



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2018 – 05:46 pm GMT

PDB ID : 4D6T
Title : Cytochrome bc1 bound to the 4(1H)-pyridone GW844520
Authors : Capper, M.J.; O'Neill, P.M.; Fisher, N.; Strange, R.W.; Moss, D.; Ward, S.A.;
Berry, N.G.; Lawrenson, A.S.; Hasnain, S.S.; Biagini, G.A.; Antonyuk, S.V.
Deposited on : 2014-11-14
Resolution : 3.57 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

<https://www.wwpdb.org/validation/2017/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 : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk30967
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30967

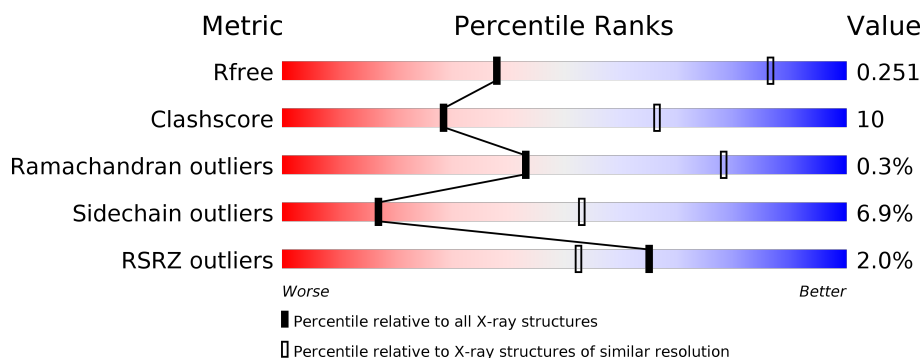
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.57 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}	111664	1163 (3.70-3.46)
Clashscore	122126	1004 (3.66-3.50)
Ramachandran outliers	120053	1011 (3.68-3.48)
Sidechain outliers	120020	1011 (3.68-3.48)
RSRZ outliers	108989	1072 (3.70-3.46)

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	480	<div> <div>2%</div> <div> <div></div> <div>75%</div> <div>16%</div> <div>• 8%</div> </div> </div>
1	N	480	<div> <div>%</div> <div> <div></div> <div>76%</div> <div>15%</div> <div>•• 8%</div> </div> </div>
2	B	453	<div> <div>6%</div> <div> <div></div> <div>71%</div> <div>19%</div> <div>• 7%</div> </div> </div>
3	C	379	<div> <div></div> <div> <div></div> <div>75%</div> <div>19%</div> <div>••</div> </div> </div>
3	P	379	<div> <div></div> <div> <div></div> <div>77%</div> <div>17%</div> <div>••</div> </div> </div>
4	D	265	<div> <div>%</div> <div> <div></div> <div>76%</div> <div>13%</div> <div>• 9%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
4	Q	265	
5	E	274	
5	I	274	
5	R	274	
6	F	111	
6	S	111	
7	G	82	
7	T	82	
8	H	91	
8	U	91	
9	J	64	
9	W	64	
10	O	453	
11	V	274	

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
14	PO4	F	501	-	-	-	X
14	PO4	N	501	-	-	-	X
14	PO4	S	501	-	-	-	X
15	PEE	C	505	X	-	-	-
15	PEE	D	506	X	-	-	-
15	PEE	P	505	X	-	-	-
15	PEE	Q	506	X	-	-	-
18	FES	R	501	-	-	X	-
19	GOL	R	502	-	-	-	X

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 31051 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 CYTOCHROME B-C1 COMPLEX SUBUNIT 1, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	444	Total	C	N	O	S	0	0	0
			3439	2148	607	664	20			
1	N	444	Total	C	N	O	S	0	0	0
			3432	2142	607	663	20			

- Molecule 2 is a protein called CYTOCHROME B-C1 COMPLEX SUBUNIT 2, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	422	Total	C	N	O	S	0	0	0
			3164	1988	561	608	7			

- Molecule 3 is a protein called CYTOCHROME B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	374	Total	C	N	O	S	0	0	0
			2968	1993	463	494	18			
3	P	370	Total	C	N	O	S	0	0	0
			2936	1973	456	489	18			

- Molecule 4 is a protein called CYTOCHROME C1, HEME PROTEIN, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	240	Total	C	N	O	S	0	0	0
			1912	1222	329	346	15			
4	Q	241	Total	C	N	O	S	0	0	0
			1918	1225	330	348	15			

- Molecule 5 is a protein called CYTOCHROME B-C1 COMPLEX SUBUNIT RIESKE, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	73	Total	C	N	O	S	0	0	0
			549	341	92	114	2			
5	I	21	Total	C	N	O	S	0	0	0
			157	97	31	28	1			
5	R	196	Total	C	N	O	S	0	0	0
			1518	957	263	290	8			

- Molecule 6 is a protein called CYTOCHROME B-C1 COMPLEX SUBUNIT 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	98	Total	C	N	O	S	0	0	0
			860	547	154	157	2			
6	S	99	Total	C	N	O	S	0	0	0
			869	553	156	158	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	56	ASP	ASN	conflict	UNP P00129
S	56	ASP	ASN	conflict	UNP P00129

- Molecule 7 is a protein called CYTOCHROME B-C1 COMPLEX SUBUNIT 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	80	Total	C	N	O	S	0	0	0
			677	439	127	110	1			
7	T	74	Total	C	N	O	S	0	0	0
			624	408	117	98	1			

- Molecule 8 is a protein called CYTOCHROME B-C1 COMPLEX SUBUNIT 6, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	65	Total	C	N	O	S	0	0	0
			529	321	96	107	5			
8	U	66	Total	C	N	O	S	0	0	0
			538	327	98	108	5			

- Molecule 9 is a protein called CYTOCHROME B-C1 COMPLEX SUBUNIT 9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	J	58	Total	C	N	O	0	0	0
			482	317	83	82			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	W	59	Total	C	N	O	0	0	0
			487	320	84	83			

- Molecule 10 is a protein called CYTOCHROME B-C1 COMPLEX SUBUNIT 2, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	O	419	Total	C	N	O	S	0	0	0
			3140	1972	555	606	7			

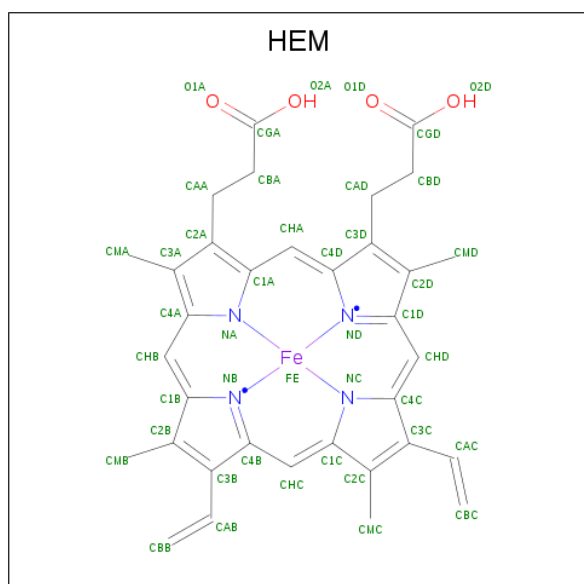
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	305	GLU	GLN	conflict	UNP P23004

- Molecule 11 is a protein called CYTOCHROME B-C1 COMPLEX SUBUNIT RIESKE, MITOCHONDRIAL.

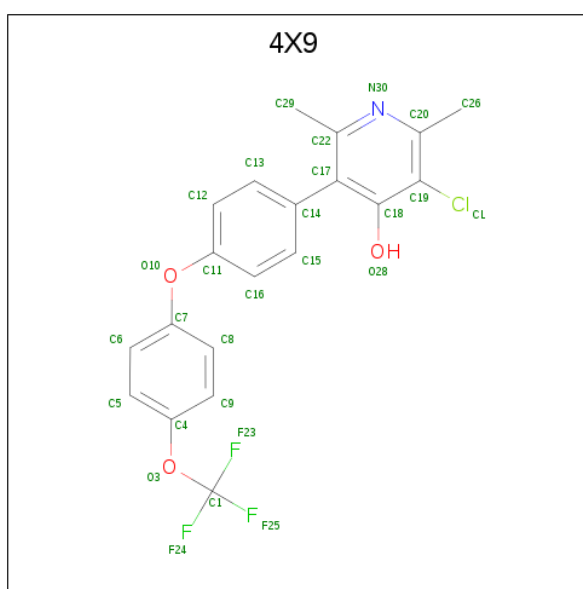
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
11	V	17	Total	C	N	O	0	0	0
			127	81	24	22			

- Molecule 12 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 13 is 3-chloro-2,6-dimethyl-5-{4-[4-(trifluoromethoxy)phenoxy]phenyl}pyridin-4-ol (three-letter code: 4X9) (formula: C₂₀H₁₅ClF₃NO₃).



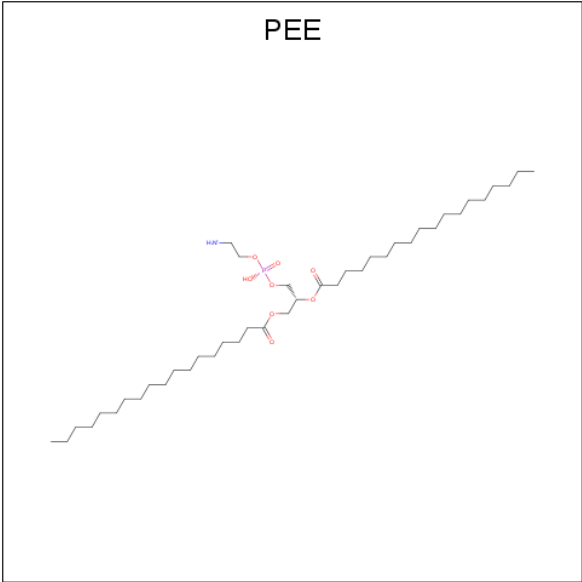
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
13	C	1	Total	C	Cl	F	N	O
			28	20	1	3	1	3
13	P	1	Total	C	Cl	F	N	O
			28	20	1	3	1	3

- Molecule 14 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



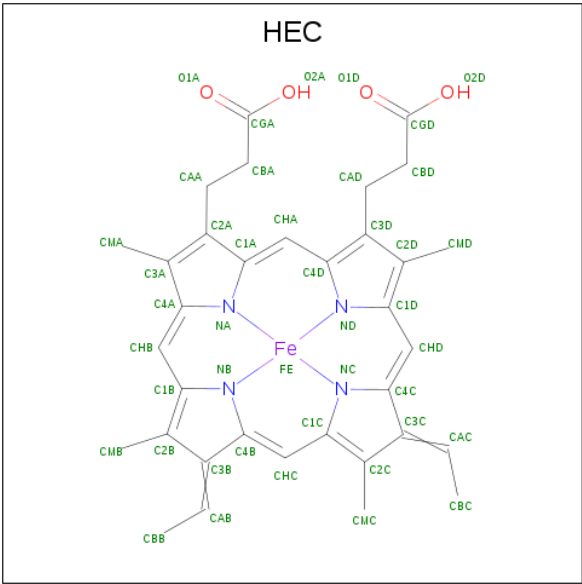
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
14	C	1	Total	O	P	0	0
			5	4	1		
14	D	1	Total	O	P	0	0
			5	4	1		
14	D	1	Total	O	P	0	0
			5	4	1		
14	D	1	Total	O	P	0	0
			5	4	1		
14	E	1	Total	O	P	0	0
			5	4	1		
14	F	1	Total	O	P	0	0
			5	4	1		
14	N	1	Total	O	P	0	0
			5	4	1		
14	N	1	Total	O	P	0	0
			5	4	1		
14	Q	1	Total	O	P	0	0
			5	4	1		
14	Q	1	Total	O	P	0	0
			5	4	1		
14	S	1	Total	O	P	0	0
			5	4	1		

- Molecule 15 is 1,2-Dioleoyl-sn-glycero-3-phosphoethanolamine (three-letter code: PEE) (formula: C₄₁H₈₃NO₈P).



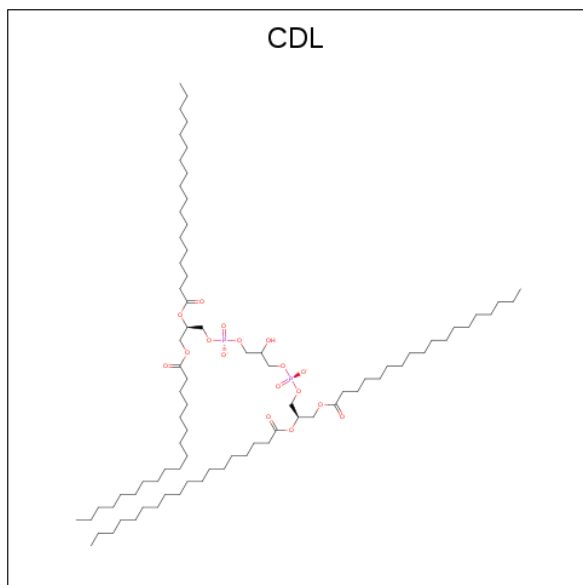
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
15	C	1	Total	C	N	O	P	0	0
			49	39	1	8	1		
15	D	1	Total	C	N	O	P	0	0
			26	16	1	8	1		
15	P	1	Total	C	N	O	P	0	0
			49	39	1	8	1		
15	Q	1	Total	C	N	O	P	0	0
			51	41	1	8	1		

- Molecule 16 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



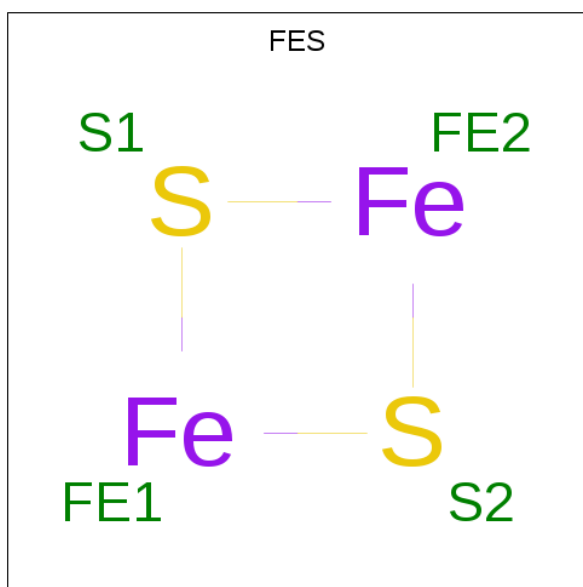
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
16	D	1	Total	C	Fe	N	O	
			43	34	1	4	4	
16	Q	1	Total	C	Fe	N	O	
			43	34	1	4	4	

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



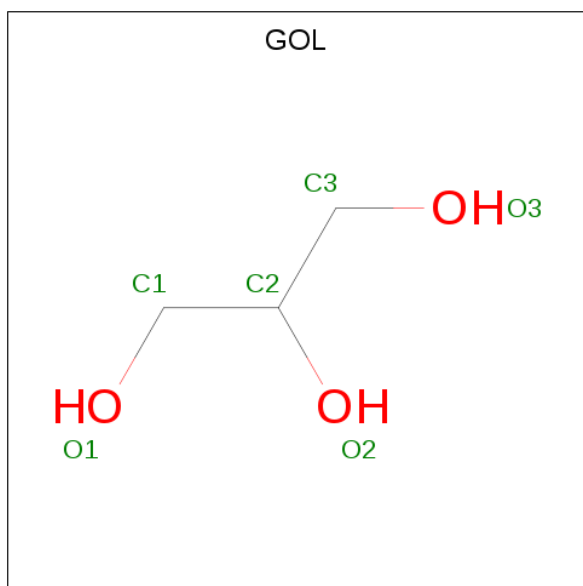
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
17	D	1	Total	C	O	P		
			39	24	13	2	0	0
17	G	1	Total	C	O	P		
			44	25	17	2	0	0
17	Q	1	Total	C	O	P		
			39	24	13	2	0	0
17	T	1	Total	C	O	P		
			49	30	17	2	0	0

