



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 01:08 AM UTC

PDB ID : 5FCR / pdb_00005fcr
Title : MOUSE COMPLEMENT FACTOR D
Authors : Mac Sweeney, A.
Deposited on : 2015-12-15
Resolution : 1.25 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

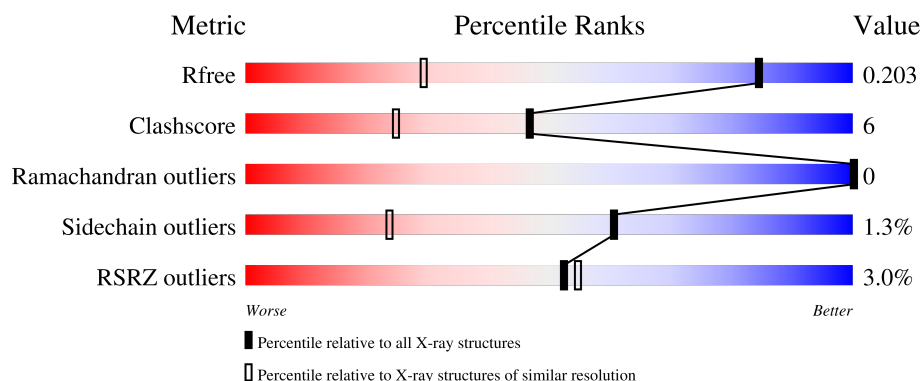
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

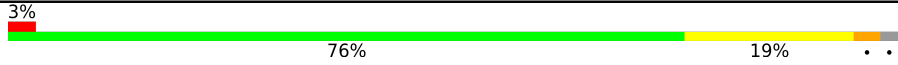
The reported resolution of this entry is 1.25 Å.

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}	180053	1693 (1.28-1.24)
Clashscore	190562	1730 (1.28-1.24)
Ramachandran outliers	187476	1695 (1.28-1.24)
Sidechain outliers	187428	1694 (1.28-1.24)
RSRZ outliers	180081	1693 (1.28-1.24)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	234	
1	B	234	
1	C	234	
1	D	234	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	B	302	-	X	X	-

2 Entry composition [i](#)

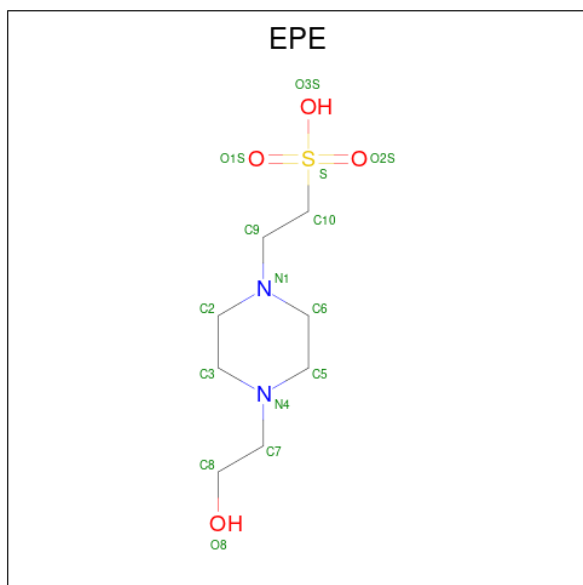
There are 6 unique types of molecules in this entry. The entry contains 8005 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Complement factor D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	11	0
			1799	1114	327	344	14			
1	B	230	Total	C	N	O	S	0	6	0
			1762	1090	318	338	16			
1	C	229	Total	C	N	O	S	0	12	0
			1784	1108	320	340	16			
1	D	230	Total	C	N	O	S	0	8	0
			1771	1097	321	337	16			

- Molecule 2 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: C₈H₁₈N₂O₄S).



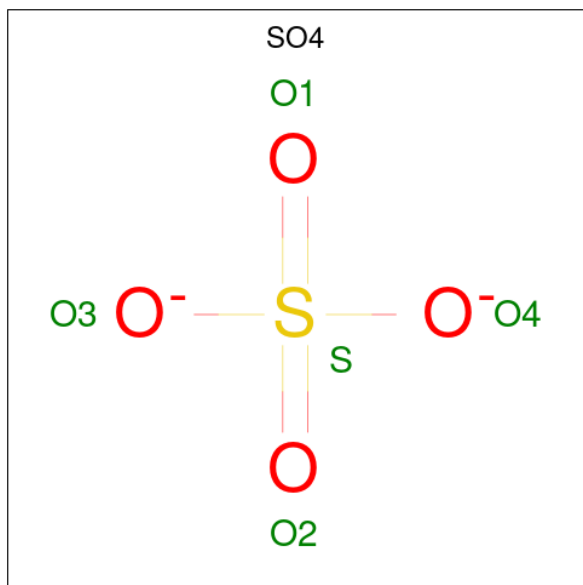
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
2	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	D	1	Total	C	O	S	0	0
			4	2	1	1		
5	D	1	Total	C	O	S	0	0
			4	2	1	1		

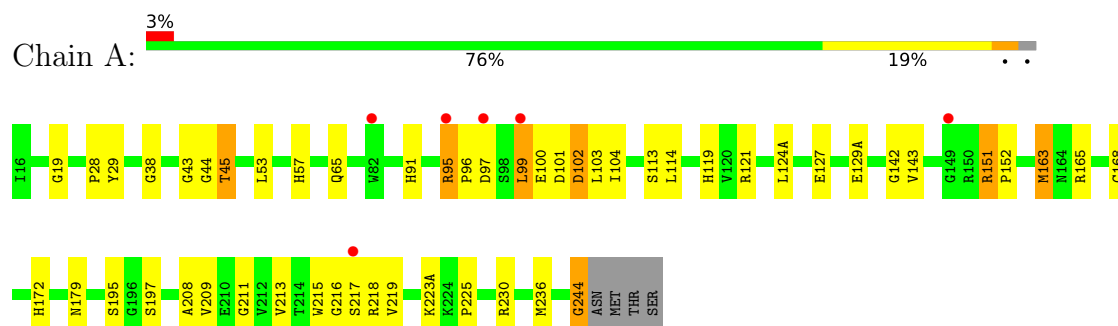
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	207	Total	O	0	0
			207	207		
6	B	234	Total	O	0	0
			234	234		
6	C	201	Total	O	0	0
			201	201		
6	D	198	Total	O	0	0
			198	198		

