



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 10:00 AM UTC

PDB ID : 5DQO / pdb_00005dgo
Title : Crystal structure of Y347F mutant of human primase p58 iron-sulfur cluster domain
Authors : Salay, L.E.; Thompson, M.K.; Chazin, W.J.
Deposited on : 2015-09-15
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<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

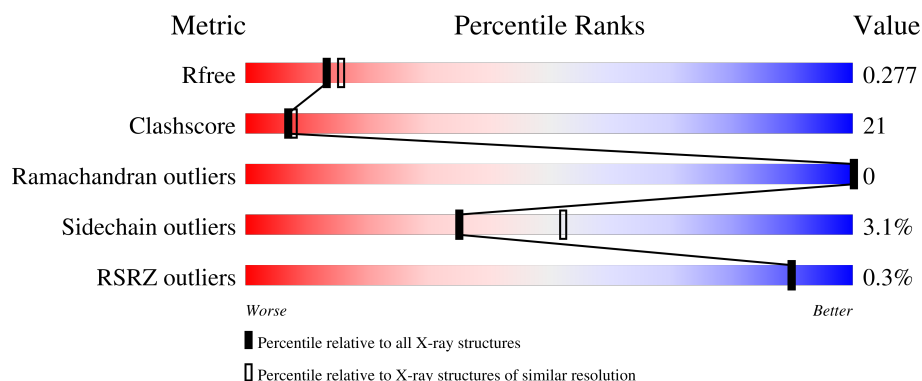
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	197	
1	B	197	
1	C	197	
1	D	197	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4911 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.

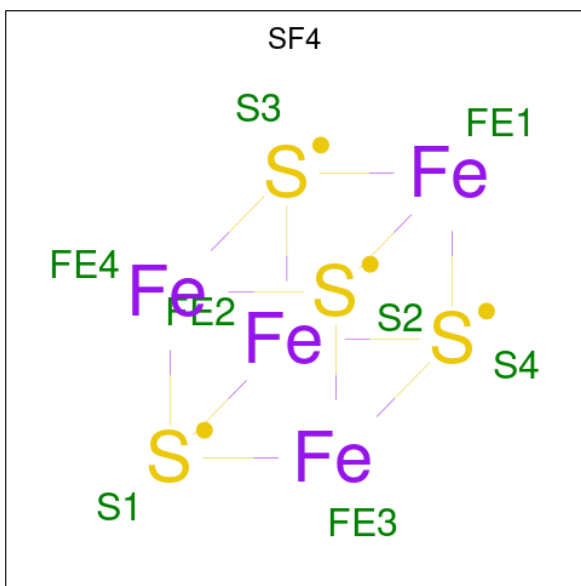
- Molecule 1 is a protein called DNA primase large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	158	Total	C	N	O	S	0	1	0
			1229	786	219	215	9			
1	B	154	Total	C	N	O	S	0	0	0
			1193	752	215	217	9			
1	C	158	Total	C	N	O	S	0	1	0
			1236	790	218	219	9			
1	D	159	Total	C	N	O	S	0	0	0
			1207	762	216	220	9			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	268	GLY	-	expression tag	UNP P49643
A	269	SER	-	expression tag	UNP P49643
A	270	PRO	-	expression tag	UNP P49643
A	271	ASN	-	expression tag	UNP P49643
A	347	PHE	TYR	engineered mutation	UNP P49643
B	268	GLY	-	expression tag	UNP P49643
B	269	SER	-	expression tag	UNP P49643
B	270	PRO	-	expression tag	UNP P49643
B	271	ASN	-	expression tag	UNP P49643
B	347	PHE	TYR	engineered mutation	UNP P49643
C	268	GLY	-	expression tag	UNP P49643
C	269	SER	-	expression tag	UNP P49643
C	270	PRO	-	expression tag	UNP P49643
C	271	ASN	-	expression tag	UNP P49643
C	347	PHE	TYR	engineered mutation	UNP P49643
D	268	GLY	-	expression tag	UNP P49643
D	269	SER	-	expression tag	UNP P49643
D	270	PRO	-	expression tag	UNP P49643
D	271	ASN	-	expression tag	UNP P49643
D	347	PHE	TYR	engineered mutation	UNP P49643

- Molecule 2 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Fe	S	0	0
			8	4	4		
2	B	1	Total	Fe	S	0	0
			8	4	4		
2	C	1	Total	Fe	S	0	0
			8	4	4		
2	D	1	Total	Fe	S	0	0
			8	4	4		