- Molecule 18 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



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

- Molecule 19 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

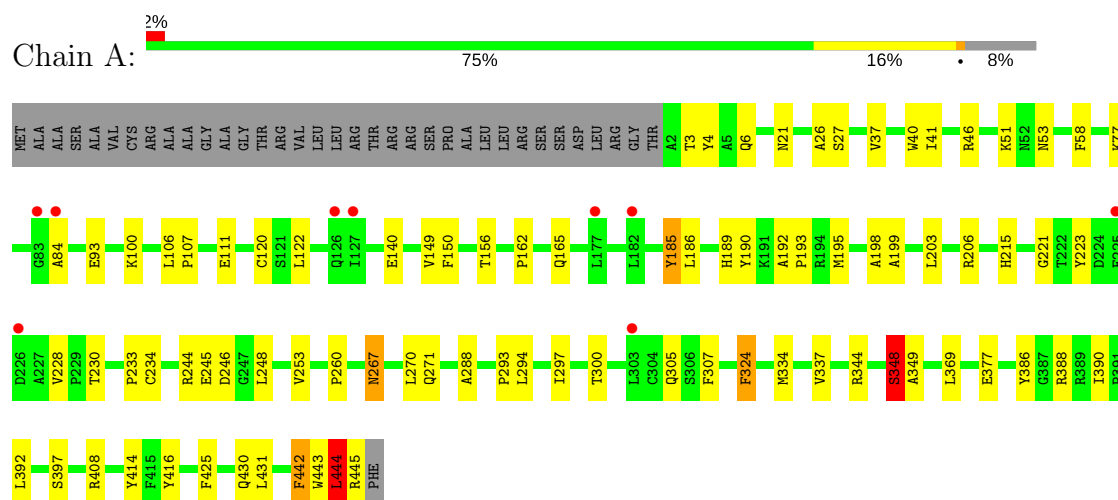


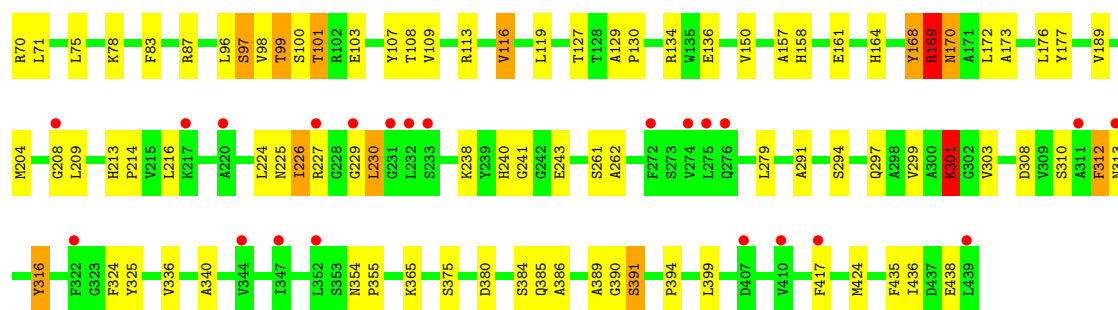
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
19	R	1	Total	C	O	0	0
			6	3	3		

3 Residue-property plots

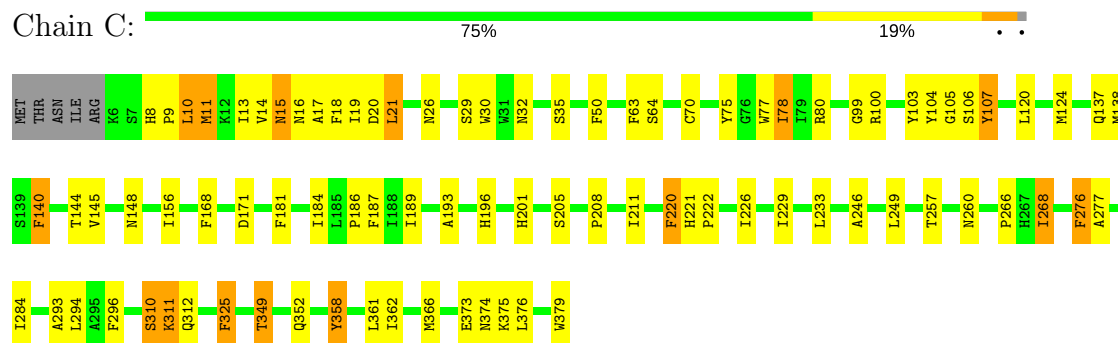
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: CYTOCHROME B-C1 COMPLEX SUBUNIT 1, MITOCHONDRIAL

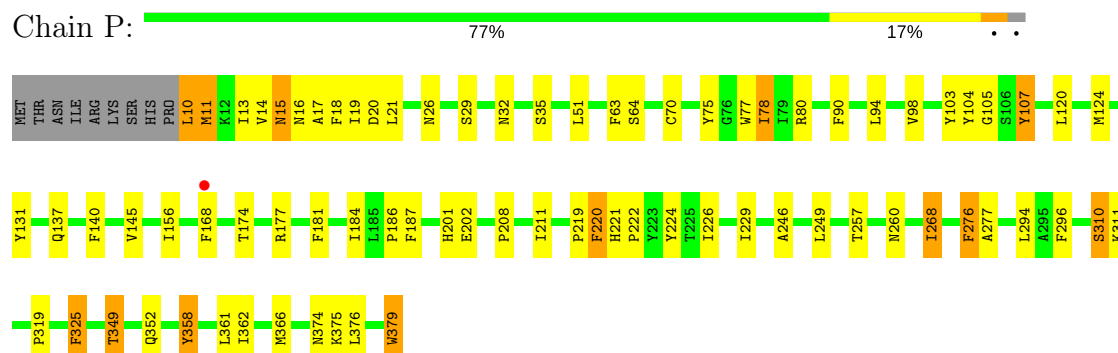




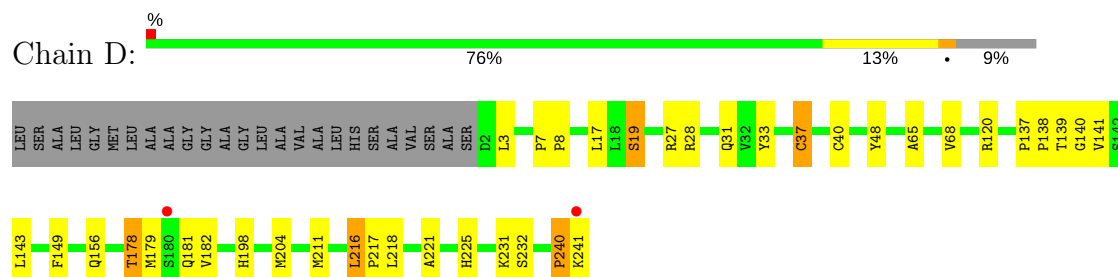
• Molecule 3: CYTOCHROME B



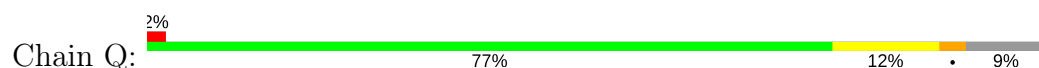
• Molecule 3: CYTOCHROME B

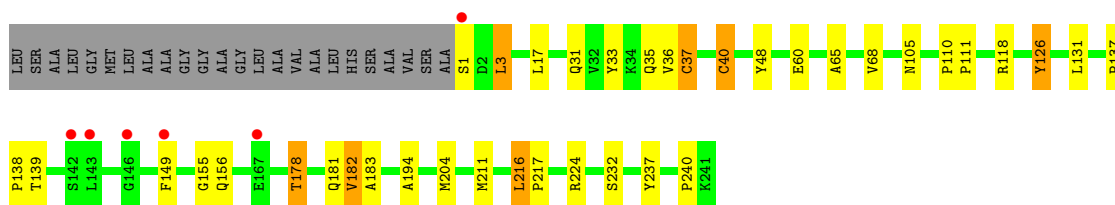


• Molecule 4: CYTOCHROME C1, HEME PROTEIN, MITOCHONDRIAL



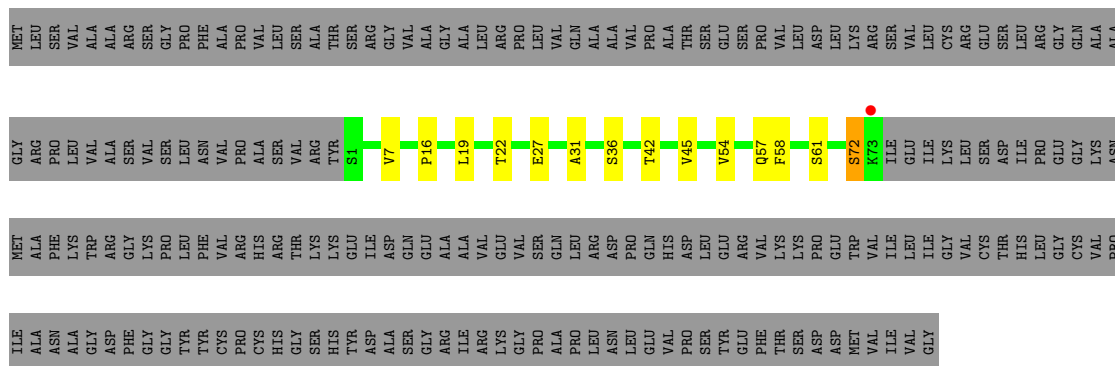
• Molecule 4: CYTOCHROME C1, HEME PROTEIN, MITOCHONDRIAL





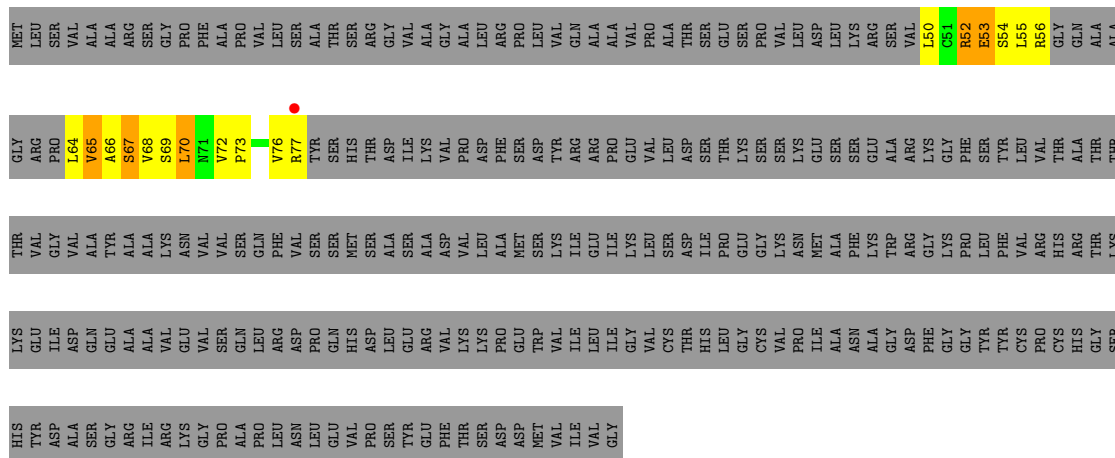
- Molecule 5: CYTOCHROME B-C1 COMPLEX SUBUNIT RIESKE, MITOCHONDRIAL

Chain E:  22% 5% 73%



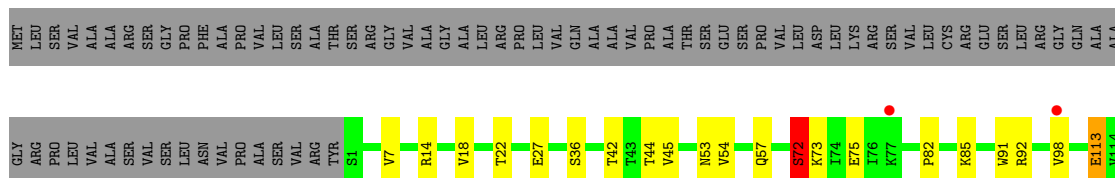
- Molecule 5: CYTOCHROME B-C1 COMPLEX SUBUNIT RIESKE, MITOCHONDRIAL

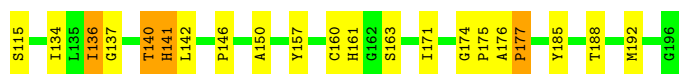
Chain I:  92%



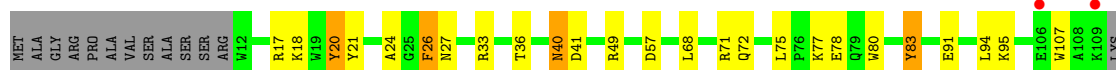
- Molecule 5: CYTOCHROME B-C1 COMPLEX SUBUNIT RIESKE, MITOCHONDRIAL

Chain R: 





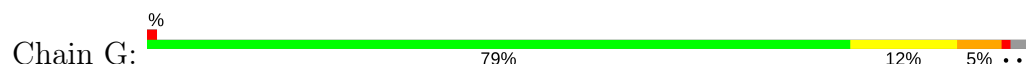
• Molecule 6: CYTOCHROME B-C1 COMPLEX SUBUNIT 7



• Molecule 6: CYTOCHROME B-C1 COMPLEX SUBUNIT 7



• Molecule 7: CYTOCHROME B-C1 COMPLEX SUBUNIT 8



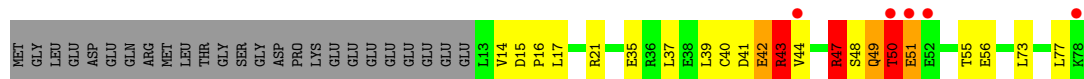
• Molecule 7: CYTOCHROME B-C1 COMPLEX SUBUNIT 8



• Molecule 8: CYTOCHROME B-C1 COMPLEX SUBUNIT 6, MITOCHONDRIAL



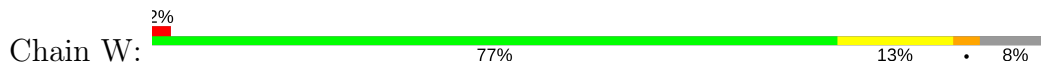
• Molecule 8: CYTOCHROME B-C1 COMPLEX SUBUNIT 6, MITOCHONDRIAL



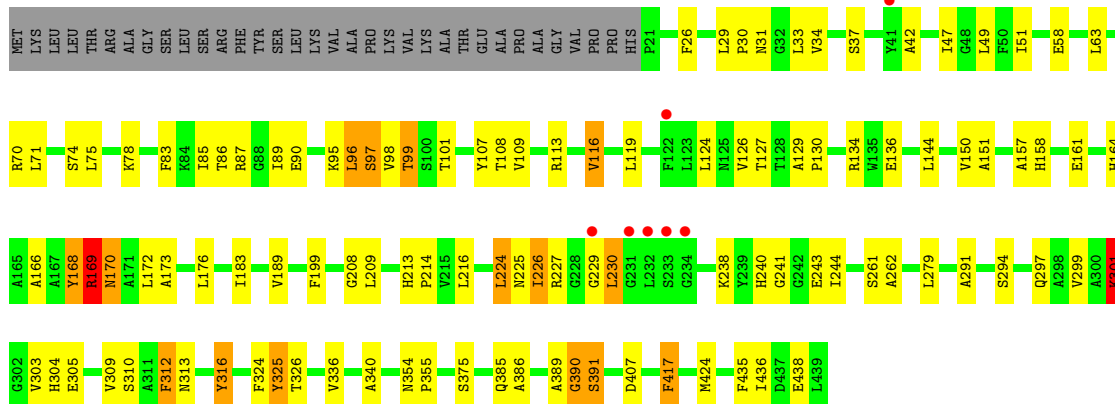
• Molecule 9: CYTOCHROME B-C1 COMPLEX SUBUNIT 9



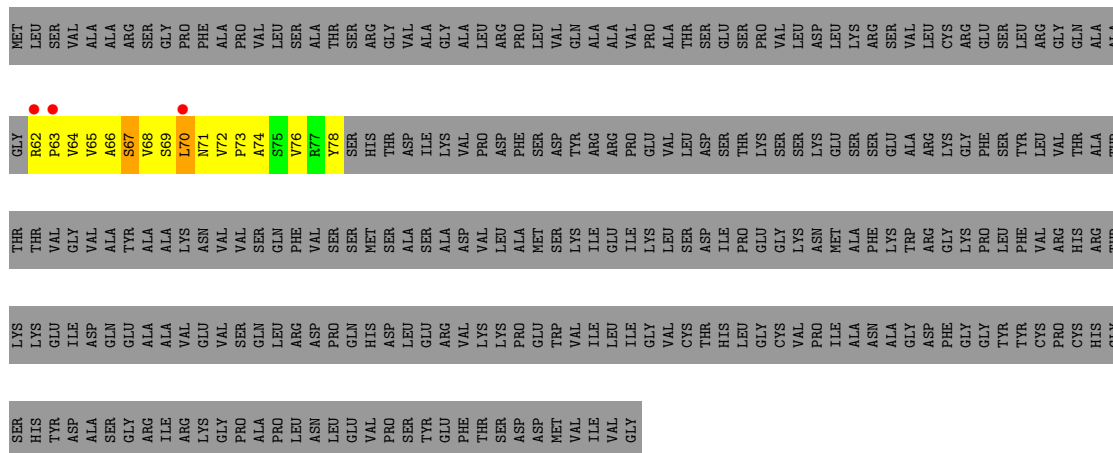
- Molecule 9: CYTOCHROME B-C1 COMPLEX SUBUNIT 9