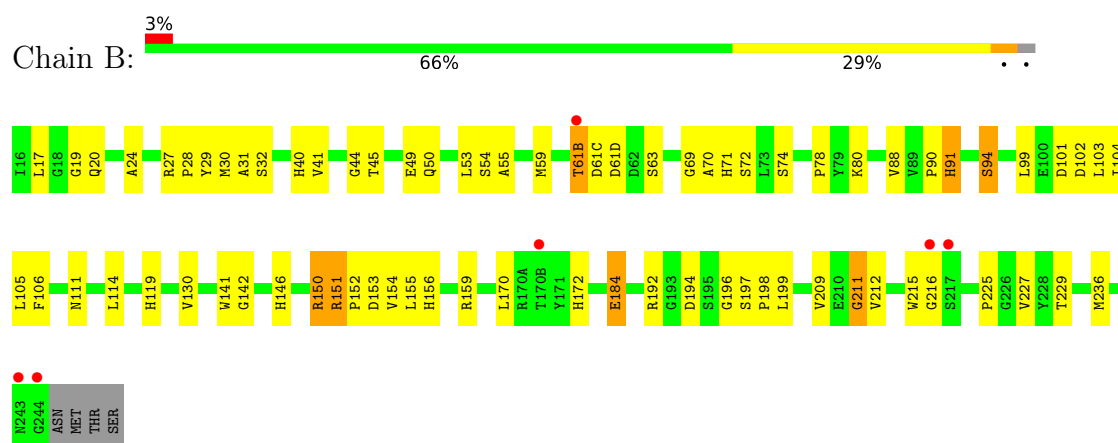
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

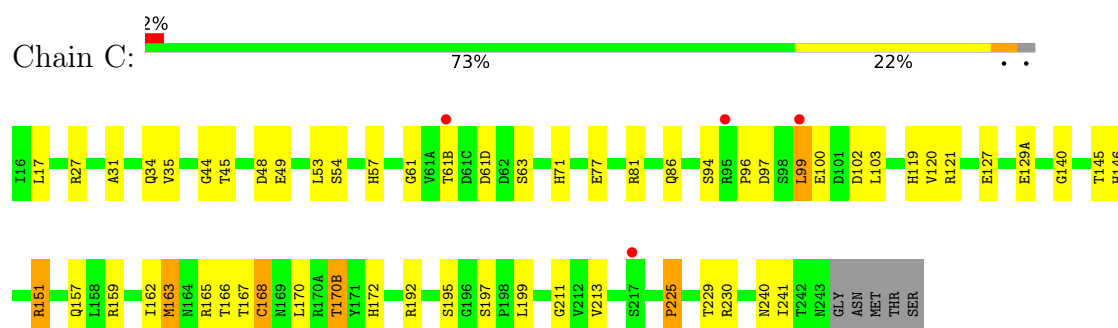
- Molecule 1: Complement factor D



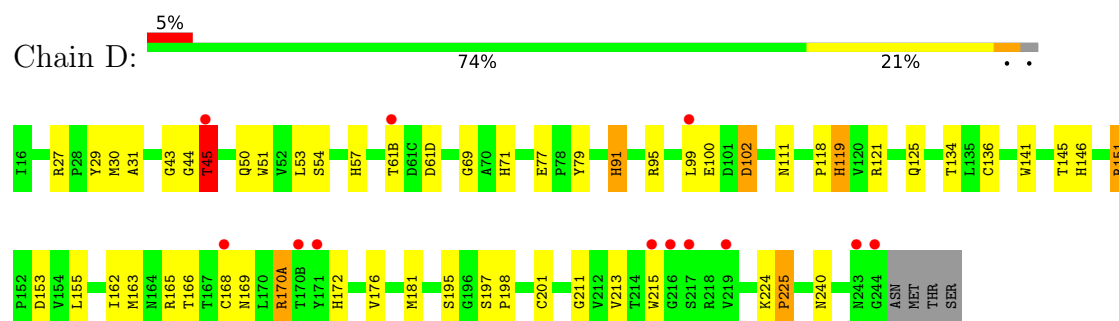
- Molecule 1: Complement factor D



- Molecule 1: Complement factor D



- Molecule 1: Complement factor D



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	51.27Å 52.87Å 84.28Å 90.46° 98.04° 90.14°	Depositor
Resolution (Å)	83.45 – 1.25 83.45 – 1.25	Depositor EDS
% Data completeness (in resolution range)	88.3 (83.45-1.25) 88.8 (83.45-1.25)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.23 (at 1.25Å)	Xtriage
Refinement program	REFMAC 5.8.0131	Depositor
R, R_{free}	0.150 , 0.196 0.160 , 0.203	Depositor DCC
R_{free} test set	10776 reflections (4.41%)	wwPDB-VP
Wilson B-factor (Å ²)	8.7	Xtriage
Anisotropy	0.867	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 34.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.137 for -h,k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8005	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 42.16 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.1252e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: SO4, EPE, DMS, GOL

