL	2.8
1	A	206	ARG	2.8
8	U	71	HIS	2.7
6	S	109	LYS	2.7
10	W	57	HIS	2.7
5	R	190	ASP	2.7
9	V	35	PRO	2.7
2	B	350	GLY	2.7
1	A	125	SER	2.7
4	D	144	ARG	2.6
7	T	42	ARG	2.6
8	H	43	ARG	2.6
3	P	25	SER	2.6
5	R	89	PHE	2.6
5	E	75	GLU	2.6
3	P	19	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
6	S	78	GLU	2.6
9	I	71	ASN	2.6
5	E	192	MET	2.6
2	O	301	LYS	2.6
10	W	30	PHE	2.6
4	Q	76	GLU	2.6
5	E	186	GLU	2.6
3	P	29	SER	2.6
9	I	75	SER	2.6
7	G	68	LYS	2.6
1	N	213	GLN	2.6
2	B	251	SER	2.5
4	Q	1	SER	2.5
3	P	26	ASN	2.5
4	Q	79	GLU	2.5
2	O	367	GLY	2.5
10	J	12	LEU	2.5
4	Q	77	ASP	2.5
3	P	314	SER	2.5
10	W	8	ARG	2.5
4	Q	75	ASN	2.5
2	O	350	GLY	2.5
2	O	304	HIS	2.5
5	R	5	ILE	2.4
9	V	68	VAL	2.4
1	A	187	SER	2.4
8	U	51	GLU	2.4
3	C	18	PHE	2.4
3	P	66	VAL	2.4
4	Q	82	MET	2.4
5	E	102	THR	2.4
3	P	27	ILE	2.4
1	N	221	GLY	2.4
7	G	75	ALA	2.4
3	P	30	TRP	2.4
2	O	399	LEU	2.4
3	P	104	TYR	2.4
9	I	64	LEU	2.4
8	H	71	HIS	2.4
4	Q	227	TRP	2.4
7	T	30	PHE	2.4
8	H	48	SER	2.4

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Mol	Chain	Res	Type	RSRZ
9	V	76	VAL	2.4
4	Q	115	TYR	2.4
4	Q	214	LEU	2.4
5	E	153	PHE	2.4
10	J	9	LEU	2.4
1	A	225	GLU	2.4
10	W	3	PRO	2.3
3	P	209	THR	2.3
1	A	127	ILE	2.3
2	O	302	GLY	2.3
6	F	110	LYS	2.3
9	I	34	VAL	2.3
7	T	34	ILE	2.3
1	A	124	ASP	2.3
8	U	34	ARG	2.3
2	B	97	SER	2.3
6	S	15	GLY	2.3
6	S	70	MET	2.3
3	P	102	LEU	2.3
8	U	49	GLN	2.3
5	E	91	TRP	2.3
3	P	207	ASN	2.3
2	O	249	GLY	2.2
9	I	42	VAL	2.2
2	B	439	LEU	2.2
9	I	58	GLN	2.2
3	C	102	LEU	2.2
9	V	77	ARG	2.2
8	H	45	SER	2.2
1	A	188	ARG	2.2
1	A	186	LEU	2.2
4	D	214	LEU	2.2
10	J	22	LEU	2.2
1	A	129	LYS	2.2
2	B	307	PHE	2.2
3	C	130	GLY	2.2
3	P	210	GLY	2.2
2	B	411	ILE	2.2
6	F	16	ILE	2.2
5	E	27	GLU	2.2
3	P	28	SER	2.2
5	E	79	SER	2.2