- Molecule 10: CYTOCHROME B-C1 COMPLEX SUBUNIT 2, MITOCHONDRIAL



- Molecule 11: CYTOCHROME B-C1 COMPLEX SUBUNIT RIESKE, MITOCHONDRIAL



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	129.90Å 129.90Å 722.15Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 3.57 49.81 – 3.57	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-3.57) 99.9 (49.81-3.57)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.86 (at 3.57Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.206 , 0.252 0.207 , 0.251	Depositor DCC
R_{free} test set	3953 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	122.6	Xtriage
Anisotropy	0.197	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 79.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.064 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	31051	wwPDB-VP
Average B, all atoms (Å ²)	135.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.68% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: GOL, CDL, PO4, FES, 4X9, HEC, HEM, PEE

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	0.46	1/3511 (0.0%)	0.69	5/4766 (0.1%)
1	N	0.42	0/3503	0.70	7/4755 (0.1%)
2	B	0.69	3/3224 (0.1%)	0.80	10/4375 (0.2%)
3	C	0.50	0/3065	0.68	0/4196
3	P	0.48	1/3031 (0.0%)	0.67	0/4150
4	D	0.42	0/1971	0.62	0/2676
4	Q	0.42	0/1977	0.61	0/2684
5	E	0.41	0/557	0.62	0/752
5	I	0.57	0/156	1.24	2/209 (1.0%)
5	R	0.43	0/1552	0.78	7/2100 (0.3%)
6	F	0.46	0/879	0.68	0/1180
6	S	0.47	0/888	0.65	0/1191
7	G	0.52	1/699 (0.1%)	1.26	6/946 (0.6%)
7	T	0.49	0/645	0.74	0/873
8	H	2.11	7/534 (1.3%)	1.96	8/718 (1.1%)
8	U	1.48	6/543 (1.1%)	2.09	10/729 (1.4%)
9	J	0.42	0/495	0.59	0/667
9	W	0.43	0/500	0.60	0/675
10	O	0.50	2/3197 (0.1%)	0.95	12/4336 (0.3%)
11	V	0.58	0/129	0.86	0/177
All	All	0.59	21/31056 (0.1%)	0.82	67/42155 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	N	0	1
2	B	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
7	G	0	1
8	H	0	1
8	U	0	3
10	O	0	2
All	All	0	11

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	169	ARG	CZ-NH2	28.39	1.70	1.33
8	H	43	ARG	CZ-NH1	26.86	1.68	1.33
8	H	47	ARG	CZ-NH2	25.79	1.66	1.33
8	U	47	ARG	CZ-NH2	25.71	1.66	1.33
8	H	43	ARG	NE-CZ	23.73	1.64	1.33
10	O	169	ARG	NE-CZ	15.59	1.53	1.33
1	A	408	ARG	CZ-NH2	13.97	1.51	1.33
2	B	169	ARG	CZ-NH1	-11.66	1.17	1.33
8	U	43	ARG	CZ-NH2	-10.62	1.19	1.33
8	U	43	ARG	CZ-NH1	9.93	1.46	1.33
8	H	47	ARG	CD-NE	9.43	1.62	1.46
8	U	43	ARG	NE-CZ	8.60	1.44	1.33
10	O	169	ARG	CZ-NH1	7.78	1.43	1.33
2	B	169	ARG	NE-CZ	6.49	1.41	1.33
8	H	42	GLU	CD-OE2	6.18	1.32	1.25
8	H	47	ARG	CZ-NH1	-5.94	1.25	1.33
8	U	50	THR	CB-CG2	5.50	1.70	1.52
3	P	220	PHE	CG-CD1	-5.38	1.30	1.38
8	H	40	CYS	CB-SG	5.23	1.91	1.82
8	U	42	GLU	CD-OE2	5.08	1.31	1.25
7	G	74	PRO	N-CD	5.01	1.54	1.47

All (67) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	U	47	ARG	NE-CZ-NH2	-37.30	101.65	120.30
8	H	47	ARG	NE-CZ-NH2	33.38	136.99	120.30
7	G	75	ALA	N-CA-CB	-19.29	83.10	110.10
8	U	43	ARG	NH1-CZ-NH2	-18.82	98.69	119.40
10	O	169	ARG	NH1-CZ-NH2	-17.91	99.70	119.40
8	U	43	ARG	NE-CZ-NH1	17.41	129.00	120.30
10	O	169	ARG	NE-CZ-NH2	17.25	128.93	120.30
8	H	43	ARG	NE-CZ-NH2	-16.30	112.15	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	43	ARG	NE-CZ-NH1	15.84	128.22	120.30
10	O	169	ARG	NE-CZ-NH1	15.61	128.10	120.30
2	B	390	GLY	N-CA-C	15.33	151.42	113.10
10	O	390	GLY	N-CA-C	15.25	151.24	113.10
8	H	47	ARG	NH1-CZ-NH2	-14.99	102.92	119.40
7	G	74	PRO	N-CA-C	14.66	150.22	112.10
10	O	301	LYS	CB-CA-C	-14.42	81.56	110.40
8	U	47	ARG	NH1-CZ-NH2	13.47	134.21	119.40
10	O	168	TYR	CB-CA-C	-12.57	85.27	110.40
10	O	301	LYS	N-CA-C	12.53	144.84	111.00
2	B	301	LYS	N-CA-C	12.14	143.79	111.00
8	U	43	ARG	CB-CG-CD	-11.76	81.03	111.60
2	B	391	SER	N-CA-CB	11.69	128.03	110.50
10	O	169	ARG	N-CA-CB	-11.51	89.89	110.60
2	B	169	ARG	NE-CZ-NH1	11.35	125.97	120.30
8	U	43	ARG	CD-NE-CZ	-11.17	107.97	123.60
10	O	391	SER	N-CA-CB	11.11	127.16	110.50
2	B	301	LYS	CB-CA-C	-11.09	88.22	110.40
7	G	77	TYR	C-N-CA	10.54	148.06	121.70
10	O	169	ARG	N-CA-C	10.10	138.26	111.00
7	G	74	PRO	CB-CA-C	-9.99	87.02	112.00
8	H	50	THR	CB-CA-C	-9.80	85.15	111.60
1	A	349	ALA	N-CA-CB	9.42	123.29	110.10
5	R	142	LEU	N-CA-C	-8.95	86.83	111.00
2	B	169	ARG	NE-CZ-NH2	-8.92	115.84	120.30
8	U	50	THR	CB-CA-C	-8.37	89.01	111.60
5	R	141	HIS	CB-CA-C	-8.23	93.95	110.40
5	I	53	GLU	N-CA-C	8.15	133.00	111.00
2	B	169	ARG	N-CA-CB	-8.15	95.94	110.60
1	N	349	ALA	N-CA-CB	8.13	121.48	110.10
8	H	43	ARG	CB-CG-CD	-7.93	90.97	111.60
5	R	72	SER	N-CA-C	7.88	132.29	111.00
5	R	142	LEU	N-CA-CB	7.80	126.00	110.40
1	A	348	SER	CB-CA-C	7.54	124.42	110.10
8	H	43	ARG	N-CA-CB	-7.47	97.14	110.60
1	A	349	ALA	N-CA-C	-7.33	91.20	111.00
8	H	47	ARG	CD-NE-CZ	7.25	133.74	123.60
7	G	77	TYR	N-CA-C	7.24	130.54	111.00
5	I	52	ARG	CB-CA-C	6.95	124.29	110.40
1	N	349	ALA	N-CA-C	-6.93	92.29	111.00
1	A	348	SER	N-CA-C	-6.65	93.04	111.00
10	O	301	LYS	C-N-CA	6.42	135.79	122.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	LYS	C-N-CA	6.40	135.75	122.30
7	G	73	ASN	C-N-CD	6.03	141.06	128.40
8	U	43	ARG	NE-CZ-NH2	5.98	123.29	120.30
1	N	445	ARG	NE-CZ-NH2	-5.96	117.32	120.30
5	R	73	LYS	N-CA-CB	5.89	121.20	110.60
5	R	72	SER	CB-CA-C	-5.87	98.94	110.10
10	O	169	ARG	CD-NE-CZ	-5.80	115.47	123.60
1	N	348	SER	N-CA-C	-5.67	95.68	111.00
2	B	169	ARG	NH1-CZ-NH2	-5.67	113.16	119.40
1	N	408	ARG	CB-CG-CD	-5.57	97.13	111.60
1	A	408	ARG	CG-CD-NE	5.51	123.37	111.80
1	N	348	SER	CB-CA-C	5.45	120.45	110.10
8	U	42	GLU	OE1-CD-OE2	5.44	129.83	123.30
8	U	47	ARG	NE-CZ-NH1	-5.42	117.59	120.30
2	B	168	TYR	CB-CA-C	-5.19	100.02	110.40
5	R	73	LYS	N-CA-C	-5.07	97.32	111.00
1	N	324	PHE	CB-CG-CD1	5.00	124.30	120.80

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	444	LEU	Peptide
2	B	169	ARG	Sidechain
2	B	301	LYS	Peptide
7	G	77	TYR	Peptide
8	H	50	THR	Peptide
1	N	444	LEU	Peptide
10	O	169	ARG	Sidechain
10	O	301	LYS	Peptide
8	U	43	ARG	Sidechain
8	U	47	ARG	Sidechain
8	U	50	THR	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3439	0	3337	45	0
1	N	3432	0	3330	42	0
2	B	3164	0	3144	80	0
3	C	2968	0	3028	82	0
3	P	2936	0	2996	71	0
4	D	1912	0	1861	42	0
4	Q	1918	0	1870	38	0
5	E	549	0	547	9	0
5	I	157	0	171	27	0
5	R	1518	0	1504	27	0
6	F	860	0	849	24	1
6	S	869	0	862	24	0
7	G	677	0	672	9	0
7	T	624	0	630	8	0
8	H	529	0	512	45	0
8	U	538	0	522	23	1
9	J	482	0	483	8	0
9	W	487	0	487	9	0
10	O	3140	0	3121	104	0
11	V	127	0	135	40	0
12	C	86	0	60	10	0
12	P	86	0	60	10	0
13	C	28	0	14	6	0
13	P	28	0	14	5	0
14	C	5	0	0	0	0
14	D	15	0	0	0	0
14	E	5	0	0	0	0
14	F	5	0	0	0	0
14	N	10	0	0	0	0
14	Q	10	0	0	0	0
14	S	5	0	0	0	0
15	C	49	0	72	1	0
15	D	26	0	26	0	0
15	P	49	0	72	1	0
15	Q	51	0	82	3	0
16	D	43	0	32	12	0
16	Q	43	0	32	10	0
17	D	39	0	39	0	0
17	G	44	0	32	0	0
17	Q	39	0	39	1	0
17	T	49	0	42	1	0
18	R	4	0	0	3	0
19	R	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	31051	0	30685	645	1