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	1.88	33/1866 (1.8%)	1.56	22/2544 (0.9%)
1	B	2.11	58/1816 (3.2%)	1.67	38/2475 (1.5%)
1	C	2.01	37/1851 (2.0%)	1.57	16/2525 (0.6%)
1	D	2.03	47/1832 (2.6%)	1.53	12/2498 (0.5%)
All	All	2.01	175/7365 (2.4%)	1.58	88/10042 (0.9%)

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

All (175) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	27	ARG	C-N	11.95	1.45	1.33
1	B	141	TRP	CA-C	10.01	1.66	1.52
1	A	53	LEU	C-N	9.70	1.42	1.33
1	B	91	HIS	CA-C	9.00	1.62	1.53
1	D	30	MET	CA-C	-8.98	1.41	1.52
1	B	30	MET	CA-C	-8.54	1.41	1.52
1	B	212	VAL	C-O	8.53	1.33	1.24
1	B	142	GLY	CA-C	-8.47	1.39	1.52
1	B	155	LEU	CA-C	-8.43	1.41	1.52
1	D	197	SER	CA-C	-8.40	1.44	1.53
1	B	111	ASN	CG-ND2	-8.36	1.15	1.33
1	B	44	GLY	N-CA	-8.27	1.36	1.45
1	A	102	ASP	CA-C	8.19	1.62	1.53
1	A	217	SER	C-O	-8.13	1.13	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	55	ALA	C-O	-8.13	1.14	1.23
1	B	24	ALA	C-O	8.11	1.34	1.23
1	B	71	HIS	C-O	8.07	1.33	1.24
1	D	165	ARG	CD-NE	-7.97	1.35	1.46
1	D	211	GLY	CA-C	-7.96	1.45	1.52
1	D	77	GLU	C-O	-7.93	1.15	1.24
1	B	54	SER	C-O	-7.81	1.17	1.24
1	D	44	GLY	CA-C	7.73	1.59	1.51
1	A	121[A]	ARG	C-N	-7.70	1.24	1.33
1	A	121[B]	ARG	C-N	-7.70	1.24	1.33
1	D	54	SER	C-O	-7.56	1.17	1.24
1	D	141	TRP	CA-C	7.51	1.63	1.52
1	B	54	SER	CA-C	7.50	1.61	1.53
1	D	30	MET	N-CA	7.50	1.55	1.46
1	C	121	ARG	C-N	-7.47	1.24	1.33
1	C	213	VAL	N-CA	7.42	1.55	1.46
1	C	44	GLY	CA-C	7.40	1.59	1.51
1	D	43	GLY	C-N	7.38	1.43	1.33
1	C	86	GLN	N-CA	7.31	1.55	1.46
1	A	100	GLU	CD-OE2	-7.26	1.11	1.25
1	D	201	CYS	CA-C	-7.20	1.44	1.52
1	D	53	LEU	C-N	7.18	1.40	1.33
1	B	102	ASP	CA-C	7.04	1.61	1.53
1	A	152	PRO	N-CA	-7.04	1.38	1.46
1	A	209	VAL	C-O	-6.96	1.17	1.24
1	D	79	TYR	CA-C	6.93	1.61	1.52
1	C	53	LEU	C-N	6.90	1.39	1.33
1	C	54	SER	C-O	-6.88	1.17	1.24
1	C	241	ILE	C-O	6.85	1.32	1.24
1	B	197	SER	CA-C	-6.85	1.45	1.53
1	B	114	LEU	C-O	6.83	1.32	1.23
1	B	40	HIS	CA-C	6.80	1.61	1.52
1	B	53	LEU	C-N	6.70	1.39	1.33
1	C	34	GLN	C-N	-6.67	1.25	1.33
1	B	103	LEU	CA-C	-6.67	1.44	1.52
1	C	211	GLY	C-N	6.63	1.42	1.33
1	C	61	GLY	N-CA	6.62	1.55	1.45
1	A	218	ARG	C-N	-6.60	1.26	1.33
1	B	196	GLY	CA-C	6.59	1.60	1.51
1	B	61(C)	ASP	C-O	-6.57	1.15	1.24
1	B	71	HIS	CA-C	-6.56	1.46	1.52
1	B	78	PRO	C-O	-6.55	1.15	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	31	ALA	C-O	6.54	1.32	1.24
1	C	103	LEU	CA-C	-6.54	1.44	1.52
1	A	168	CYS	CB-SG	-6.45	1.59	1.81
1	C	77	GLU	N-CA	-6.44	1.37	1.45
1	C	27	ARG	CA-C	-6.42	1.45	1.52
1	B	99	LEU	N-CA	-6.39	1.37	1.46
1	A	43	GLY	C-N	6.39	1.41	1.33
1	C	163	MET	N-CA	6.38	1.53	1.46
1	D	155	LEU	CA-C	-6.36	1.44	1.52
1	D	51	TRP	C-N	6.36	1.41	1.33
1	B	194	ASP	CG-OD1	6.34	1.37	1.25
1	D	31	ALA	C-O	6.34	1.32	1.24
1	B	45	THR	N-CA	6.32	1.53	1.46
1	D	71	HIS	C-O	6.25	1.31	1.24
1	B	154	VAL	C-N	-6.24	1.25	1.33
1	D	71	HIS	CA-C	-6.24	1.46	1.52
1	D	165	ARG	CZ-NH2	6.24	1.41	1.33
1	A	19	GLY	N-CA	-6.21	1.36	1.45
1	A	216	GLY	N-CA	6.18	1.53	1.45
1	B	236	MET	N-CA	-6.14	1.39	1.46
1	B	28	PRO	C-O	-6.08	1.16	1.24
1	C	120	VAL	C-O	6.07	1.31	1.24
1	C	159	ARG	CZ-NH2	-6.01	1.25	1.33
1	C	140	GLY	C-O	-6.00	1.17	1.23
1	D	95	ARG	CA-C	-5.96	1.45	1.52
1	D	102	ASP	CA-C	5.96	1.60	1.53