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Mol	Chain	Res	Type	RSRZ
5	E	115	SER	2.2
3	P	224	TYR	2.2
2	O	401	GLN	2.1
4	Q	3	LEU	2.1
1	A	224	ASP	2.1
2	O	236	LYS	2.1
5	E	167	ALA	2.1
4	Q	80	MET	2.1
2	O	264	ILE	2.1
5	E	113	GLU	2.1
9	V	52	ARG	2.1
3	C	31	TRP	2.1
9	V	72	VAL	2.1
5	E	152	ASP	2.1
5	E	100	HIS	2.1
1	N	6	GLN	2.1
2	B	348	ALA	2.1
2	B	23	ASP	2.1
4	Q	2	ASP	2.1
7	G	53	VAL	2.1
10	W	53	LYS	2.0
2	B	232	LEU	2.0
3	C	160	LEU	2.0
1	A	202	GLY	2.0
10	J	28	ALA	2.0
10	W	60	GLU	2.0
2	B	98	VAL	2.0
4	Q	139	THR	2.0
5	E	188	THR	2.0
9	V	37	THR	2.0
7	T	70	LYS	2.0
9	I	54	SER	2.0
2	O	388	ALA	2.0
5	E	98	VAL	2.0
3	P	24	PRO	2.0
5	E	151	GLY	2.0
1	N	51	LYS	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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
11	BHG	F	3011	18/18	0.48	0.59	23.77	114,118,122,122	0
11	BHG	S	2011	18/18	0.30	0.43	17.13	73,86,91,91	0
11	BHG	A	4002	18/18	0.27	0.63	13.84	130,143,145,145	0
11	BHG	C	2008	18/18	0.45	0.42	12.49	109,112,116,116	0
21	GOL	P	3009	6/6	0.81	0.35	10.95	59,65,67,68	0
20	PEE	T	3005	49/51	0.71	0.53	10.57	96,121,136,136	0
11	BHG	P	3008	18/18	0.57	0.40	10.48	100,102,107,109	0
13	AZI	C	2014	3/3	0.52	0.38	10.23	53,53,57,59	0
21	GOL	C	2009	6/6	0.85	0.39	9.74	56,59,63,67	0
20	PEE	G	2005	49/51	0.62	0.43	8.00	105,123,129,129	0
21	GOL	B	2013	6/6	0.10	0.92	7.65	145,148,148,149	0
13	AZI	P	3014	3/3	0.40	0.43	6.68	54,54,55,61	0
21	GOL	O	3013	6/6	0.35	0.68	5.35	112,115,116,116	0
13	AZI	D	4004	3/3	0.54	0.30	5.04	69,69,72,73	0
18	UQ	P	3002	14/63	0.71	0.37	4.63	90,93,97,97	0
20	PEE	C	2007	49/51	0.88	0.25	2.96	39,53,68,69	0
20	PEE	D	2006	51/51	0.90	0.21	2.85	52,66,94,95	0
13	AZI	A	4005	3/3	0.79	0.31	2.61	72,72,73,74	0
19	CDL	G	2004	44/100	0.88	0.25	2.35	62,79,105,107	0
19	CDL	G	2003	50/100	0.74	0.27	2.35	62,96,113,113	0
20	PEE	Q	3006	51/51	0.92	0.18	1.73	45,59,83,83	0
19	CDL	T	3004	49/100	0.87	0.26	1.56	54,69,98,101	0
20	PEE	P	3007	49/51	0.93	0.22	1.31	35,54,62,63	0
19	CDL	Q	3003	50/100	0.85	0.21	1.01	55,78,90,92	0
18	UQ	C	2002	14/63	0.78	0.28	0.89	74,78,80,82	0
17	SMA	P	3001	37/37	0.92	0.15	0.74	24,32,37,37	0
14	HEM	P	501	43/43	0.98	0.14	0.27	25,29,37,42	0
15	HEC	D	501	43/43	0.97	0.12	0.22	29,33,36,38	0
14	HEM	P	502	43/43	0.97	0.14	0.15	24,27,32,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
14	HEM	C	501	43/43	0.98	0.14	0.13	21,26,33,37	0
17	SMA	C	2001	37/37	0.94	0.13	0.07	25,30,32,38	0
14	HEM	C	502	43/43	0.98	0.13	-0.01	22,26,31,33	0
16	FES	E	501	4/4	0.98	0.10	-0.36	34,35,37,37	0
16	FES	R	501	4/4	0.99	0.09	-0.75	31,31,33,33	0
15	HEC	Q	501	43/43	0.98	0.10	-0.78	32,35,36,37	0
20	PEE	A	4003	6/51	0.68	0.32	-	110,111,112,113	0
12	PO4	B	3010	5/5	0.86	0.16	-	99,100,100,100	0
20	PEE	N	3012	5/51	0.78	0.19	-	94,94,94,96	0
12	PO4	O	2010	5/5	0.92	0.11	-	106,106,107,108	0
11	BHG	F	4001	18/18	0.32	0.52	-	168,171,173,173	0
20	PEE	C	2012	5/51	0.72	0.26	-	116,116,116,116	0

6.5 Other polymers [i](#)

There are no such residues in this entry.