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

All (645) 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)
8:H:43:ARG:NH1	8:H:43:ARG:CZ	1.68	1.56
2:B:169:ARG:NH2	2:B:169:ARG:CZ	1.70	1.49
8:H:47:ARG:CD	8:H:50:THR:HG21	1.35	1.44
8:H:47:ARG:CD	8:H:50:THR:CG2	2.07	1.32
8:H:47:ARG:HD2	8:H:50:THR:CG2	1.62	1.28
4:D:139:THR:OG1	8:H:41:ASP:OD1	1.55	1.22
8:H:44:VAL:CG2	8:H:47:ARG:HH21	1.53	1.20
10:O:168:TYR:O	10:O:173:ALA:HB2	1.41	1.17
1:N:284:TYR:CE1	11:V:73:PRO:HB3	1.80	1.16
8:H:47:ARG:HD2	8:H:50:THR:HG22	1.28	1.15
8:H:44:VAL:HG22	8:H:47:ARG:HH21	1.10	1.12
4:Q:139:THR:OG1	8:U:41:ASP:OD1	1.68	1.08
10:O:89:ILE:HD12	11:V:70:LEU:HD22	1.36	1.03
4:Q:37:CYS:SG	16:Q:501:HEC:CAB	2.48	1.02
8:H:47:ARG:CZ	8:H:50:THR:OG1	1.88	1.01
1:A:344:ARG:O	1:A:348:SER:O	1.79	1.01
8:U:37:LEU:O	8:U:41:ASP:HB2	1.61	1.01
10:O:85:ILE:HG22	11:V:70:LEU:HD13	1.43	0.99
4:D:40:CYS:SG	16:D:501:HEC:HBC3	2.02	0.99
10:O:90:GLU:HG2	11:V:71:ASN:OD1	1.64	0.97
2:B:168:TYR:HD2	2:B:172:LEU:HB2	1.27	0.96
8:H:37:LEU:O	8:H:41:ASP:HB2	1.64	0.96
8:H:44:VAL:HG22	8:H:47:ARG:NH2	1.80	0.94
10:O:168:TYR:HD2	10:O:172:LEU:HB2	1.33	0.93
3:C:376:LEU:HD12	6:F:20:TYR:HD2	1.33	0.93
1:N:344:ARG:O	1:N:348:SER:O	1.86	0.91
2:B:99:THR:CG2	5:I:67:SER:OG	2.19	0.91
8:U:43:ARG:O	8:U:47:ARG:HG2	1.72	0.89
10:O:85:ILE:HG22	11:V:70:LEU:CD1	2.02	0.89
4:Q:1:SER:HA	4:Q:155:GLY:HA2	1.54	0.88
4:D:178:THR:HG21	8:H:16:PRO:HD2	1.57	0.87
8:U:43:ARG:O	8:U:47:ARG:CG	2.23	0.87
8:H:44:VAL:CG2	8:H:47:ARG:NH2	2.36	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:376:LEU:CD1	6:F:20:TYR:HD2	1.90	0.84
2:B:99:THR:HG22	5:I:67:SER:OG	1.77	0.84
4:Q:37:CYS:SG	16:Q:501:HEC:CBB	2.66	0.83
3:P:276:PHE:HD1	3:P:277:ALA:N	1.74	0.83
4:D:37:CYS:SG	16:D:501:HEC:CAB	2.66	0.83
8:H:44:VAL:HG23	8:H:47:ARG:HH21	1.44	0.83
10:O:90:GLU:CG	11:V:71:ASN:OD1	2.26	0.83
3:C:376:LEU:HD12	6:F:20:TYR:CD2	2.14	0.82
3:C:276:PHE:HD1	3:C:277:ALA:N	1.78	0.82
2:B:168:TYR:CD2	2:B:172:LEU:HB2	2.14	0.81
10:O:169:ARG:HH21	10:O:238:LYS:HG2	1.45	0.81
8:H:50:THR:OG1	8:H:51:GLU:N	2.10	0.80
8:H:47:ARG:HH12	8:H:50:THR:C	1.85	0.80
10:O:168:TYR:CD2	10:O:172:LEU:HB2	2.17	0.80
8:U:50:THR:OG1	8:U:51:GLU:N	2.05	0.80
10:O:169:ARG:NH2	10:O:238:LYS:HG2	1.97	0.79
4:D:40:CYS:SG	16:D:501:HEC:CBC	2.69	0.79
3:C:145:VAL:HG21	3:C:268:ILE:HD12	1.64	0.79
8:H:47:ARG:NH1	8:H:50:THR:O	2.15	0.78
3:P:145:VAL:HG21	3:P:268:ILE:HD12	1.65	0.78
8:U:48:SER:C	8:U:49:GLN:HG2	2.04	0.78
4:D:37:CYS:SG	16:D:501:HEC:CBB	2.72	0.78
4:D:40:CYS:SG	16:D:501:HEC:CAC	2.71	0.78
12:C:502:HEM:HMC2	12:C:502:HEM:HBC2	1.64	0.77
4:D:140:GLY:HA3	8:H:53:ASP:HB3	1.64	0.76
4:D:37:CYS:SG	16:D:501:HEC:HBB3	2.25	0.76
10:O:89:ILE:HB	11:V:70:LEU:CD2	2.16	0.75
8:U:44:VAL:HG23	8:U:47:ARG:NH2	2.02	0.74
2:B:169:ARG:NH2	2:B:238:LYS:HG2	2.03	0.74
2:B:99:THR:HG23	5:I:67:SER:OG	1.87	0.74
4:D:120:ARG:NE	16:D:501:HEC:O1A	2.21	0.74
12:C:501:HEM:HBC2	12:C:501:HEM:HMC1	1.70	0.73
8:H:48:SER:C	8:H:49:GLN:HG2	2.09	0.73
5:I:53:GLU:HG3	5:I:53:GLU:O	1.88	0.73
13:P:503:4X9:C6	13:P:503:4X9:H16	2.18	0.72
7:G:77:TYR:O	7:G:80:ASP:O	2.07	0.72
10:O:89:ILE:CD1	11:V:70:LEU:HD22	2.16	0.72
6:F:20:TYR:HD1	6:F:20:TYR:O	1.73	0.72
2:B:78:LYS:HB2	2:B:129:ALA:HB1	1.72	0.71
3:C:106:SER:HB3	12:C:502:HEM:HBD2	1.71	0.71
8:H:43:ARG:O	8:H:47:ARG:HG2	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:438:GLU:OE2	10:O:169:ARG:NH1	2.23	0.71
12:P:501:HEM:HMC1	12:P:501:HEM:HBC2	1.71	0.71
2:B:227:ARG:HE	2:B:227:ARG:HA	1.55	0.70
2:B:168:TYR:O	2:B:173:ALA:HB2	1.92	0.70
3:C:205:SER:OG	13:C:503:4X9:H26B	1.91	0.70
1:N:253:VAL:HB	1:N:324:PHE:CE1	2.26	0.70
12:P:501:HEM:HBB2	12:P:501:HEM:HMB1	1.74	0.70
5:R:98:VAL:O	5:R:98:VAL:HG23	1.92	0.70
8:H:40:CYS:HA	8:H:43:ARG:HG2	1.74	0.70
2:B:169:ARG:NH1	10:O:438:GLU:OE2	2.24	0.70
4:Q:40:CYS:SG	16:Q:501:HEC:HBC3	2.31	0.69
8:H:47:ARG:NH2	8:H:50:THR:OG1	2.23	0.69
10:O:168:TYR:O	10:O:173:ALA:CB	2.30	0.69
1:A:21:ASN:O	1:A:221:GLY:O	2.10	0.69
10:O:78:LYS:HB2	10:O:129:ALA:HB1	1.75	0.69
3:P:276:PHE:CD1	3:P:277:ALA:N	2.60	0.69
10:O:227:ARG:HA	10:O:227:ARG:HE	1.57	0.68
8:H:44:VAL:HA	8:H:47:ARG:HE	1.58	0.68
10:O:304:HIS:O	10:O:305:GLU:HG3	1.93	0.68
4:Q:37:CYS:SG	16:Q:501:HEC:HBB3	2.33	0.68
2:B:29:LEU:HD23	2:B:30:PRO:HD2	1.75	0.67
3:P:276:PHE:HD1	3:P:276:PHE:C	1.97	0.67
11:V:72:VAL:HG13	11:V:73:PRO:HD2	1.77	0.67
3:C:187:PHE:CZ	3:P:184:ILE:CD1	2.78	0.66
3:C:276:PHE:CD1	3:C:277:ALA:N	2.61	0.66
3:C:201:HIS:CE1	13:C:503:4X9:H29	2.30	0.65
2:B:170:ASN:ND2	2:B:170:ASN:H	1.93	0.65
6:F:20:TYR:HD1	6:F:20:TYR:C	1.99	0.65
11:V:72:VAL:HG12	11:V:73:PRO:O	1.95	0.65
3:P:78:ILE:HD11	4:Q:204:MET:CE	2.27	0.65
3:C:220:PHE:O	3:C:220:PHE:HD1	1.80	0.65
5:R:163:SER:HA	5:R:174:GLY:HA3	1.79	0.65
8:H:43:ARG:O	8:H:47:ARG:CG	2.45	0.65
8:H:44:VAL:HA	8:H:47:ARG:NE	2.12	0.65
11:V:70:LEU:O	11:V:70:LEU:HG	1.97	0.65
10:O:29:LEU:HD23	10:O:30:PRO:HD2	1.78	0.64
1:A:253:VAL:HB	1:A:324:PHE:CE1	2.33	0.64
3:P:276:PHE:C	3:P:276:PHE:CD1	2.71	0.64
1:N:21:ASN:O	1:N:221:GLY:O	2.16	0.64
6:F:20:TYR:CD1	6:F:20:TYR:C	2.71	0.64
1:N:324:PHE:CE2	1:N:334:MET:HB3	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:78:ILE:HD11	4:D:204:MET:CE	2.28	0.64
5:I:70:LEU:O	5:I:70:LEU:HG	1.96	0.64
5:R:175:PRO:HG2	18:R:501:FES:S1	2.38	0.63
6:F:20:TYR:HE1	6:F:24:ALA:HB2	1.64	0.63
6:S:40:ASN:C	6:S:40:ASN:OD1	2.35	0.63
3:C:379:TRP:CE2	6:F:33:ARG:HD3	2.34	0.63
5:I:72:VAL:HG12	5:I:73:PRO:O	1.99	0.62
3:P:220:PHE:CD1	3:P:224:TYR:HB2	2.34	0.62
4:D:178:THR:HG21	8:H:16:PRO:CD	2.29	0.62
11:V:62:ARG:O	11:V:78:TYR:HB3	2.00	0.62
10:O:98:VAL:O	11:V:67:SER:HA	2.00	0.62
3:C:168:PHE:HE2	5:R:72:SER:HB2	1.65	0.62
3:P:103:TYR:HB2	3:P:325:PHE:HE2	1.65	0.61
3:C:276:PHE:HD1	3:C:276:PHE:C	2.03	0.61
1:A:293:PRO:O	1:A:297:ILE:HG12	2.01	0.61
2:B:261:SER:OG	2:B:262:ALA:N	2.32	0.61
1:N:284:TYR:CE1	11:V:73:PRO:CB	2.71	0.61
10:O:170:ASN:ND2	10:O:170:ASN:H	1.96	0.61
2:B:169:ARG:CD	10:O:435:PHE:CZ	2.83	0.61
10:O:169:ARG:HH21	10:O:238:LYS:CG	2.12	0.61
1:N:253:VAL:HB	1:N:324:PHE:HE1	1.64	0.61
2:B:435:PHE:CZ	10:O:169:ARG:CD	2.84	0.61
3:P:376:LEU:HB2	6:S:20:TYR:HD2	1.64	0.61
12:C:501:HEM:HHC	12:C:501:HEM:HBB2	1.83	0.60
11:V:76:VAL:HG12	11:V:76:VAL:O	2.01	0.60
3:C:277:ALA:HB1	3:C:294:LEU:CD1	2.31	0.60
9:W:58:LYS:C	9:W:59:TYR:HD1	2.05	0.60
5:I:72:VAL:HG13	5:I:73:PRO:HD2	1.83	0.60
2:B:169:ARG:HD3	10:O:435:PHE:CE2	2.36	0.60
3:P:277:ALA:HB1	3:P:294:LEU:CD1	2.32	0.60
2:B:134:ARG:NH2	6:S:49:ARG:O	2.34	0.60
3:P:376:LEU:CB	6:S:20:TYR:HD2	2.15	0.60
1:A:324:PHE:CE2	1:A:334:MET:HB3	2.37	0.59
4:D:178:THR:CG2	8:H:15:ASP:HA	2.32	0.59
1:A:443:TRP:CD1	1:A:444:LEU:HD23	2.37	0.59
3:C:220:PHE:CD1	3:C:220:PHE:O	2.55	0.59
10:O:89:ILE:HB	11:V:70:LEU:HD23	1.83	0.59
5:R:161:HIS:HB2	18:R:501:FES:S1	2.43	0.59
4:D:33:TYR:HA	4:D:37:CYS:SG	2.43	0.58
2:B:279:LEU:HA	2:B:294:SER:HB3	1.85	0.58
4:Q:181:GLN:HB2	8:U:77:LEU:HD22	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:U:40:CYS:HA	8:U:43:ARG:HG2	1.84	0.58
3:C:375:LYS:O	6:F:17:ARG:NH1	2.36	0.58
7:G:59:TYR:C	7:G:59:TYR:CD1	2.75	0.58
5:I:64:LEU:HD21	5:I:76:VAL:HG13	1.84	0.58
3:C:106:SER:HB3	12:C:502:HEM:CBD	2.33	0.57
2:B:98:VAL:O	5:I:68:VAL:O	2.22	0.57
3:C:120:LEU:HG	3:C:124:MET:HE2	1.86	0.57
3:C:361:LEU:O	3:C:366:MET:HG3	2.04	0.57
3:C:276:PHE:C	3:C:276:PHE:CD1	2.77	0.57
3:C:220:PHE:CZ	13:C:503:4X9:H15	2.39	0.57
1:N:3:THR:HG23	1:N:6:GLN:H	1.69	0.57
8:U:47:ARG:HB2	8:U:50:THR:HG22	1.85	0.57
3:C:103:TYR:HB2	3:C:325:PHE:HE2	1.68	0.57
3:C:220:PHE:CD1	3:C:220:PHE:C	2.78	0.57
10:O:261:SER:OG	10:O:262:ALA:N	2.38	0.57
13:P:503:4X9:H6	13:P:503:4X9:H16	1.87	0.57
3:P:349:THR:HA	3:P:352:GLN:HG2	1.86	0.56
1:A:223:TYR:HB2	1:A:228:VAL:HG21	1.87	0.56
3:P:376:LEU:HB2	6:S:20:TYR:CD2	2.40	0.56
6:F:40:ASN:OD1	6:F:41:ASP:N	2.38	0.56
4:Q:40:CYS:SG	16:Q:501:HEC:CAC	2.93	0.56
6:F:49:ARG:O	10:O:134:ARG:NH2	2.39	0.56
2:B:71:LEU:HD23	5:I:68:VAL:HG11	1.88	0.56
3:P:18:PHE:O	3:P:220:PHE:HD2	1.88	0.56
4:Q:33:TYR:HA	4:Q:37:CYS:SG	2.45	0.56
1:A:253:VAL:HB	1:A:324:PHE:HE1	1.70	0.56
4:D:178:THR:HG21	8:H:15:ASP:HA	1.87	0.56
10:O:97:SER:HA	11:V:69:SER:OG	2.06	0.56
2:B:169:ARG:NH2	2:B:238:LYS:CG	2.69	0.56
5:E:58:PHE:O	5:E:61:SER:HB3	2.06	0.56
5:I:52:ARG:HD2	5:I:53:GLU:H	1.71	0.56
3:P:145:VAL:HG21	3:P:268:ILE:CD1	2.36	0.56
6:S:40:ASN:OD1	6:S:41:ASP:N	2.38	0.56
8:H:48:SER:C	8:H:49:GLN:CG	2.75	0.56
10:O:86:THR:HA	11:V:70:LEU:HD11	1.87	0.56
10:O:71:LEU:HD23	11:V:68:VAL:HG21	1.87	0.55
3:P:103:TYR:HD1	3:P:325:PHE:HD2	1.53	0.55
3:P:70:CYS:SG	3:P:80:ARG:HD3	2.46	0.55
8:H:40:CYS:CA	8:H:43:ARG:HG2	2.36	0.55
3:C:21:LEU:HD23	3:C:220:PHE:HD2	1.72	0.55
7:G:59:TYR:C	7:G:59:TYR:HD1	2.08	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:176:LEU:HD13	5:I:66:ALA:HB2	1.88	0.55
1:A:27:SER:HA	1:A:199:ALA:O	2.06	0.55
4:Q:1:SER:CA	4:Q:155:GLY:HA2	2.32	0.55
8:H:35:GLU:C	8:H:39:LEU:HD12	2.27	0.55
10:O:31:ASN:ND2	10:O:225:ASN:OD1	2.39	0.55
8:H:35:GLU:O	8:H:39:LEU:HD12	2.07	0.55
2:B:75:LEU:HD22	2:B:136:GLU:HB3	1.89	0.55
16:D:501:HEC:HBD2	16:D:501:HEC:HHA	1.88	0.55
3:C:105:GLY:HA2	3:C:107:TYR:CE2	2.42	0.55
4:Q:204:MET:HG2	15:Q:506:PEE:H2	1.88	0.55
1:A:3:THR:HG23	1:A:6:GLN:H	1.71	0.54
3:C:220:PHE:C	3:C:220:PHE:HD1	2.11	0.54
10:O:90:GLU:HA	11:V:71:ASN:HD21	1.71	0.54
16:D:501:HEC:HHA	16:D:501:HEC:CBD	2.37	0.54
6:F:40:ASN:OD1	6:F:40:ASN:C	2.44	0.54
5:I:53:GLU:O	5:I:53:GLU:CG	2.56	0.54
10:O:176:LEU:HD12	11:V:64:VAL:HG23	1.90	0.54
1:N:284:TYR:CD1	11:V:73:PRO:HB3	2.38	0.54
10:O:226:ILE:HD12	10:O:227:ARG:N	2.23	0.54
3:C:8:HIS:N	3:C:9:PRO:HD3	2.23	0.54
1:A:233:PRO:O	5:E:22:THR:HA	2.07	0.54
1:N:288:ALA:HB2	1:N:300:THR:HG22	1.90	0.54
2:B:169:ARG:HD3	10:O:435:PHE:CZ	2.43	0.53
8:U:48:SER:C	8:U:49:GLN:CG	2.77	0.53
3:C:75:TYR:CE2	5:E:57:GLN:HG2	2.42	0.53
2:B:99:THR:CG2	5:I:67:SER:HG	2.22	0.53
3:C:184:ILE:CD1	3:P:187:PHE:CZ	2.91	0.53
2:B:299:VAL:HG11	2:B:336:VAL:HG13	1.90	0.53
3:C:104:TYR:CD1	3:C:208:PRO:HA	2.43	0.53
3:P:221:HIS:ND1	3:P:222:PRO:HA	2.24	0.53
4:D:211:MET:HG2	9:J:35:PHE:CE2	2.43	0.53
7:T:59:TYR:C	7:T:59:TYR:CD1	2.82	0.53
3:P:376:LEU:HD12	6:S:20:TYR:CD2	2.44	0.53
1:N:219:LEU:HG	1:N:220:SER:O	2.08	0.53
3:C:11:MET:C	3:C:11:MET:SD	2.88	0.53
13:P:503:4X9:C6	13:P:503:4X9:C16	2.84	0.53
1:A:162:PRO:HD2	1:A:234:CYS:SG	2.48	0.52
8:H:44:VAL:HG23	8:H:47:ARG:NH2	2.14	0.52
2:B:157:ALA:O	2:B:161:GLU:HG2	2.09	0.52
2:B:168:TYR:CE2	2:B:172:LEU:HD12	2.44	0.52
1:N:106:LEU:HB3	1:N:107:PRO:HD3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:O:299:VAL:HG11	10:O:336:VAL:HG13	1.91	0.52
4:Q:178:THR:HG21	8:U:16:PRO:HD2	1.90	0.52
3:P:375:LYS:O	6:S:17:ARG:NH1	2.37	0.52
1:N:283:THR:HB	11:V:74:ALA:HB3	1.91	0.52
6:F:107:TRP:HE1	10:O:87:ARG:HB3	1.75	0.52
3:C:11:MET:SD	3:C:11:MET:O	2.67	0.52
6:F:20:TYR:CE1	6:F:24:ALA:HB2	2.43	0.52
12:P:502:HEM:HMB1	12:P:502:HEM:HBB2	1.92	0.52
9:W:59:TYR:CD1	9:W:59:TYR:N	2.75	0.52
2:B:169:ARG:NH1	2:B:169:ARG:NH2	2.41	0.52
9:J:58:LYS:C	9:J:59:TYR:HD1	2.13	0.52
10:O:42:ALA:O	10:O:113:ARG:NH1	2.41	0.52
3:P:103:TYR:HD1	3:P:325:PHE:CD2	2.28	0.52
3:C:246:ALA:HB1	3:C:249:LEU:HB2	1.92	0.51
5:I:64:LEU:HD23	5:I:65:VAL:N	2.24	0.51
10:O:279:LEU:HA	10:O:294:SER:HB3	1.91	0.51
10:O:96:LEU:O	11:V:69:SER:HA	2.10	0.51
3:P:226:ILE:HA	3:P:229:ILE:HD12	1.92	0.51
3:P:361:LEU:O	3:P:366:MET:HG3	2.10	0.51
2:B:101:THR:HG1	2:B:103:GLU:H	1.57	0.51
3:C:277:ALA:HB1	3:C:294:LEU:HD12	1.92	0.51
4:D:141:VAL:HG23	8:H:53:ASP:OD2	2.10	0.51
2:B:435:PHE:CE2	10:O:169:ARG:HD3	2.45	0.51
10:O:49:LEU:HD23	10:O:127:THR:HG21	1.91	0.51
3:P:103:TYR:HB2	3:P:325:PHE:CE2	2.44	0.51
10:O:168:TYR:CE2	10:O:172:LEU:HD12	2.45	0.51
3:C:145:VAL:HG21	3:C:268:ILE:CD1	2.36	0.51
3:P:211:ILE:HD11	6:S:36:THR:HG22	1.93	0.51
7:T:73:ASN:HB3	7:T:75:ALA:H	1.76	0.51
2:B:226:ILE:HD12	2:B:227:ARG:N	2.25	0.51
5:I:65:VAL:HG23	5:I:77:ARG:HB2	1.91	0.51
10:O:85:ILE:HG22	11:V:70:LEU:HD11	1.90	0.51
5:I:76:VAL:O	5:I:76:VAL:HG12	2.10	0.51
1:N:27:SER:HA	1:N:199:ALA:O	2.11	0.51
2:B:435:PHE:CZ	10:O:169:ARG:HD2	2.46	0.51
3:C:181:PHE:HA	3:C:184:ILE:HG22	1.92	0.51
3:C:349:THR:HA	3:C:352:GLN:HG2	1.93	0.51
12:C:502:HEM:HBC2	12:C:502:HEM:CMC	2.38	0.51
3:P:246:ALA:HB1	3:P:249:LEU:HB2	1.92	0.51
3:P:277:ALA:HB1	3:P:294:LEU:HD12	1.93	0.51
3:C:120:LEU:HG	3:C:124:MET:CE	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:O:75:LEU:HD22	10:O:136:GLU:HB3	1.93	0.51
3:P:120:LEU:HG	3:P:124:MET:HE2	1.93	0.51
1:A:244:ARG:CZ	7:G:10:VAL:HB	2.41	0.50
3:C:19:ILE:HG22	3:C:20:ASP:OD1	2.11	0.50
10:O:90:GLU:HG3	11:V:71:ASN:OD1	2.09	0.50
6:S:71:ARG:O	6:S:72:GLN:HB2	2.12	0.50
4:D:137:PRO:HA	4:D:149:PHE:CD2	2.46	0.50
10:O:98:VAL:HG22	10:O:107:TYR:CD1	2.46	0.50
17:Q:505:CDL:C42	17:T:501:CDL:C78	2.90	0.50
3:C:75:TYR:CD2	5:E:57:GLN:HG2	2.47	0.50
3:P:325:PHE:C	3:P:325:PHE:CD1	2.85	0.50
12:P:502:HEM:CMB	12:P:502:HEM:HBB2	2.42	0.50
4:Q:40:CYS:SG	16:Q:501:HEC:CBC	2.98	0.50
5:R:134:ILE:HD11	5:R:185:TYR:CG	2.47	0.50
2:B:177:TYR:OH	5:I:76:VAL:CG2	2.60	0.50
1:N:223:TYR:CB	1:N:228:VAL:HG21	2.41	0.49
1:N:293:PRO:O	1:N:297:ILE:HG12	2.12	0.49
10:O:157:ALA:O	10:O:161:GLU:HG2	2.12	0.49
6:S:12:TRP:CD1	6:S:13:LEU:HD23	2.47	0.49
3:C:226:ILE:HA	3:C:229:ILE:HD12	1.94	0.49
3:P:51:LEU:HD13	12:P:501:HEM:HBD1	1.94	0.49
5:R:150:ALA:O	5:R:157:TYR:HB2	2.12	0.49
10:O:385:GLN:O	10:O:389:ALA:O	2.29	0.49
3:P:137:GLN:OE1	3:P:260:ASN:N	2.45	0.49
3:P:14:VAL:HG12	3:P:14:VAL:O	2.11	0.49
1:A:288:ALA:HB2	1:A:300:THR:HG22	1.93	0.49
3:C:70:CYS:SG	3:C:80:ARG:HD3	2.52	0.49
1:N:3:THR:OG1	1:N:4:TYR:N	2.46	0.49
2:B:83:PHE:CZ	6:S:107:TRP:HD1	2.31	0.49
2:B:308:ASP:HB2	5:I:55:LEU:CB	2.42	0.49
2:B:435:PHE:CZ	10:O:169:ARG:HD3	2.47	0.49
5:R:171:ILE:HD11	5:R:176:ALA:HB3	1.95	0.49
1:A:106:LEU:HB3	1:A:107:PRO:HD3	1.95	0.49
1:A:223:TYR:CB	1:A:228:VAL:HG21	2.42	0.49
3:C:10:LEU:HD12	3:C:10:LEU:C	2.32	0.49
4:D:231:LYS:O	6:F:71:ARG:HD3	2.13	0.49
2:B:100:SER:O	5:I:66:ALA:O	2.30	0.49
5:R:140:THR:HB	5:R:177:PRO:HD2	1.95	0.49
4:Q:211:MET:HG2	9:W:35:PHE:CE2	2.48	0.49
1:A:223:TYR:HB2	1:A:228:VAL:CG2	2.42	0.49
2:B:316:TYR:N	2:B:316:TYR:CD1	2.80	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:380:ASP:O	2:B:384:SER:HB2	2.13	0.49