1	D	100	GLU	CD-OE2	-5.90	1.14	1.25
1	B	61(B)	THR	CB-CG2	-5.90	1.33	1.52
1	A	114	LEU	C-N	-5.90	1.24	1.33
1	C	167	THR	C-O	5.88	1.30	1.24
1	B	104	ILE	CA-C	5.87	1.60	1.52
1	D	118	PRO	CA-C	5.86	1.61	1.52
1	B	211	GLY	CA-C	-5.83	1.45	1.51
1	D	43	GLY	CA-C	-5.82	1.40	1.52
1	A	143	VAL	CA-CB	-5.82	1.48	1.54
1	D	95	ARG	N-CA	5.78	1.53	1.46
1	C	157	GLN	CD-NE2	-5.78	1.21	1.33
1	B	105	LEU	N-CA	5.77	1.53	1.46
1	C	48	ASP	CA-C	-5.76	1.46	1.53
1	D	121	ARG	C-N	-5.72	1.25	1.33
1	B	69	GLY	CA-C	-5.72	1.43	1.51
1	D	91	HIS	CA-C	5.71	1.58	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	95	ARG	N-CA	5.71	1.53	1.46
1	B	72	SER	CA-C	-5.68	1.45	1.52
1	D	29	TYR	C-N	-5.67	1.25	1.33
1	C	71	HIS	CA-C	-5.66	1.48	1.52
1	D	213	VAL	C-O	-5.66	1.18	1.24
1	B	88	VAL	C-N	-5.65	1.26	1.33
1	B	198	PRO	N-CA	-5.61	1.40	1.46
1	D	27	ARG	N-CA	5.61	1.52	1.46
1	B	184	GLU	CD-OE2	-5.59	1.14	1.25
1	C	35	VAL	CA-CB	-5.58	1.46	1.54
1	B	80	LYS	CA-C	-5.57	1.45	1.52
1	B	27	ARG	N-CA	5.55	1.52	1.46
1	A	29	TYR	C-N	-5.54	1.25	1.33
1	B	99	LEU	CA-C	5.53	1.60	1.52
1	D	119	HIS	C-O	5.49	1.31	1.24
1	C	63	SER	C-O	-5.48	1.17	1.24
1	D	166	THR	C-O	-5.47	1.17	1.24
1	B	74	SER	N-CA	5.45	1.53	1.45
1	B	24	ALA	CA-C	-5.44	1.45	1.52
1	B	41	VAL	CA-C	-5.43	1.45	1.52
1	D	197	SER	C-N	5.42	1.40	1.33
1	C	45	THR	C-O	-5.41	1.17	1.23
1	B	19	GLY	C-N	-5.40	1.26	1.33
1	D	45[A]	THR	C-N	5.40	1.41	1.33
1	D	45[B]	THR	C-N	5.40	1.41	1.33
1	D	145	THR	CA-C	-5.39	1.46	1.52
1	C	86	GLN	CA-CB	-5.38	1.44	1.53
1	C	241	ILE	CB-CG1	-5.38	1.42	1.53
1	C	17	LEU	N-CA	5.37	1.53	1.46
1	A	114	LEU	C-O	5.37	1.30	1.23
1	D	69	GLY	C-N	5.36	1.41	1.33
1	A	103	LEU	CA-C	-5.35	1.46	1.52
1	B	215	TRP	CA-C	5.34	1.59	1.53
1	A	45[A]	THR	C-N	5.33	1.41	1.33
1	A	45[B]	THR	C-N	5.33	1.41	1.33
1	C	162	ILE	C-O	-5.33	1.17	1.24
1	A	95	ARG	C-N	5.32	1.40	1.34
1	A	213	VAL	N-CA	5.32	1.52	1.46
1	A	215	TRP	CB-CG	5.30	1.66	1.50
1	B	55	ALA	C-N	5.27	1.41	1.34
1	C	49	GLU	C-O	-5.27	1.17	1.24
1	C	199	LEU	C-O	-5.27	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	142	GLY	C-O	-5.27	1.18	1.23
1	D	215	TRP	CB-CG	5.27	1.66	1.50
1	A	91	HIS	CA-C	5.27	1.58	1.53
1	D	141	TRP	N-CA	-5.27	1.40	1.46
1	B	142	GLY	N-CA	5.25	1.52	1.45
1	D	181	MET	C-O	-5.25	1.17	1.23
1	D	176	VAL	CA-C	-5.24	1.47	1.53
1	A	101	ASP	N-CA	5.24	1.54	1.46
1	B	209	VAL	C-O	-5.22	1.19	1.24
1	C	97	ASP	CG-OD2	-5.20	1.15	1.25
1	C	192	ARG	CA-CB	5.20	1.61	1.53
1	B	29	TYR	C-N	-5.20	1.26	1.33
1	D	43	GLY	N-CA	5.19	1.51	1.45
1	C	230	ARG	CD-NE	-5.19	1.39	1.46
1	C	45	THR	C-N	5.18	1.40	1.33
1	D	111	ASN	CG-ND2	-5.18	1.22	1.33
1	B	17	LEU	N-CA	5.16	1.52	1.46
1	B	30	MET	CA-CB	-5.14	1.45	1.53
1	D	224	LYS	C-O	5.14	1.30	1.24
1	B	211	GLY	C-N	5.13	1.40	1.33
1	A	219	VAL	CA-CB	5.12	1.59	1.54
1	B	130	VAL	C-O	-5.10	1.17	1.24
1	A	211	GLY	CA-C	-5.09	1.46	1.51
1	B	199	LEU	C-O	-5.09	1.17	1.24
1	A	28	PRO	C-O	-5.09	1.17	1.24
1	B	94[A]	SER	C-O	5.08	1.30	1.23
1	B	94[B]	SER	C-O	5.08	1.30	1.23
1	D	170(A)	ARG	N-CA	5.08	1.52	1.46
1	D	50	GLN	N-CA	5.07	1.52	1.45
1	D	51	TRP	CA-C	-5.05	1.46	1.52
1	A	124(A)	LEU	CA-C	-5.04	1.46	1.52
1	C	170(B)	THR	CB-CG2	-5.02	1.35	1.52
1	B	216	GLY	C-O	5.00	1.30	1.23
1	A	113[A]	SER	N-CA	-5.00	1.40	1.46
1	A	113[B]	SER	N-CA	-5.00	1.40	1.46

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	121[A]	ARG	O-C-N	9.67	129.38	121.84
1	A	121[B]	ARG	O-C-N	9.67	129.38	121.84
1	B	196	GLY	O-C-N	8.59	132.98	122.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	55	ALA	CA-C-O	8.20	129.90	120.80
1	A	99	LEU	N-CA-CB	8.03	123.49	110.40
1	C	163	MET	CG-SD-CE	-7.76	83.83	100.90
1	A	236	MET	CG-SD-CE	7.53	117.47	100.90
1	C	99	LEU	N-CA-CB	7.38	122.43	110.40
1	D	30	MET	CA-C-O	7.29	129.36	121.05
1	B	159	ARG	CG-CD-NE	6.93	127.25	112.00
1	A	53	LEU	CA-C-O	6.92	128.49	120.80
1	B	32	SER	CA-C-O	6.92	127.93	120.32
1	B	151	ARG	CB-CG-CD	-6.70	95.90	111.30
1	B	45	THR	CA-C-O	6.60	128.52	120.60
1	B	40	HIS	O-C-N	6.58	130.96	123.06
1	C	170[A]	LEU	CA-C-O	6.58	129.50	121.87
1	B	196	GLY	CA-C-O	-6.56	112.70	119.20
1	A	163	MET	CG-SD-CE	-6.51	86.59	100.90
1	B	104	ILE	O-C-N	6.49	130.62	123.09
1	D	51	TRP	CA-C-O	6.39	127.61	120.70
1	B	150	ARG	CD-NE-CZ	6.35	133.29	124.40
1	D	45[A]	THR	CA-C-O	6.25	127.85	120.66
1	D	45[B]	THR	CA-C-O	6.25	127.85	120.66
1	A	168	CYS	N-CA-CB	6.20	119.89	110.28
1	C	27	ARG	O-C-N	-6.20	115.79	121.37
1	B	27	ARG	O-C-N	-6.19	115.83	121.34
1	C	27	ARG	CA-C-O	6.16	129.15	120.83
1	C	159	ARG	CG-CD-NE	6.09	125.40	112.00
1	A	45[A]	THR	CA-C-O	6.03	127.59	120.66
1	A	45[B]	THR	CA-C-O	6.03	127.59	120.66
1	B	44	GLY	CA-C-O	-6.02	115.29	121.61
1	A	44	GLY	O-C-N	6.01	130.51	123.66
1	A	209	VAL	O-C-N	6.00	129.56	122.66
1	B	70	ALA	N-CA-C	5.96	119.77	110.17
1	B	63	SER	CA-C-O	-5.86	114.30	120.80
1	B	197	SER	O-C-N	-5.84	114.89	121.43
1	D	27	ARG	O-C-N	-5.80	116.17	121.34
1	B	54	SER	O-C-N	5.79	129.92	122.68
1	B	106	PHE	CA-C-O	-5.76	113.98	120.32
1	D	30	MET	O-C-N	-5.71	116.27	123.01
1	B	184	GLU	CA-C-O	-5.68	115.53	121.55
1	C	99	LEU	CA-CB-CG	5.67	136.16	116.30
1	B	24	ALA	O-C-N	-5.65	115.33	123.07
1	D	151	ARG	CB-CG-CD	-5.63	98.35	111.30
1	D	169	ASN	N-CA-C	5.62	120.13	113.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	244	GLY	CA-C-O	-5.62	109.00	120.80
1	C	121	ARG	CA-C-O	-5.60	113.57	119.50
1	A	121[A]	ARG	CA-C-O	-5.58	113.55	119.13
1	A	121[B]	ARG	CA-C-O	-5.58	113.55	119.13
1	A	179	ASN	N-CA-C	-5.58	106.36	112.72
1	B	151	ARG	NE-CZ-NH1	-5.56	115.94	121.50
1	B	24	ALA	CA-C-N	5.54	131.95	123.47
1	B	24	ALA	C-N-CA	5.54	131.95	123.47
1	B	30	MET	CA-C-O	5.54	127.18	120.81
1	A	151	ARG	CB-CG-CD	-5.51	98.63	111.30
1	C	199	LEU	O-C-N	5.47	129.46	123.22
1	B	90	PRO	CA-C-O	-5.47	114.74	121.31
1	A	230	ARG	CA-C-O	5.47	126.83	120.49
1	B	216	GLY	N-CA-C	5.46	120.40	113.24
1	C	81	ARG	NE-CZ-NH2	-5.46	114.29	119.20
1	C	168[A]	CYS	O-C-N	5.44	129.72	122.43
1	C	168[B]	CYS	O-C-N	5.44	129.72	122.43
1	C	35	VAL	O-C-N	5.43	128.30	123.03
1	B	192	ARG	NH1-CZ-NH2	5.42	126.35	119.30
1	C	225	PRO	CA-C-O	5.38	127.80	121.56
1	B	71	HIS	CA-C-N	5.38	129.11	121.42
1	B	71	HIS	C-N-CA	5.38	129.11	121.42
1	A	208	ALA	O-C-N	5.32	129.32	123.25
1	B	59	MET	O-C-N	5.32	128.72	122.34
1	B	216	GLY	O-C-N	5.29	127.85	122.24
1	C	229	THR	CA-C-O	-5.27	114.68	120.69
1	B	141	TRP	CG-CD1-NE1	-5.27	103.35	110.20
1	C	151	ARG	CB-CG-CD	-5.26	99.20	111.30
1	A	104	ILE	O-C-N	5.25	128.77	123.00
1	D	197	SER	CA-C-O	5.21	126.58	120.69
1	A	99	LEU	CA-CB-CG	5.17	134.38	116.30
1	B	150	ARG	CG-CD-NE	-5.17	100.63	112.00
1	A	97	ASP	N-CA-C	5.15	119.20	113.02
1	B	192	ARG	NE-CZ-NH2	-5.13	114.58	119.20
1	A	216	GLY	O-C-N	5.12	127.67	122.24
1	B	227	VAL	O-C-N	5.10	128.69	123.18
1	D	71	HIS	CA-C-N	5.10	128.71	121.42
1	D	71	HIS	C-N-CA	5.10	128.71	121.42
1	B	27	ARG	CA-C-N	5.07	125.14	119.87
1	B	27	ARG	C-N-CA	5.07	125.14	119.87
1	B	50	GLN	CB-CG-CD	-5.05	104.01	112.60
1	B	31	ALA	CA-C-O	-5.03	115.42	121.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	225	PRO	CB-CA-C	-5.01	104.82	111.23