10:O:169:ARG:HH21	10:O:238:LYS:HB3	1.77	0.49
3:P:105:GLY:HA2	3:P:107:TYR:CE2	2.48	0.49
1:N:443:TRP:CD1	1:N:444:LEU:HD23	2.48	0.49
1:A:294:LEU:HD13	1:A:337:VAL:HG12	1.95	0.48
1:N:386:TYR:CD2	1:N:390:ILE:HD12	2.47	0.48
2:B:169:ARG:HD2	10:O:435:PHE:CZ	2.48	0.48
2:B:129:ALA:N	2:B:130:PRO:CD	2.77	0.48
9:J:59:TYR:CD1	9:J:59:TYR:N	2.82	0.48
10:O:164:HIS:NE2	10:O:316:TYR:OH	2.40	0.48
3:P:13:ILE:O	3:P:16:ASN:ND2	2.46	0.48
12:P:502:HEM:HBC2	12:P:502:HEM:HHD	1.95	0.48
4:Q:149:PHE:CE1	4:Q:156:GLN:HB3	2.48	0.48
4:Q:36:VAL:O	16:Q:501:HEC:HMC3	2.14	0.48
7:T:25:ALA:O	7:T:27:PRO:HD3	2.14	0.48
10:O:95:LYS:HG3	11:V:72:VAL:CG2	2.44	0.48
1:A:53:ASN:HD21	1:A:165:GLN:HB3	1.79	0.48
3:C:137:GLN:OE1	3:C:260:ASN:N	2.46	0.48
3:C:312:GLN:HG3	3:C:379:TRP:CZ3	2.47	0.48
2:B:49:LEU:HD23	2:B:127:THR:HG21	1.94	0.48
3:C:103:TYR:HB2	3:C:325:PHE:CE2	2.48	0.48
2:B:97:SER:HA	5:I:69:SER:HB3	1.96	0.48
3:P:120:LEU:HG	3:P:124:MET:CE	2.43	0.48
8:U:35:GLU:C	8:U:39:LEU:HD12	2.34	0.48
10:O:95:LYS:HG3	11:V:72:VAL:HG23	1.95	0.48
10:O:229:GLY:O	10:O:230:LEU:C	2.51	0.48
10:O:96:LEU:HG	10:O:96:LEU:O	2.13	0.48
6:S:20:TYR:CD1	6:S:20:TYR:O	2.66	0.48
1:A:40:TRP:CZ2	1:A:377:GLU:HA	2.49	0.48
3:C:15:ASN:N	3:C:15:ASN:OD1	2.46	0.48
4:D:140:GLY:CA	8:H:53:ASP:HB3	2.39	0.48
3:P:131:TYR:HA	12:P:501:HEM:HAA1	1.94	0.48
3:C:103:TYR:HD1	3:C:325:PHE:HD2	1.61	0.48
1:N:245:GLU:HG3	1:N:248:LEU:HG	1.96	0.48
2:B:209:LEU:CD2	2:B:375:SER:HB2	2.43	0.48
3:C:14:VAL:HG12	3:C:14:VAL:O	2.14	0.48
3:C:29:SER:O	3:C:32:ASN:HB2	2.13	0.48
16:D:501:HEC:HMB1	16:D:501:HEC:CBB	2.44	0.48
8:H:41:ASP:O	8:H:45:SER:OG	2.19	0.48
5:I:52:ARG:HD2	5:I:53:GLU:N	2.28	0.48
3:P:104:TYR:CD1	3:P:208:PRO:HA	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:386:TYR:CD2	1:A:390:ILE:HD12	2.49	0.48
2:B:229:GLY:O	2:B:230:LEU:C	2.53	0.48
3:C:325:PHE:C	3:C:325:PHE:CD1	2.87	0.48
10:O:312:PHE:HD1	10:O:313:ASN:N	2.11	0.48
10:O:243:GLU:HA	10:O:424:MET:O	2.13	0.48
6:S:20:TYR:CD1	6:S:20:TYR:C	2.85	0.48
4:D:225:HIS:CE1	7:G:20:PRO:HB2	2.49	0.47
1:N:85:HIS:HB2	1:N:100:LYS:HB2	1.96	0.47
10:O:85:ILE:CG2	11:V:70:LEU:HD13	2.29	0.47
3:P:75:TYR:CE2	5:R:57:GLN:HG2	2.49	0.47
1:A:3:THR:OG1	1:A:4:TYR:N	2.47	0.47
2:B:29:LEU:CD2	2:B:30:PRO:HD2	2.43	0.47
2:B:385:GLN:O	2:B:389:ALA:O	2.32	0.47
1:A:267:ASN:O	1:A:271:GLN:HG2	2.15	0.47
3:C:211:ILE:HD11	6:F:36:THR:HG22	1.95	0.47
4:D:211:MET:HG2	9:J:35:PHE:HE2	1.79	0.47
10:O:301:LYS:HG3	10:O:301:LYS:O	2.13	0.47
10:O:316:TYR:N	10:O:316:TYR:CD1	2.80	0.47
3:P:10:LEU:HD12	3:P:10:LEU:C	2.35	0.47
4:Q:3:LEU:HD21	8:U:56:GLU:HG3	1.96	0.47
2:B:227:ARG:NE	2:B:227:ARG:HA	2.26	0.47
4:D:218:LEU:O	4:D:221:ALA:HB3	2.13	0.47
2:B:354:ASN:N	2:B:355:PRO:HD2	2.30	0.47
16:Q:501:HEC:CBB	16:Q:501:HEC:HMB1	2.45	0.47
5:R:98:VAL:O	5:R:98:VAL:CG2	2.62	0.47
8:U:35:GLU:O	8:U:39:LEU:HD12	2.15	0.47
10:O:86:THR:HA	11:V:70:LEU:HD21	1.97	0.47
3:P:14:VAL:CG1	3:P:14:VAL:O	2.63	0.47
3:P:77:TRP:CZ3	3:P:78:ILE:HG13	2.50	0.47
2:B:435:PHE:CD1	2:B:435:PHE:N	2.82	0.47
11:V:62:ARG:HB3	11:V:63:PRO:HD2	1.97	0.47
5:R:45:VAL:HG13	9:W:28:ALA:HA	1.96	0.47
15:Q:506:PEE:H11	5:R:53:ASN:OD1	2.15	0.47
7:T:59:TYR:C	7:T:59:TYR:HD1	2.17	0.47
10:O:209:LEU:CD2	10:O:375:SER:HB2	2.45	0.46
12:P:501:HEM:HHA	12:P:501:HEM:CBA	2.45	0.46
5:R:171:ILE:CD1	5:R:176:ALA:HB3	2.45	0.46
13:C:503:4X9:C12	13:C:503:4X9:C6	2.89	0.46
5:E:31:ALA:HB2	9:J:7:ALA:HB2	1.96	0.46
3:P:379:TRP:CE3	6:S:33:ARG:HD3	2.51	0.46
4:D:138:PRO:HG3	8:H:55:THR:HA	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:358:TYR:HE1	3:P:362:ILE:HD11	1.80	0.46
8:H:40:CYS:O	8:H:43:ARG:CG	2.64	0.46
1:N:294:LEU:HD13	1:N:337:VAL:HG12	1.97	0.46
10:O:34:VAL:HG11	10:O:386:ALA:HB1	1.98	0.46
12:P:501:HEM:HBB2	12:P:501:HEM:CMB	2.42	0.46
3:C:373:GLU:HA	6:F:20:TYR:HE2	1.80	0.46
8:U:17:LEU:HD11	8:U:21:ARG:NE	2.30	0.46
1:N:442:PHE:CD1	1:N:442:PHE:C	2.89	0.46
5:R:91:TRP:HZ3	5:R:136:ILE:HD11	1.81	0.46
1:A:245:GLU:HG3	1:A:248:LEU:HG	1.97	0.46
2:B:308:ASP:HB2	5:I:55:LEU:HB2	1.97	0.46
4:D:138:PRO:HD3	4:D:149:PHE:CE2	2.50	0.46
4:D:181:GLN:OE1	8:H:77:LEU:HB3	2.16	0.46
3:P:103:TYR:CD1	3:P:325:PHE:CD2	3.04	0.46
2:B:87:ARG:HB3	6:S:107:TRP:NE1	2.30	0.46
3:C:186:PRO:HG2	12:C:501:HEM:HMC3	1.96	0.46
2:B:109:VAL:HB	2:B:119:LEU:HD12	1.98	0.46
1:A:77:LYS:HE3	2:B:291:ALA:HB1	1.97	0.46
2:B:70:ARG:HG2	5:I:68:VAL:HB	1.98	0.46
1:N:219:LEU:O	1:N:220:SER:C	2.54	0.46
10:O:169:ARG:HH21	10:O:238:LYS:CB	2.29	0.46
10:O:354:ASN:N	10:O:355:PRO:HD2	2.31	0.45
3:P:319:PRO:HD2	6:S:20:TYR:CE1	2.51	0.45
3:C:14:VAL:CG1	3:C:14:VAL:O	2.64	0.45
12:C:502:HEM:HBB2	12:C:502:HEM:CMB	2.47	0.45
4:D:40:CYS:SG	16:D:501:HEC:C3C	3.04	0.45
10:O:26:PHE:CE2	10:O:391:SER:HA	2.52	0.45
10:O:99:THR:HG23	11:V:67:SER:OG	2.15	0.45
4:Q:149:PHE:CD1	4:Q:156:GLN:HB3	2.50	0.45
3:C:233:LEU:HD22	4:D:216:LEU:HG	1.98	0.45
4:D:37:CYS:HG	16:D:501:HEC:HBB3	1.80	0.45
8:H:17:LEU:HD11	8:H:21:ARG:NE	2.31	0.45
1:N:442:PHE:C	1:N:442:PHE:HD1	2.20	0.45
10:O:213:HIS:N	10:O:214:PRO:CD	2.79	0.45
3:C:10:LEU:HD21	3:P:202:GLU:HG3	1.99	0.45
4:Q:137:PRO:HA	4:Q:149:PHE:CD2	2.52	0.45
10:O:129:ALA:N	10:O:130:PRO:CD	2.80	0.45
3:P:103:TYR:CD1	3:P:325:PHE:HD2	2.34	0.45
4:Q:3:LEU:CD2	8:U:56:GLU:HG3	2.47	0.45
4:D:216:LEU:N	4:D:217:PRO:HD2	2.31	0.45
1:N:77:LYS:HE3	10:O:291:ALA:HB1	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:111:GLU:HG3	1:A:215:HIS:CE1	2.52	0.45
2:B:303:VAL:HG23	2:B:303:VAL:O	2.16	0.45
7:G:75:ALA:O	7:G:77:TYR:CD2	2.69	0.45
1:N:233:PRO:O	5:R:22:THR:HA	2.17	0.45
10:O:291:ALA:HA	10:O:297:GLN:NE2	2.31	0.45
6:S:68:LEU:HD11	6:S:75:LEU:HG	1.99	0.45
3:C:221:HIS:ND1	3:C:222:PRO:HA	2.32	0.45
8:H:73:LEU:HD23	8:H:73:LEU:O	2.17	0.45
5:I:70:LEU:CG	5:I:70:LEU:O	2.64	0.45
3:P:103:TYR:CE2	15:P:505:PEE:H2	2.51	0.45
1:A:140:GLU:OE2	5:I:52:ARG:O	2.35	0.45
3:P:15:ASN:OD1	3:P:15:ASN:N	2.49	0.45
2:B:87:ARG:HB3	6:S:107:TRP:HE1	1.82	0.45
6:F:26:PHE:HD1	6:F:27:ASN:N	2.15	0.44
6:F:77:LYS:HA	6:F:80:TRP:CE2	2.52	0.44
13:P:503:4X9:H6	13:P:503:4X9:C16	2.47	0.44
5:R:175:PRO:CG	18:R:501:FES:S1	3.04	0.44
3:C:144:THR:O	3:C:148:ASN:HB2	2.17	0.44
8:H:40:CYS:CB	8:H:54:CYS:SG	3.05	0.44
5:E:45:VAL:HG13	9:J:28:ALA:HA	1.99	0.44
10:O:227:ARG:NE	10:O:227:ARG:HA	2.28	0.44
10:O:325:TYR:HD1	10:O:326:THR:N	2.14	0.44
8:U:73:LEU:O	8:U:73:LEU:HD23	2.17	0.44
1:A:149:VAL:HG23	1:A:425:PHE:CB	2.47	0.44
1:A:84:ALA:HB1	1:A:100:LYS:O	2.18	0.44
4:Q:31:GLN:O	4:Q:35:GLN:HG2	2.17	0.44
1:A:120:CYS:SG	1:A:122:LEU:HG	2.57	0.44
5:E:72:SER:HB2	3:P:168:PHE:HE2	1.81	0.44
8:U:40:CYS:O	8:U:43:ARG:HG3	2.18	0.44
2:B:164:HIS:NE2	2:B:316:TYR:OH	2.43	0.44
13:C:503:4X9:H12	13:C:503:4X9:C6	2.47	0.44
10:O:58:GLU:OE1	10:O:63:LEU:HA	2.16	0.44
10:O:85:ILE:O	11:V:70:LEU:HD21	2.17	0.44
10:O:151:ALA:HB2	11:V:76:VAL:HG21	1.98	0.44
2:B:213:HIS:N	2:B:214:PRO:CD	2.81	0.44
2:B:31:ASN:ND2	2:B:225:ASN:OD1	2.51	0.44
2:B:34:VAL:HG11	2:B:386:ALA:HB1	1.99	0.44
3:C:312:GLN:HG3	3:C:379:TRP:HZ3	1.82	0.44
10:O:124:LEU:HD22	10:O:224:LEU:HD12	2.00	0.44
10:O:70:ARG:NE	11:V:66:ALA:HB3	2.33	0.44
3:P:181:PHE:HA	3:P:184:ILE:HG22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:29:SER:O	3:P:32:ASN:HB2	2.18	0.44
4:Q:138:PRO:HD3	4:Q:149:PHE:CE2	2.53	0.44
3:C:103:TYR:HD1	3:C:325:PHE:CD2	2.35	0.44
3:C:220:PHE:CE2	13:C:503:4X9:H15	2.52	0.44
1:N:41:ILE:HG12	1:N:195:MET:HG2	1.99	0.44
3:P:219:PRO:HB2	3:P:221:HIS:O	2.17	0.44
2:B:83:PHE:CZ	6:S:107:TRP:CD1	3.06	0.44
1:N:162:PRO:HD2	1:N:234:CYS:SG	2.58	0.44
10:O:168:TYR:N	10:O:168:TYR:CD1	2.86	0.44
10:O:208:GLY:HA3	10:O:216:LEU:HD11	2.00	0.44
2:B:98:VAL:HG22	2:B:107:TYR:CD1	2.53	0.43
3:C:99:GLY:O	3:C:100:ARG:C	2.57	0.43
3:C:50:PHE:HE2	5:E:58:PHE:HB3	1.82	0.43
1:N:84:ALA:HB1	1:N:100:LYS:O	2.18	0.43
5:R:72:SER:O	5:R:92:ARG:NE	2.50	0.43
1:A:442:PHE:CD1	1:A:442:PHE:C	2.91	0.43
2:B:47:ILE:HD11	2:B:116:VAL:HG12	1.99	0.43
12:C:501:HEM:HBC2	12:C:501:HEM:CMC	2.43	0.43
3:P:26:ASN:ND2	3:P:208:PRO:HD2	2.33	0.43
4:Q:178:THR:HG21	8:U:15:ASP:HA	2.00	0.43
2:B:291:ALA:HA	2:B:297:GLN:NE2	2.33	0.43
3:C:358:TYR:HE1	3:C:362:ILE:HD11	1.83	0.43
4:Q:48:TYR:CE2	4:Q:65:ALA:HA	2.54	0.43
1:A:369:LEU:HD12	1:A:392:LEU:HD21	2.00	0.43
2:B:299:VAL:O	2:B:299:VAL:HG12	2.18	0.43
4:D:137:PRO:HA	4:D:149:PHE:HD2	1.83	0.43
1:N:252:HIS:CE1	1:N:325:VAL:HG22	2.54	0.43
5:R:75:GLU:OE1	5:R:75:GLU:HA	2.19	0.43
10:O:47:ILE:HD11	10:O:116:VAL:HG12	1.99	0.43
2:B:243:GLU:HA	2:B:424:MET:O	2.18	0.43
1:N:267:ASN:O	1:N:271:GLN:HG2	2.18	0.43
1:A:41:ILE:HD13	1:A:190:TYR:CE1	2.54	0.43
4:D:240:PRO:O	4:D:241:LYS:HG3	2.19	0.43
5:I:68:VAL:HG12	5:I:69:SER:N	2.34	0.43
1:A:192:ALA:N	1:A:193:PRO:HD2	2.34	0.43
2:B:26:PHE:CE1	2:B:391:SER:HA	2.54	0.43
3:C:77:TRP:CZ3	3:C:78:ILE:HG13	2.54	0.43
10:O:37:SER:HA	10:O:208:GLY:O	2.19	0.43
3:P:94:LEU:O	3:P:98:VAL:HG23	2.19	0.43
1:A:246:ASP:OD2	7:G:9:ARG:HA	2.18	0.43
1:A:430:GLN:O	1:A:431:LEU:C	2.56	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:20:TYR:O	6:F:21:TYR:C	2.57	0.42
1:N:192:ALA:N	1:N:193:PRO:HD2	2.33	0.42
3:C:187:PHE:HZ	3:P:184:ILE:CD1	2.31	0.42
3:P:201:HIS:NE2	13:P:503:4X9:H29	2.35	0.42
6:S:18:LYS:HA	6:S:83:TYR:CD2	2.54	0.42
1:A:185:TYR:CD1	1:A:189:HIS:CD2	3.07	0.42
3:P:11:MET:C	3:P:11:MET:SD	2.97	0.42
1:N:123:GLU:HB2	1:N:126:GLN:HB2	2.00	0.42
1:N:379:ILE:HG12	1:N:389:ARG:CD	2.49	0.42
3:P:75:TYR:CD2	5:R:57:GLN:HG2	2.55	0.42
5:R:141:HIS:O	5:R:141:HIS:CG	2.72	0.42
1:A:21:ASN:HB2	1:A:221:GLY:CA	2.49	0.42
2:B:42:ALA:O	2:B:113:ARG:NH1	2.49	0.42
4:Q:216:LEU:N	4:Q:217:PRO:HD2	2.35	0.42
2:B:169:ARG:HH22	2:B:238:LYS:HG2	1.78	0.42
2:B:312:PHE:HD1	2:B:313:ASN:N	2.17	0.42
1:N:204:GLU:O	1:N:205:HIS:C	2.57	0.42
3:C:21:LEU:HD23	3:C:220:PHE:CD2	2.53	0.42
10:O:299:VAL:HG21	10:O:340:ALA:HB2	2.01	0.42
3:P:174:THR:O	3:P:177:ARG:HG2	2.20	0.42
4:Q:105:ASN:HD22	16:Q:501:HEC:HMD3	1.85	0.42
8:U:44:VAL:HA	8:U:47:ARG:CZ	2.49	0.42
3:C:26:ASN:ND2	3:C:208:PRO:HD2	2.35	0.42
3:C:310:SER:HA	3:C:374:ASN:HD21	1.85	0.42
10:O:26:PHE:HZ	10:O:390:GLY:O	2.01	0.42
10:O:83:PHE:CE1	10:O:87:ARG:HG3	2.55	0.42
3:P:17:ALA:O	3:P:18:PHE:CD1	2.72	0.42
3:P:19:ILE:HG22	3:P:20:ASP:OD1	2.19	0.42
1:A:270:LEU:HD21	1:A:414:TYR:HD2	1.85	0.42
2:B:208:GLY:HA3	2:B:216:LEU:HD11	2.01	0.42
4:D:149:PHE:CD1	4:D:156:GLN:HB3	2.55	0.42
3:P:16:ASN:N	3:P:16:ASN:HD22	2.17	0.42
4:D:143:LEU:HD11	4:D:149:PHE:HB2	2.02	0.42
4:Q:126:TYR:C	4:Q:126:TYR:CD1	2.93	0.42
4:Q:182:VAL:HG12	4:Q:183:ALA:N	2.35	0.42
3:C:140:PHE:C	3:C:140:PHE:CD1	2.93	0.42
10:O:240:HIS:ND1	10:O:241:GLY:O	2.52	0.42
5:R:44:THR:HG21	9:W:24:ILE:HD13	2.02	0.42
1:A:46:ARG:NH1	1:A:93:GLU:OE2	2.49	0.41
2:B:51:ILE:HG12	2:B:204:MET:HG2	2.02	0.41
4:Q:118:ARG:HD2	4:Q:194:ALA:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:224:ARG:HG3	7:T:26:PHE:CE1	2.55	0.41
3:C:284:ILE:HD12	3:C:293:ALA:HB2	2.01	0.41
4:D:48:TYR:CE2	4:D:65:ALA:HA	2.55	0.41
1:N:280:TYR:HB3	1:N:307:PHE:CE2	2.55	0.41
10:O:96:LEU:C	11:V:69:SER:HB3	2.41	0.41
3:P:310:SER:HA	3:P:374:ASN:HD21	1.85	0.41
2:B:299:VAL:HG21	2:B:340:ALA:HB2	2.02	0.41
3:C:13:ILE:O	3:C:16:ASN:ND2	2.52	0.41
1:N:327:ASP:OD1	1:N:328:HIS:N	2.53	0.41
1:N:40:TRP:CZ2	1:N:377:GLU:HA	2.56	0.41
10:O:435:PHE:CD1	10:O:435:PHE:N	2.88	0.41
4:Q:237:TYR:HB2	6:S:60:PHE:CD1	2.54	0.41
5:R:113:GLU:OE1	5:R:115:SER:N	2.52	0.41
3:C:17:ALA:O	3:C:18:PHE:CD1	2.74	0.41
3:C:193:ALA:O	3:C:196:HIS:HB3	2.21	0.41
1:N:149:VAL:HG23	1:N:425:PHE:CB	2.50	0.41
4:Q:131:LEU:HD11	16:Q:501:HEC:HMB2	2.02	0.41
1:A:442:PHE:HD1	1:A:442:PHE:C	2.23	0.41
4:D:198:HIS:C	4:D:198:HIS:ND1	2.73	0.41
4:D:28:ARG:HA	4:D:31:GLN:HE21	1.85	0.41
11:V:70:LEU:O	11:V:70:LEU:CG	2.66	0.41
3:C:187:PHE:CZ	3:P:184:ILE:HD11	2.56	0.41
10:O:303:VAL:O	10:O:303:VAL:HG23	2.20	0.41
10:O:417:PHE:CD1	10:O:417:PHE:C	2.94	0.41
4:Q:110:PRO:HA	4:Q:111:PRO:HD2	1.97	0.41
7:T:34:ILE:N	7:T:35:PRO:HD2	2.35	0.41
1:A:41:ILE:HG12	1:A:195:MET:HG2	2.03	0.41
1:A:37:VAL:HG23	1:A:199:ALA:HB2	2.03	0.41
4:D:140:GLY:HA3	8:H:53:ASP:CB	2.42	0.41
7:G:79:ASN:ND2	8:H:52:GLU:OE2	2.53	0.41
10:O:172:LEU:HD13	10:O:316:TYR:CD2	2.56	0.41
3:P:186:PRO:HG2	12:P:501:HEM:HMC3	2.03	0.41
4:Q:204:MET:HE3	15:Q:506:PEE:O4	2.21	0.41
1:A:294:LEU:HG	1:A:307:PHE:CZ	2.56	0.41
12:C:502:HEM:HMB1	12:C:502:HEM:HBB2	2.02	0.41
6:F:71:ARG:O	6:F:72:GLN:HB2	2.20	0.41
1:N:246:ASP:OD2	7:T:9:ARG:HA	2.20	0.41
10:O:166:ALA:HB2	10:O:244:ILE:HG13	2.03	0.41
10:O:86:THR:N	11:V:70:LEU:HD11	2.36	0.41
5:R:137:GLY:O	5:R:146:PRO:HD2	2.21	0.41
5:R:14:ARG:NH1	5:R:18:VAL:O	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:188:THR:HG23	5:R:192:MET:HB2	2.02	0.41
3:C:311:LYS:HE2	3:C:379:TRP:CD1	2.56	0.41
3:C:30:TRP:NE1	15:C:505:PEE:O4	2.53	0.41
10:O:144:LEU:HB2	10:O:183:ILE:HG23	2.02	0.41
4:D:7:PRO:HA	4:D:8:PRO:HD3	1.92	0.41
5:R:82:PRO:HD2	5:R:85:LYS:HD3	2.03	0.41
8:U:47:ARG:CD	8:U:50:THR:CG2	2.99	0.41
2:B:209:LEU:HD23	2:B:375:SER:HB2	2.02	0.40
4:D:27:ARG:NH1	9:J:59:TYR:CE2	2.90	0.40
6:F:18:LYS:HG3	6:F:83:TYR:HD2	1.86	0.40
3:P:376:LEU:CD1	6:S:20:TYR:CD2	3.03	0.40
10:O:74:SER:CB	11:V:70:LEU:HD12	2.51	0.40
4:Q:60:GLU:OE2	9:W:59:TYR:HB3	2.20	0.40
2:B:365:LYS:HG2	2:B:399:LEU:HD23	2.03	0.40
4:D:179:MET:HB3	8:H:15:ASP:OD2	2.21	0.40
5:E:16:PRO:HA	5:E:19:LEU:HD12	2.03	0.40
6:F:18:LYS:HA	6:F:83:TYR:CD2	2.57	0.40
4:Q:204:MET:HB3	4:Q:204:MET:HE3	1.86	0.40
4:Q:211:MET:HG2	9:W:35:PHE:HE2	1.84	0.40
9:W:58:LYS:C	9:W:59:TYR:CD1	2.90	0.40
4:D:19:SER:HA	9:J:47:ASN:OD1	2.21	0.40
1:N:244:ARG:CZ	7:T:10:VAL:HB	2.51	0.40
10:O:109:VAL:HB	10:O:119:LEU:HD12	2.02	0.40
10:O:309:VAL:HA	10:O:325:TYR:O	2.20	0.40
3:P:17:ALA:O	3:P:18:PHE:HD1	2.04	0.40
3:P:276:PHE:CE1	3:P:277:ALA:HB2	2.57	0.40
8:U:40:CYS:O	8:U:43:ARG:CG	2.69	0.40
9:W:4:THR:HG22	9:W:5:LEU:H	1.86	0.40
1:A:26:ALA:O	1:A:198:ALA:HA	2.21	0.40
2:B:240:HIS:ND1	2:B:241:GLY:O	2.54	0.40
3:C:138:MET:HE2	3:C:138:MET:HA	2.03	0.40
3:C:186:PRO:O	3:C:189:ILE:HB	2.21	0.40
6:F:68:LEU:HD11	6:F:75:LEU:HG	2.04	0.40
10:O:29:LEU:CD2	10:O:30:PRO:HD2	2.47	0.40
6:S:77:LYS:HA	6:S:80:TRP:CE2	2.56	0.40
10:O:89:ILE:CG1	11:V:70:LEU:HD22	2.52	0.40
7:G:79:ASN:H	7:G:79:ASN:ND2	2.19	0.40
10:O:51:ILE:HD13	10:O:199:PHE:CE2	2.55	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:57:ASP:OD2	8:U:42:GLU:OE2[1_655]	1.73	0.47