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	95	ARG	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1799	0	1751	15	4
1	B	1762	0	1698	23	0
1	C	1784	0	1735	16	3
1	D	1771	0	1709	29	0
2	B	15	0	18	1	0
2	C	15	0	18	1	0
3	B	6	0	6	6	0
4	C	5	0	0	0	0
5	D	8	0	12	4	0
6	A	207	0	0	9	4
6	B	234	0	0	8	1
6	C	201	0	0	9	3
6	D	198	0	0	8	3
All	All	8005	0	6947	80	9

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 6.

All (80) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:136:CYS:SG	1:D:162:ILE:HD11	2.01	1.00
1:D:45[B]:THR:HG22	1:D:198:PRO:HG3	1.53	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:134:THR:O	1:D:162:ILE:HD12	1.76	0.84
1:D:91:HIS:HE2	5:D:301:DMS:C1	1.91	0.83
1:B:49:GLU:HG2	6:B:585:HOH:O	1.84	0.76
1:B:184:GLU:HB2	6:B:484:HOH:O	1.84	0.76
1:D:91:HIS:HE2	5:D:301:DMS:H12	1.52	0.74
1:B:152:PRO:HA	3:B:302:GOL:H11	1.68	0.73
1:C:195[B]:SER:HB3	6:C:512:HOH:O	1.89	0.72
1:B:172:HIS:HD2	6:B:596:HOH:O	1.74	0.71
1:B:153:ASP:H	3:B:302:GOL:H11	1.56	0.71
1:D:45[B]:THR:HG21	1:D:198:PRO:HB3	1.74	0.69
1:C:94[B]:SER:OG	6:C:401:HOH:O	2.12	0.67
1:B:172:HIS:HE1	1:B:225:PRO:O	1.78	0.66
1:D:146:HIS:HD2	6:D:538:HOH:O	1.79	0.65
1:D:151:ARG:HD3	6:D:494:HOH:O	1.96	0.65
1:B:61(B):THR:HG23	1:B:61(D):ASP:H	1.64	0.63
1:C:166[A]:THR:HG23	6:C:458:HOH:O	1.99	0.63
1:A:119:HIS:HD2	6:A:384:HOH:O	1.82	0.62
1:C:172:HIS:HE1	1:C:225:PRO:O	1.83	0.62
1:D:153:ASP:H	5:D:302:DMS:H12	1.64	0.62
1:C:100:GLU:OE1	2:C:301:EPE:O8	2.07	0.61
1:B:153:ASP:H	3:B:302:GOL:C1	2.12	0.61
1:C:146:HIS:HD2	6:C:530:HOH:O	1.82	0.61
1:D:45[B]:THR:HG22	1:D:198:PRO:CG	2.29	0.60
1:D:172:HIS:HD2	6:D:465:HOH:O	1.85	0.60
1:D:119:HIS:HD2	6:D:478:HOH:O	1.86	0.59
1:D:45[B]:THR:CG2	1:D:198:PRO:HG3	2.30	0.59
1:A:172:HIS:HE1	1:A:225:PRO:O	1.87	0.58
1:D:61(B):THR:HG23	1:D:61(D):ASP:H	1.68	0.58
1:A:195[B]:SER:HB3	6:A:437:HOH:O	2.03	0.58
1:C:61(B):THR:HG23	1:C:61(D):ASP:H	1.67	0.58
1:D:45[B]:THR:CG2	1:D:198:PRO:HB3	2.34	0.57
1:B:91:HIS:O	1:B:94[B]:SER:HB3	2.05	0.56
1:D:172:HIS:HE1	1:D:225:PRO:O	1.88	0.56
1:A:129(A):GLU:OE1	1:A:165:ARG:NH1	2.35	0.56
1:C:172:HIS:HD2	6:C:560:HOH:O	1.89	0.55
1:C:119:HIS:HD2	6:C:508:HOH:O	1.89	0.55
1:A:172:HIS:HD2	6:A:406:HOH:O	1.89	0.55
1:D:170(A):ARG:HG3	1:D:170(A):ARG:HH11	1.72	0.55
1:D:57[A]:HIS:ND1	1:D:102:ASP:OD2	2.40	0.54
1:D:45[B]:THR:HG23	6:D:402:HOH:O	2.07	0.53
1:A:38:GLY:HA2	6:A:310:HOH:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:119:HIS:HD2	6:B:522:HOH:O	1.91	0.52
1:D:153:ASP:H	5:D:302:DMS:C1	2.21	0.52
1:C:57[A]:HIS:ND1	1:C:102:ASP:OD2	2.40	0.52
1:D:45[B]:THR:CG2	1:D:198:PRO:CG	2.88	0.51
1:D:163:MET:HE2	1:D:168[B]:CYS:SG	2.50	0.51
1:A:65:GLN:OE1	1:B:170:LEU:HD21	2.11	0.51
1:B:20:GLN:HE22	1:D:125:GLN:HE22	1.58	0.51
1:D:134:THR:HB	1:D:162:ILE:HD13	1.93	0.51
1:A:151:ARG:HD3	6:A:330:HOH:O	2.10	0.51
1:C:129(A):GLU:OE1	1:C:165:ARG:NH1	2.38	0.50
1:D:195[B]:SER:HB3	6:D:520:HOH:O	2.12	0.49
1:B:49:GLU:CG	6:B:585:HOH:O	2.49	0.49
1:D:45[A]:THR:HG22	6:D:429:HOH:O	2.13	0.49
1:C:166[A]:THR:HG22	6:C:556:HOH:O	2.12	0.48
1:A:57[A]:HIS:ND1	1:A:102:ASP:OD2	2.42	0.48
1:C:163:MET:SD	1:C:168[B]:CYS:HB3	2.54	0.48
1:D:170(A):ARG:HH11	1:D:170(A):ARG:CG	2.27	0.48
1:C:151:ARG:HD3	6:C:538:HOH:O	2.16	0.45
1:A:45[A]:THR:HG22	6:A:334:HOH:O	2.16	0.45
1:B:151:ARG:CZ	6:B:451:HOH:O	2.64	0.45
1:B:61(B):THR:HG23	1:B:61(D):ASP:N	2.31	0.44
1:B:153:ASP:N	3:B:302:GOL:H11	2.29	0.44
1:A:195[A]:SER:HB2	6:A:437:HOH:O	2.16	0.44
1:B:146:HIS:HD2	6:B:459:HOH:O	2.01	0.43
1:A:45[A]:THR:CG2	6:A:334:HOH:O	2.68	0.42
1:A:151:ARG:NH2	6:A:301:HOH:O	2.32	0.42
1:B:20:GLN:HE22	1:D:125:GLN:NE2	2.17	0.42
1:C:163:MET:HB3	1:C:163:MET:HE3	1.73	0.42
1:A:163:MET:HE2	1:A:163:MET:HB2	1.75	0.42
1:B:156:HIS:HE1	3:B:302:GOL:O3	2.03	0.42
1:B:119:HIS:HE1	6:B:584:HOH:O	2.01	0.42
1:B:101:ASP:OD2	2:B:301:EPE:H82	2.20	0.41
1:C:170(B):THR:HG21	6:C:405:HOH:O	2.19	0.41
1:B:211:GLY:HA2	1:B:229:THR:O	2.22	0.40
1:D:151:ARG:NH2	6:D:406:HOH:O	2.54	0.40
1:A:223(A):LYS:HA	1:A:223(A):LYS:HD2	1.92	0.40
1:B:150:ARG:NH2	3:B:302:GOL:H31	2.37	0.40