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	442/480 (92%)	405 (92%)	35 (8%)	2 (0%)	31	71
1	N	442/480 (92%)	407 (92%)	33 (8%)	2 (0%)	31	71
2	B	420/453 (93%)	375 (89%)	44 (10%)	1 (0%)	49	83
3	C	372/379 (98%)	347 (93%)	23 (6%)	2 (0%)	31	71
3	P	368/379 (97%)	337 (92%)	30 (8%)	1 (0%)	43	78
4	D	238/265 (90%)	216 (91%)	21 (9%)	1 (0%)	36	75
4	Q	239/265 (90%)	218 (91%)	20 (8%)	1 (0%)	36	75
5	E	71/274 (26%)	64 (90%)	7 (10%)	0	100	100
5	I	17/274 (6%)	12 (71%)	5 (29%)	0	100	100
5	R	194/274 (71%)	174 (90%)	19 (10%)	1 (0%)	31	71
6	F	96/111 (86%)	87 (91%)	9 (9%)	0	100	100
6	S	97/111 (87%)	89 (92%)	8 (8%)	0	100	100
7	G	78/82 (95%)	67 (86%)	10 (13%)	1 (1%)	13	54
7	T	72/82 (88%)	62 (86%)	10 (14%)	0	100	100
8	H	63/91 (69%)	59 (94%)	4 (6%)	0	100	100
8	U	64/91 (70%)	61 (95%)	3 (5%)	0	100	100
9	J	56/64 (88%)	51 (91%)	5 (9%)	0	100	100
9	W	57/64 (89%)	51 (90%)	6 (10%)	0	100	100
10	O	417/453 (92%)	376 (90%)	41 (10%)	0	100	100
11	V	15/274 (6%)	12 (80%)	3 (20%)	0	100	100
All	All	3818/4946 (77%)	3470 (91%)	336 (9%)	12 (0%)	43	78