All (9) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:GLU:OE2	6:C:459:HOH:O[1_645]	0.33	1.87
1:C:127:GLU:OE2	6:A:404:HOH:O[1_455]	0.35	1.85
1:C:127:GLU:CD	6:A:404:HOH:O[1_455]	1.27	0.93
6:B:401:HOH:O	6:D:510:HOH:O[1_445]	1.31	0.89
1:A:127:GLU:CD	6:C:459:HOH:O[1_645]	1.38	0.82
6:A:491:HOH:O	6:C:410:HOH:O[1_545]	1.59	0.61
1:C:145:THR:OG1	6:A:491:HOH:O[1_565]	1.75	0.45
1:A:244:GLY:CA	6:D:580:HOH:O[1_545]	1.91	0.29
1:A:244:GLY:C	6:D:596:HOH:O[1_545]	1.93	0.27

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	239/234 (102%)	232 (97%)	7 (3%)	0	100	100
1	B	234/234 (100%)	223 (95%)	11 (5%)	0	100	100
1	C	238/234 (102%)	229 (96%)	9 (4%)	0	100	100
1	D	236/234 (101%)	225 (95%)	11 (5%)	0	100	100
All	All	947/936 (101%)	909 (96%)	38 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	202/197 (102%)	198 (98%)	4 (2%)	48	12
1	B	196/197 (100%)	196 (100%)	0	100	100
1	C	201/197 (102%)	195 (97%)	6 (3%)	36	5
1	D	197/197 (100%)	192 (98%)	5 (2%)	42	8
All	All	796/788 (101%)	781 (98%)	15 (2%)	61	13

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	96	PRO
1	A	99	LEU
1	A	197[A]	SER
1	A	197[B]	SER
1	C	96	PRO
1	C	99	LEU
1	C	197[A]	SER
1	C	197[B]	SER
1	C	240[A]	ASN
1	C	240[B]	ASN
1	D	45[A]	THR
1	D	45[B]	THR
1	D	99	LEU
1	D	240[A]	ASN
1	D	240[B]	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	119	HIS
1	A	172	HIS
1	B	20	GLN
1	B	111	ASN
1	B	119	HIS
1	B	146	HIS
1	B	156	HIS
1	B	172	HIS
1	B	240	ASN
1	C	20	GLN
1	C	119	HIS

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Mol	Chain	Res	Type
1	C	146	HIS
1	C	172	HIS
1	D	119	HIS
1	D	146	HIS
1	D	156	HIS
1	D	172	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 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	$\# Z > 2$
5	DMS	D	302	-	3,3,3	1.24	0	3,3,3	3.28	1 (33%)
2	EPE	B	301	-	15,15,15	1.59	3 (20%)	19,20,20	2.31	9 (47%)
5	DMS	D	301	-	3,3,3	2.00	1 (33%)	3,3,3	1.99	1 (33%)
4	SO4	C	302	-	4,4,4	0.78	0	6,6,6	0.93	0
2	EPE	C	301	-	15,15,15	1.88	2 (13%)	19,20,20	2.79	6 (31%)
3	GOL	B	302	-	5,5,5	2.34	3 (60%)	5,5,5	2.59	2 (40%)

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
3	GOL	B	302	-	-	1/4/4/4	-
2	EPE	C	301	-	-	2/9/19/19	0/1/1/1
2	EPE	B	301	-	-	3/9/19/19	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	EPE	O2S-S	4.76	1.58	1.45
2	B	301	EPE	C10-S	-4.06	1.71	1.77
2	C	301	EPE	C10-S	-3.92	1.72	1.77
5	D	301	DMS	C1-S	-3.45	1.51	1.76
3	B	302	GOL	C3-C2	-3.24	1.39	1.51
2	B	301	EPE	O2S-S	2.95	1.53	1.45
3	B	302	GOL	O2-C2	-2.67	1.35	1.43
2	B	301	EPE	C9-C10	2.57	1.59	1.52
3	B	302	GOL	C1-C2	-2.48	1.42	1.51

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	301	EPE	O3S-S-O1S	7.09	129.13	111.40
2	C	301	EPE	O3S-S-O2S	-7.00	93.90	111.40
5	D	302	DMS	C2-S-C1	5.58	127.03	98.42
2	B	301	EPE	O3S-S-C10	-5.22	95.79	106.00
2	B	301	EPE	O1S-S-C10	4.43	113.42	106.73
2	C	301	EPE	C2-C3-N4	4.02	118.76	110.65
3	B	302	GOL	O3-C3-C2	3.94	128.12	110.38
3	B	302	GOL	O1-C1-C2	3.45	125.89	110.38
2	B	301	EPE	O3S-S-O1S	2.96	118.82	111.40
5	D	301	DMS	C2-S-C1	2.86	113.09	98.42
2	C	301	EPE	O1S-S-C10	-2.82	102.47	106.73
2	B	301	EPE	C6-N1-C2	-2.77	102.88	108.84
2	B	301	EPE	C5-C6-N1	2.73	116.15	110.65
2	B	301	EPE	C7-N4-C5	-2.53	104.49	111.24
2	B	301	EPE	O8-C8-C7	-2.37	101.44	111.22
2	B	301	EPE	C6-C5-N4	-2.20	106.21	110.65
2	C	301	EPE	C5-N4-C3	-2.16	104.20	108.84
2	B	301	EPE	O2S-S-O1S	-2.10	106.98	113.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	301	EPE	C9-N1-C2	-2.03	105.83	111.24

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	301	EPE	S-C10-C9-N1
2	B	301	EPE	S-C10-C9-N1
3	B	302	GOL	O1-C1-C2-O2
2	B	301	EPE	C8-C7-N4-C3
2	B	301	EPE	N4-C7-C8-O8
2	C	301	EPE	C8-C7-N4-C3

There are no ring outliers.

5 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	302	DMS	2	0
2	B	301	EPE	1	0
5	D	301	DMS	2	0
2	C	301	EPE	1	0
3	B	302	GOL	6	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	230/234 (98%)	-0.01	6 (2%) 57 59	6, 15, 36, 71	11 (4%)
1	B	230/234 (98%)	-0.05	6 (2%) 57 59	5, 13, 33, 64	6 (2%)
1	C	229/234 (97%)	0.04	4 (1%) 69 69	5, 14, 34, 66	12 (5%)
1	D	230/234 (98%)	0.13	12 (5%) 33 34	6, 14, 36, 66	8 (3%)
All	All	919/936 (98%)	0.03	28 (3%) 52 55	5, 14, 36, 71	37 (4%)

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	45[A]	THR	4.6
1	B	243	ASN	3.8
1	D	219	VAL	3.6
1	D	170(B)	THR	3.5
1	D	168[A]	CYS	3.2
1	B	244	GLY	3.2
1	A	99	LEU	3.2
1	D	171	TYR	3.1
1	B	170(B)	THR	3.0
1	D	216	GLY	3.0
1	A	97	ASP	3.0
1	C	99	LEU	2.9
1	D	243	ASN	2.9
1	B	217	SER	2.9
1	C	95	ARG	2.8
1	C	61(B)	THR	2.8
1	A	95	ARG	2.7
1	D	61(B)	THR	2.7
1	D	217	SER	2.6
1	D	244	GLY	2.6
1	D	99	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	215	TRP	2.5
1	C	217	SER	2.3
1	B	216	GLY	2.3
1	A	82	TRP	2.3
1	A	217	SER	2.3
1	B	61(B)	THR	2.2
1	A	149	GLY	2.1

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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($\text{\AA}^2$)	Q<0.9
4	SO4	C	302	5/5	0.92	0.12	28,40,47,77	0
3	GOL	B	302	6/6	0.93	0.09	18,21,29,34	0
2	EPE	C	301	15/15	0.95	0.09	19,29,42,44	0
5	DMS	D	302	4/4	0.95	0.10	19,23,26,27	0
5	DMS	D	301	4/4	0.97	0.08	13,20,24,29	0
2	EPE	B	301	15/15	0.97	0.09	18,24,32,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.