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	267	ASN
1	N	267	ASN
3	P	107	TYR
5	R	177	PRO
3	C	107	TYR
2	B	394	PRO
7	G	74	PRO
1	N	260	PRO
4	D	240	PRO
1	A	260	PRO
3	C	266	PRO
4	Q	240	PRO

5.3.2 Protein sidechains [i](#)

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	368/394 (93%)	350 (95%)	18 (5%)	27	64
1	N	367/394 (93%)	347 (95%)	20 (5%)	24	61
2	B	331/355 (93%)	309 (93%)	22 (7%)	18	55
3	C	322/327 (98%)	301 (94%)	21 (6%)	19	55
3	P	318/327 (97%)	297 (93%)	21 (7%)	18	55
4	D	205/218 (94%)	196 (96%)	9 (4%)	31	68
4	Q	206/218 (94%)	196 (95%)	10 (5%)	27	64
5	E	63/228 (28%)	57 (90%)	6 (10%)	9	41
5	I	19/228 (8%)	13 (68%)	6 (32%)	0	3
5	R	168/228 (74%)	158 (94%)	10 (6%)	21	58
6	F	90/99 (91%)	82 (91%)	8 (9%)	11	43
6	S	91/99 (92%)	84 (92%)	7 (8%)	14	48
7	G	71/72 (99%)	64 (90%)	7 (10%)	8	39
7	T	66/72 (92%)	59 (89%)	7 (11%)	7	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H	62/85 (73%)	54 (87%)	8 (13%)	5	27
8	U	63/85 (74%)	56 (89%)	7 (11%)	7	35
9	J	49/54 (91%)	45 (92%)	4 (8%)	12	46
9	W	49/54 (91%)	44 (90%)	5 (10%)	8	37
10	O	328/355 (92%)	304 (93%)	24 (7%)	15	51
11	V	15/228 (7%)	12 (80%)	3 (20%)	1	10
All	All	3251/4120 (79%)	3028 (93%)	223 (7%)	17	53

All (223) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	LYS
1	A	58	PHE
1	A	150	PHE
1	A	156	THR
1	A	185	TYR
1	A	186	LEU
1	A	203	LEU
1	A	206	ARG
1	A	230	THR
1	A	305	GLN
1	A	324	PHE
1	A	348	SER
1	A	388	ARG
1	A	397	SER
1	A	416	TYR
1	A	442	PHE
1	A	444	LEU
1	A	445	ARG
2	B	33	LEU
2	B	96	LEU
2	B	97	SER
2	B	99	THR
2	B	101	THR
2	B	108	THR
2	B	116	VAL
2	B	150	VAL
2	B	158	HIS
2	B	170	ASN
2	B	189	VAL

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Mol	Chain	Res	Type
2	B	224	LEU
2	B	226	ILE
2	B	230	LEU
2	B	301	LYS
2	B	310	SER
2	B	312	PHE
2	B	316	TYR
2	B	324	PHE
2	B	325	TYR
2	B	417	PHE
2	B	436	ILE
3	C	10	LEU
3	C	11	MET
3	C	15	ASN
3	C	21	LEU
3	C	35	SER
3	C	63	PHE
3	C	64	SER
3	C	78	ILE
3	C	140	PHE
3	C	156	ILE
3	C	171	ASP
3	C	220	PHE
3	C	257	THR
3	C	268	ILE
3	C	276	PHE
3	C	296	PHE
3	C	310	SER
3	C	311	LYS
3	C	325	PHE
3	C	349	THR
3	C	358	TYR
4	D	3	LEU
4	D	17	LEU
4	D	19	SER
4	D	37	CYS
4	D	68	VAL
4	D	178	THR
4	D	182	VAL
4	D	216	LEU
4	D	232	SER
5	E	7	VAL

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Mol	Chain	Res	Type
5	E	27	GLU
5	E	36	SER
5	E	42	THR
5	E	54	VAL
5	E	72	SER
6	F	20	TYR
6	F	26	PHE
6	F	40	ASN
6	F	78	GLU
6	F	83	TYR
6	F	91	GLU
6	F	94	LEU
6	F	95	LYS
7	G	9	ARG
7	G	17	SER
7	G	18	LEU
7	G	41	THR
7	G	46	LEU
7	G	59	TYR
7	G	60	THR
8	H	14	VAL
8	H	43	ARG
8	H	44	VAL
8	H	47	ARG
8	H	49	GLN
8	H	50	THR
8	H	51	GLU
8	H	55	THR
5	I	50	LEU
5	I	54	SER
5	I	56	ARG
5	I	65	VAL
5	I	67	SER
5	I	70	LEU
9	J	13	LEU
9	J	20	PHE
9	J	37	GLN
9	J	59	TYR
1	N	27	SER
1	N	51	LYS
1	N	58	PHE
1	N	150	PHE

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Mol	Chain	Res	Type
1	N	156	THR
1	N	185	TYR
1	N	186	LEU
1	N	203	LEU
1	N	206	ARG
1	N	230	THR
1	N	305	GLN
1	N	324	PHE
1	N	327	ASP
1	N	348	SER
1	N	388	ARG
1	N	397	SER
1	N	416	TYR
1	N	442	PHE
1	N	444	LEU
1	N	445	ARG
10	O	33	LEU
10	O	96	LEU
10	O	97	SER
10	O	99	THR
10	O	101	THR
10	O	108	THR
10	O	116	VAL
10	O	126	VAL
10	O	150	VAL
10	O	158	HIS
10	O	170	ASN
10	O	189	VAL
10	O	224	LEU
10	O	226	ILE
10	O	230	LEU
10	O	301	LYS
10	O	310	SER
10	O	312	PHE
10	O	316	TYR
10	O	324	PHE
10	O	325	TYR
10	O	407	ASP
10	O	417	PHE
10	O	436	ILE
3	P	10	LEU
3	P	11	MET

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Mol	Chain	Res	Type
3	P	15	ASN
3	P	21	LEU
3	P	35	SER
3	P	63	PHE
3	P	64	SER
3	P	78	ILE
3	P	90	PHE
3	P	140	PHE
3	P	156	ILE
3	P	257	THR
3	P	268	ILE
3	P	276	PHE
3	P	296	PHE
3	P	310	SER
3	P	311	LYS
3	P	325	PHE
3	P	349	THR
3	P	358	TYR
3	P	379	TRP
4	Q	3	LEU
4	Q	17	LEU
4	Q	37	CYS
4	Q	40	CYS
4	Q	68	VAL
4	Q	126	TYR
4	Q	178	THR
4	Q	182	VAL
4	Q	216	LEU
4	Q	232	SER
5	R	7	VAL
5	R	27	GLU
5	R	36	SER
5	R	42	THR
5	R	54	VAL
5	R	72	SER
5	R	113	GLU
5	R	136	ILE
5	R	140	THR
5	R	160	CYS
6	S	26	PHE
6	S	40	ASN
6	S	78	GLU

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Mol	Chain	Res	Type
6	S	83	TYR
6	S	91	GLU
6	S	94	LEU
6	S	95	LYS
7	T	9	ARG
7	T	17	SER
7	T	18	LEU
7	T	41	THR
7	T	46	LEU
7	T	59	TYR
7	T	60	THR
8	U	14	VAL
8	U	43	ARG
8	U	47	ARG
8	U	49	GLN
8	U	50	THR
8	U	51	GLU
8	U	55	THR
11	V	65	VAL
11	V	67	SER
11	V	70	LEU
9	W	4	THR
9	W	13	LEU
9	W	20	PHE
9	W	37	GLN
9	W	59	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	ASN
1	A	118	GLN
1	A	189	HIS
1	A	215	HIS
1	A	271	GLN
2	B	22	GLN
2	B	104	ASN
2	B	170	ASN
2	B	290	ASN
2	B	297	GLN
2	B	343	GLN
2	B	400	GLN

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Mol	Chain	Res	Type
3	C	8	HIS
3	C	16	ASN
4	D	225	HIS
7	G	73	ASN
7	G	79	ASN
1	N	118	GLN
1	N	189	HIS
1	N	215	HIS
1	N	271	GLN
10	O	104	ASN
10	O	297	GLN
10	O	400	GLN
3	P	16	ASN
4	Q	31	GLN
6	S	79	GLN

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](#)

29 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
12	HEM	C	501	3	27,50,50	1.16	2 (7%)	17,82,82	1.57	1 (5%)
12	HEM	C	502	3	27,50,50	0.99	2 (7%)	17,82,82	1.17	1 (5%)
13	4X9	C	503	-	30,30,30	3.01	7 (23%)	41,44,44	1.21	2 (4%)
14	PO4	C	504	-	4,4,4	0.88	0	6,6,6	0.37	0
15	PEE	C	505	-	48,48,50	0.99	2 (4%)	51,53,55	0.97	4 (7%)
16	HEC	D	501	4	26,50,50	2.43	11 (42%)	18,82,82	3.12	9 (50%)
14	PO4	D	502	-	4,4,4	0.63	0	6,6,6	0.55	0
14	PO4	D	503	-	4,4,4	0.76	0	6,6,6	0.58	0
14	PO4	D	504	-	4,4,4	0.72	0	6,6,6	0.51	0
17	CDL	D	505	-	38,38,99	1.27	3 (7%)	43,47,111	1.20	4 (9%)
15	PEE	D	506	-	25,25,50	1.49	2 (8%)	28,30,55	1.50	4 (14%)
14	PO4	E	501	-	4,4,4	0.58	0	6,6,6	0.71	0
14	PO4	F	501	-	4,4,4	0.72	0	6,6,6	0.55	0
17	CDL	G	501	-	43,43,99	1.54	4 (9%)	49,55,111	1.59	8 (16%)
14	PO4	N	1001	-	4,4,4	0.67	0	6,6,6	0.69	0
14	PO4	N	501	-	4,4,4	0.69	0	6,6,6	0.86	0
12	HEM	P	501	3	27,50,50	0.88	2 (7%)	17,82,82	1.68	5 (29%)
12	HEM	P	502	3	27,50,50	1.04	2 (7%)	17,82,82	1.53	4 (23%)
13	4X9	P	503	-	30,30,30	2.85	6 (20%)	41,44,44	1.45	6 (14%)
15	PEE	P	505	-	48,48,50	1.08	2 (4%)	51,53,55	0.85	3 (5%)
14	PO4	Q	1001	-	4,4,4	0.74	0	6,6,6	0.42	0
14	PO4	Q	1002	-	4,4,4	0.74	0	6,6,6	0.43	0
16	HEC	Q	501	4	26,50,50	2.44	12 (46%)	18,82,82	2.61	6 (33%)
17	CDL	Q	505	-	38,38,99	1.25	3 (7%)	43,47,111	1.23	5 (11%)
15	PEE	Q	506	-	50,50,50	1.05	2 (4%)	53,55,55	1.27	5 (9%)
18	FES	R	501	5	0,4,4	0.00	-	0,4,4	0.00	-
19	GOL	R	502	-	5,5,5	0.31	0	5,5,5	0.45	0
14	PO4	S	501	-	4,4,4	0.72	0	6,6,6	0.42	0
17	CDL	T	501	-	48,48,99	1.39	4 (8%)	54,60,111	1.19	5 (9%)

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
12	HEM	C	501	3	-	0/6/54/54	0/0/8/8
12	HEM	C	502	3	-	0/6/54/54	0/0/8/8
13	4X9	C	503	-	-	0/13/13/13	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
14	PO4	C	504	-	-	0/0/0/0	0/0/0/0
15	PEE	C	505	-	1/1/4/4	0/52/52/54	0/0/0/0
16	HEC	D	501	4	-	0/6/54/54	0/0/8/8
14	PO4	D	502	-	-	0/0/0/0	0/0/0/0
14	PO4	D	503	-	-	0/0/0/0	0/0/0/0
14	PO4	D	504	-	-	0/0/0/0	0/0/0/0
17	CDL	D	505	-	-	0/43/43/110	0/0/0/0
15	PEE	D	506	-	1/1/4/4	0/29/29/54	0/0/0/0
14	PO4	E	501	-	-	0/0/0/0	0/0/0/0
14	PO4	F	501	-	-	0/0/0/0	0/0/0/0
17	CDL	G	501	-	-	0/52/52/110	0/0/0/0
14	PO4	N	1001	-	-	0/0/0/0	0/0/0/0
14	PO4	N	501	-	-	0/0/0/0	0/0/0/0
12	HEM	P	501	3	-	0/6/54/54	0/0/8/8
12	HEM	P	502	3	-	0/6/54/54	0/0/8/8
13	4X9	P	503	-	-	0/13/13/13	0/3/3/3
15	PEE	P	505	-	1/1/4/4	0/52/52/54	0/0/0/0
14	PO4	Q	1001	-	-	0/0/0/0	0/0/0/0
14	PO4	Q	1002	-	-	0/0/0/0	0/0/0/0
16	HEC	Q	501	4	-	0/6/54/54	0/0/8/8
17	CDL	Q	505	-	-	0/43/43/110	0/0/0/0
15	PEE	Q	506	-	1/1/4/4	0/54/54/54	0/0/0/0
18	FES	R	501	5	-	0/0/4/4	0/1/1/1
19	GOL	R	502	-	-	0/4/4/4	0/0/0/0
14	PO4	S	501	-	-	0/0/0/0	0/0/0/0
17	CDL	T	501	-	-	0/57/57/110	0/0/0/0

All (66) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	P	503	4X9	O28-C18	-4.80	1.25	1.37
13	C	503	4X9	O28-C18	-4.58	1.26	1.37
12	C	501	HEM	C3B-C2B	-4.51	1.34	1.40
12	P	502	HEM	C3B-C2B	-2.77	1.36	1.40
12	C	502	HEM	C3B-C2B	-2.18	1.37	1.40
12	P	501	HEM	C3B-C2B	-2.07	1.37	1.40
12	C	502	HEM	C3C-C2C	-2.05	1.37	1.40
13	C	503	4X9	O3-C1	2.12	1.44	1.31
16	Q	501	HEC	C4D-CHA	2.28	1.46	1.40
17	D	505	CDL	PB2-OB5	2.34	1.64	1.54
12	C	501	HEM	C4D-C3D	2.41	1.48	1.42
16	Q	501	HEC	C3C-C4C	2.42	1.47	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	Q	505	CDL	PB2-OB5	2.47	1.64	1.54
17	T	501	CDL	OA8-CA7	2.47	1.45	1.33
16	D	501	HEC	C4D-CHA	2.48	1.46	1.40
12	P	501	HEM	C4D-C3D	2.51	1.48	1.42
16	D	501	HEC	C4A-C3A	2.60	1.48	1.42
16	D	501	HEC	C3C-C4C	2.64	1.47	1.43
12	P	502	HEM	C4D-C3D	2.69	1.48	1.42
16	D	501	HEC	C1D-CHD	2.71	1.47	1.40
16	D	501	HEC	C1B-CHB	2.73	1.47	1.40
16	Q	501	HEC	C1D-CHD	2.78	1.47	1.40
16	Q	501	HEC	C1C-CHC	2.91	1.47	1.40
16	Q	501	HEC	C1A-C2A	2.93	1.49	1.42
16	D	501	HEC	C3D-C2D	2.96	1.46	1.37
16	Q	501	HEC	C3B-C4B	2.97	1.48	1.43
17	G	501	CDL	OA8-CA7	3.01	1.48	1.33
13	C	503	4X9	C19-CL	3.04	1.79	1.72
16	Q	501	HEC	C4A-C3A	3.04	1.49	1.42
16	Q	501	HEC	C1B-CHB	3.07	1.48	1.40
16	D	501	HEC	C1C-CHC	3.18	1.48	1.40
16	Q	501	HEC	C3D-C2D	3.19	1.47	1.37
16	D	501	HEC	C2A-C3A	3.27	1.47	1.37
16	Q	501	HEC	C2A-C3A	3.30	1.47	1.37
16	D	501	HEC	C3B-C4B	3.39	1.49	1.43
13	P	503	4X9	C19-CL	3.41	1.79	1.72
15	C	505	PEE	O3-C30	4.16	1.45	1.33
15	Q	506	PEE	O3-C30	4.32	1.45	1.33
13	P	503	4X9	C18-C19	4.33	1.46	1.39
15	D	506	PEE	O2-C10	4.42	1.47	1.34
17	D	505	CDL	OA8-CA7	4.53	1.46	1.33
15	C	505	PEE	O2-C10	4.55	1.47	1.34
17	Q	505	CDL	OA8-CA7	4.58	1.46	1.33
17	T	501	CDL	OA6-CA5	4.65	1.45	1.35
17	D	505	CDL	OA6-CA5	4.65	1.47	1.34
15	Q	506	PEE	O2-C10	4.67	1.47	1.34
15	P	505	PEE	O2-C10	4.73	1.48	1.34
15	P	505	PEE	O3-C30	4.74	1.47	1.33
17	Q	505	CDL	OA6-CA5	4.76	1.48	1.34
17	T	501	CDL	OB8-CB7	4.78	1.47	1.33
17	G	501	CDL	OB6-CB5	4.78	1.48	1.34
17	T	501	CDL	OB6-CB5	4.83	1.48	1.34
17	G	501	CDL	OB8-CB7	4.90	1.47	1.33
16	D	501	HEC	C3B-C2B	4.90	1.46	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	D	506	PEE	O3-C30	5.05	1.48	1.33
16	Q	501	HEC	C3B-C2B	5.06	1.46	1.40
17	G	501	CDL	OA6-CA5	5.21	1.47	1.35
13	C	503	4X9	C18-C19	5.72	1.49	1.39
16	Q	501	HEC	C3C-C2C	6.38	1.47	1.40
16	D	501	HEC	C3C-C2C	6.70	1.47	1.40
13	P	503	4X9	C17-C18	6.90	1.48	1.40
13	P	503	4X9	C17-C22	7.03	1.48	1.39
13	C	503	4X9	C19-C20	7.84	1.49	1.40
13	C	503	4X9	C17-C22	7.95	1.49	1.39
13	C	503	4X9	C17-C18	8.27	1.50	1.40
13	P	503	4X9	C19-C20	8.84	1.50	1.40

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Q	501	HEC	C1D-C2D-C3D	-6.86	102.23	107.00
16	D	501	HEC	C1D-C2D-C3D	-6.10	102.75	107.00
16	D	501	HEC	CAA-CBA-CGA	-4.75	104.54	112.66
13	P	503	4X9	C18-C19-CL	-4.46	113.39	118.09
12	C	501	HEM	CBA-CAA-C2A	-4.07	104.71	112.48
13	C	503	4X9	C18-C17-C22	-3.51	116.06	119.59
16	D	501	HEC	CAD-CBD-CGD	-3.36	106.91	112.66
16	Q	501	HEC	CAD-CBD-CGD	-3.33	106.97	112.66
12	P	501	HEM	C1D-C2D-C3D	-3.13	104.81	107.00
13	P	503	4X9	C29-C22-C17	-3.10	117.85	122.19
12	P	502	HEM	CBA-CAA-C2A	-3.09	106.57	112.48
17	D	505	CDL	OA8-CA7-OA9	-2.82	116.71	123.58
16	Q	501	HEC	CAA-CBA-CGA	-2.74	107.97	112.66
15	C	505	PEE	O3-C30-O5	-2.65	117.12	123.58
17	Q	505	CDL	OA8-CA7-OA9	-2.63	117.16	123.58
15	D	506	PEE	O2-C10-O4	-2.61	117.25	123.69
12	P	501	HEM	CAD-CBD-CGD	-2.57	108.27	112.66
17	T	501	CDL	OA6-CA5-OA7	-2.57	117.76	122.94
17	G	501	CDL	OB8-CB7-OB9	-2.53	117.40	123.58
17	G	501	CDL	OB6-CB5-OB7	-2.53	117.44	123.69
13	P	503	4X9	C17-C22-N30	-2.49	120.97	122.47
16	D	501	HEC	C4C-C3C-C2C	-2.31	103.86	106.35
12	P	502	HEM	CAD-C3D-C2D	-2.23	122.65	129.00
15	Q	506	PEE	O3-C30-O5	-2.17	118.29	123.58
12	P	501	HEM	CMA-C3A-C4A	-2.16	125.14	128.46
15	D	506	PEE	O3-C30-O5	-2.15	118.33	123.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	C	505	PEE	C3-C2-C1	-2.13	107.06	111.86
12	P	502	HEM	CMA-C3A-C4A	-2.12	125.20	128.46
12	P	502	HEM	C3C-C4C-NC	-2.11	106.97	110.94
17	T	501	CDL	OB8-CB7-OB9	-2.05	118.58	123.58
16	D	501	HEC	CAD-C3D-C2D	-2.01	123.26	129.00
15	P	505	PEE	O3-C3-C2	2.01	113.64	108.64
15	P	505	PEE	O3-C30-C31	2.01	117.73	111.92
16	Q	501	HEC	CBA-CAA-C2A	2.05	116.38	112.47
16	D	501	HEC	CMA-C3A-C2A	2.06	128.82	124.94
12	C	502	HEM	CBD-CAD-C3D	2.08	116.44	112.47
13	P	503	4X9	O28-C18-C17	2.12	124.34	119.51
17	D	505	CDL	OB4-PB2-OB3	2.15	119.00	110.60
17	G	501	CDL	OA8-CA7-C31	2.22	122.39	112.43
17	Q	505	CDL	PB2-OB2-CB2	2.24	124.48	118.30
12	P	501	HEM	C4A-C3A-C2A	2.28	108.58	107.00
17	Q	505	CDL	OB4-PB2-OB3	2.58	120.68	110.60
13	P	503	4X9	C22-N30-C20	2.66	123.56	119.69
12	P	501	HEM	CAA-CBA-CGA	2.81	117.46	112.66
15	Q	506	PEE	O3-C30-C31	2.91	120.34	111.92
17	G	501	CDL	CA6-OA8-CA7	2.91	124.55	117.14
15	C	505	PEE	O2-C10-C11	3.00	117.88	111.55
17	Q	505	CDL	OA8-CA7-C31	3.04	120.70	111.92
17	T	501	CDL	OB8-CB7-C71	3.11	120.92	111.92
13	P	503	4X9	C29-C22-N30	3.13	121.18	116.45
17	G	501	CDL	OB8-CB6-CB4	3.18	116.56	108.64
15	C	505	PEE	O3-C30-C31	3.19	121.15	111.92
13	C	503	4X9	C22-N30-C20	3.21	124.37	119.69
15	Q	506	PEE	O3-C3-C2	3.34	116.95	108.64
15	D	506	PEE	O3-C30-C31	3.40	121.75	111.92
15	P	505	PEE	O2-C10-C11	3.40	118.73	111.55
17	D	505	CDL	OA8-CA7-C31	3.71	122.63	111.92
17	T	501	CDL	OB6-CB5-C51	3.80	119.55	111.55
16	Q	501	HEC	CMC-C2C-C3C	3.80	130.29	125.82
17	Q	505	CDL	OA6-CA5-C11	3.83	119.61	111.55
15	Q	506	PEE	O2-C10-C11	3.86	119.68	111.55
17	D	505	CDL	OA6-CA5-C11	4.05	120.08	111.55
16	D	501	HEC	CMB-C2B-C3B	4.08	130.62	125.82
17	T	501	CDL	OA6-CA5-C11	4.14	118.85	111.10
17	G	501	CDL	OB8-CB7-C71	4.28	124.29	111.92
17	G	501	CDL	OB6-CB5-C51	4.38	123.37	110.74
16	Q	501	HEC	CMB-C2B-C3B	4.46	131.07	125.82
17	G	501	CDL	OA6-CA5-C11	4.73	119.95	111.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	Q	506	PEE	C2-O2-C10	4.79	129.18	117.88
15	D	506	PEE	O2-C10-C11	5.16	122.42	111.55
16	D	501	HEC	CMC-C2C-C3C	5.18	131.91	125.82
16	D	501	HEC	CBA-CAA-C2A	5.75	123.43	112.47

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
15	Q	506	PEE	C2
15	C	505	PEE	C2
15	D	506	PEE	C2
15	P	505	PEE	C2

There are no torsion outliers.

There are no ring outliers.

14 monomers are involved in 62 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	C	501	HEM	4	0
12	C	502	HEM	6	0
13	C	503	4X9	6	0
15	C	505	PEE	1	0
16	D	501	HEC	12	0
12	P	501	HEM	7	0
12	P	502	HEM	3	0
13	P	503	4X9	5	0
15	P	505	PEE	1	0
16	Q	501	HEC	10	0
17	Q	505	CDL	1	0
15	Q	506	PEE	3	0
18	R	501	FES	3	0
17	T	501	CDL	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	444/480 (92%)	-0.14	9 (2%) 65 52	92, 150, 191, 255	0
1	N	444/480 (92%)	-0.33	7 (1%) 72 60	87, 132, 176, 243	0
2	B	422/453 (93%)	0.14	29 (6%) 17 12	108, 157, 200, 247	0
3	C	374/379 (98%)	-0.50	0 100 100	77, 103, 137, 225	0
3	P	370/379 (97%)	-0.44	1 (0%) 93 89	79, 112, 148, 183	0
4	D	240/265 (90%)	-0.31	2 (0%) 86 76	92, 121, 153, 178	0
4	Q	241/265 (90%)	-0.10	6 (2%) 57 44	86, 131, 168, 211	0
5	E	73/274 (26%)	-0.36	1 (1%) 75 63	93, 130, 158, 170	0
5	I	21/274 (7%)	0.63	1 (4%) 30 22	146, 192, 220, 228	0
5	R	196/274 (71%)	-0.15	2 (1%) 82 71	91, 150, 193, 230	0
6	F	98/111 (88%)	-0.44	2 (2%) 65 52	91, 124, 157, 171	0
6	S	99/111 (89%)	-0.44	0 100 100	85, 122, 168, 182	0
7	G	80/82 (97%)	-0.29	1 (1%) 77 65	88, 119, 189, 293	0
7	T	74/82 (90%)	-0.40	2 (2%) 54 42	83, 124, 181, 201	0
8	H	65/91 (71%)	-0.47	0 100 100	103, 136, 171, 223	0
8	U	66/91 (72%)	0.09	5 (7%) 14 10	132, 163, 213, 245	0
9	J	58/64 (90%)	-0.06	0 100 100	103, 137, 165, 175	0
9	W	59/64 (92%)	-0.19	1 (1%) 70 58	102, 121, 153, 162	0
10	O	419/453 (92%)	-0.21	7 (1%) 70 58	97, 146, 193, 250	0
11	V	17/274 (6%)	1.19	3 (17%) 1 1	176, 209, 228, 268	0
All	All	3860/4946 (78%)	-0.23	79 (2%) 65 52	77, 133, 189, 293	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	226	ASP	5.9
11	V	62	ARG	4.8
2	B	232	LEU	4.7
1	N	225	GLU	4.2
2	B	21	PRO	4.0
10	O	232	LEU	4.0
2	B	36	ALA	4.0
8	U	44	VAL	3.8
8	U	50	THR	3.8
2	B	23	ASP	3.7
11	V	63	PRO	3.6
1	N	243	HIS	3.6
8	U	51	GLU	3.4
10	O	231	GLY	3.4
2	B	19	PRO	3.4
10	O	233	SER	3.4
5	E	73	LYS	3.3
10	O	234	GLY	3.3
2	B	274	VAL	3.3
4	Q	1	SER	3.1
1	A	225	GLU	3.1
1	N	226	ASP	3.1
2	B	272	PHE	3.0
2	B	208	GLY	3.0
4	D	241	LYS	3.0
5	I	77	ARG	3.0
6	F	109	LYS	3.0
2	B	439	LEU	2.9
4	Q	143	LEU	2.9
9	W	2	ALA	2.9
2	B	276	GLN	2.8
2	B	322	PHE	2.8
2	B	233	SER	2.8
2	B	220	ALA	2.7
4	Q	146	GLY	2.7
2	B	417	PHE	2.7
8	U	78	LYS	2.7
2	B	352	LEU	2.7
1	A	127	ILE	2.7
2	B	275	LEU	2.6
1	A	177	LEU	2.6
2	B	407	ASP	2.5
2	B	38	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	182	LEU	2.5
2	B	344	VAL	2.4
11	V	70	LEU	2.4
6	F	106	GLU	2.4
2	B	229	GLY	2.3
10	O	41	TYR	2.3
3	P	168	PHE	2.3
2	B	231	GLY	2.3
4	Q	142	SER	2.3
1	A	83	GLY	2.3
1	A	303	LEU	2.3
7	T	74	PRO	2.3
10	O	122	PHE	2.3
2	B	20	HIS	2.2
5	R	77	LYS	2.2
2	B	311	ALA	2.2
1	A	126	GLN	2.2
7	T	14	ILE	2.2
1	N	394	GLU	2.2
1	N	424	GLY	2.2
2	B	227	ARG	2.2
1	N	425	PHE	2.2
4	Q	167	GLU	2.2
7	G	76	ALA	2.1
2	B	410	VAL	2.1
4	Q	149	PHE	2.1
5	R	98	VAL	2.1
2	B	347	ILE	2.1
1	A	84	ALA	2.1
2	B	313	ASN	2.1
4	D	180	SER	2.1
10	O	229	GLY	2.1
8	U	52	GLU	2.1
2	B	217	LYS	2.1
2	B	43	PRO	2.0
1	N	393	ALA	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. 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	B-factors(\AA^2)	Q<0.9
14	PO4	S	501	5/5	0.39	0.52	225,226,243,252	0
14	PO4	F	501	5/5	0.51	0.58	242,243,245,246	0
14	PO4	D	504	5/5	0.57	0.23	179,190,194,195	0
14	PO4	Q	1001	5/5	0.66	0.20	194,205,216,232	0
14	PO4	N	501	5/5	0.67	0.45	112,126,127,137	0
14	PO4	D	502	5/5	0.71	0.27	176,192,199,203	0
19	GOL	R	502	6/6	0.72	1.89	169,181,193,193	0
14	PO4	Q	1002	5/5	0.72	0.20	210,211,220,230	0
14	PO4	E	501	5/5	0.74	0.32	124,134,144,145	0
14	PO4	D	503	5/5	0.82	0.61	168,169,177,181	0
14	PO4	C	504	5/5	0.82	0.39	121,121,134,149	0
13	4X9	P	503	28/28	0.88	0.32	109,147,226,261	0
15	PEE	Q	506	51/51	0.90	0.40	100,134,171,187	0
13	4X9	C	503	28/28	0.90	0.39	116,143,206,215	0
15	PEE	C	505	49/51	0.91	0.49	94,116,135,137	0
17	CDL	D	505	39/100	0.91	0.27	85,124,146,148	0
17	CDL	G	501	44/100	0.92	0.28	95,115,153,168	0
17	CDL	T	501	49/100	0.92	0.31	93,129,160,167	0
15	PEE	P	505	49/51	0.93	0.33	100,122,154,156	0
14	PO4	N	1001	5/5	0.93	0.42	120,127,135,137	0
17	CDL	Q	505	39/100	0.93	0.28	100,126,146,148	0
15	PEE	D	506	26/51	0.93	0.26	107,127,169,176	0
18	FES	R	501	4/4	0.97	0.14	125,158,164,170	0
12	HEM	C	502	43/43	0.98	0.26	71,85,99,106	0
12	HEM	P	502	43/43	0.98	0.23	74,89,104,106	0
12	HEM	P	501	43/43	0.98	0.30	86,101,116,124	0
12	HEM	C	501	43/43	0.98	0.27	89,99,107,115	0
16	HEC	D	501	43/43	0.98	0.24	80,111,127,138	0
16	HEC	Q	501	43/43	0.98	0.28	106,117,136,143	0

6.5 Other polymers [i](#)

There are no such residues in this entry.