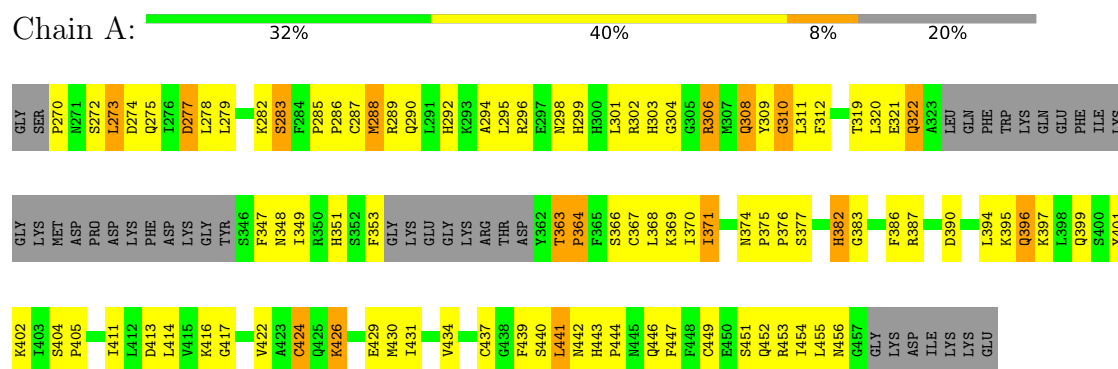
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	O	0	0
			4	4		
3	B	3	Total	O	0	0
			3	3		
3	C	5	Total	O	0	0
			5	5		
3	D	2	Total	O	0	0
			2	2		

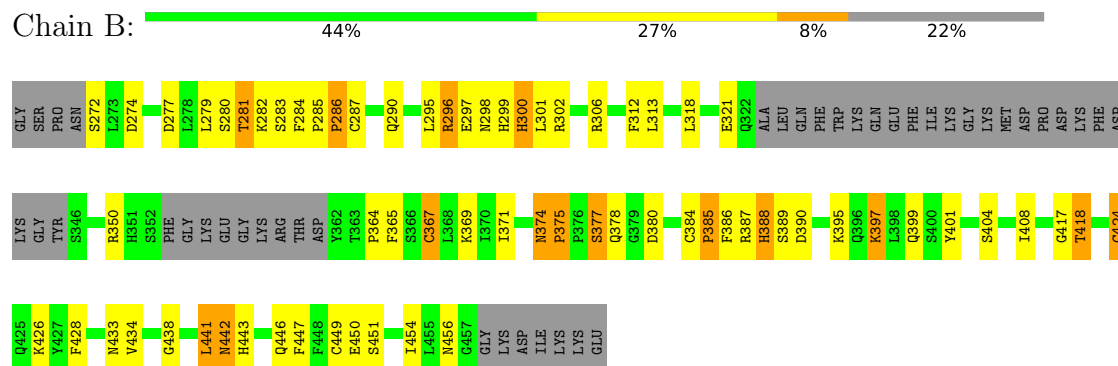
3 Residue-property plots [i](#)

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.

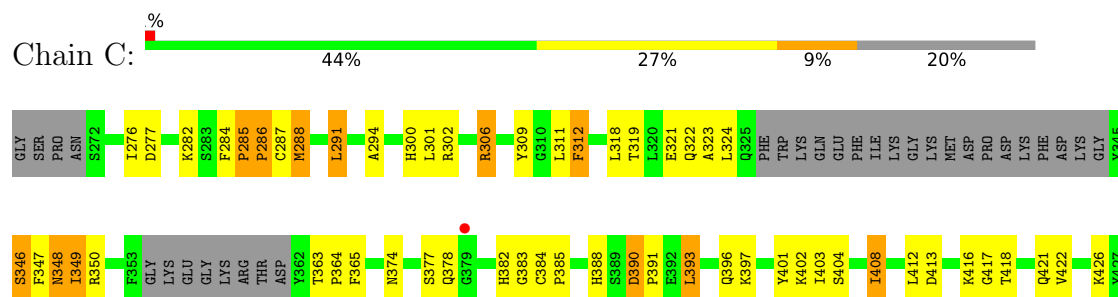
• Molecule 1: DNA primase large subunit



• Molecule 1: DNA primase large subunit



• Molecule 1: DNA primase large subunit





● Molecule 1: DNA primase large subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	60.40Å 60.40Å 246.73Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.14 – 2.30 44.14 – 2.30	Depositor EDS
% Data completeness (in resolution range)	95.3 (44.14-2.30) 95.3 (44.14-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.19 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.251 , 0.275 0.251 , 0.277	Depositor DCC
R_{free} test set	2045 reflections (4.57%)	wwPDB-VP
Wilson B-factor (Å ²)	58.1	Xtriage
Anisotropy	0.066	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 49.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l 0.300 for h,-h-k,-l 0.037 for -k,-h,-l	Xtriage
Reported twinning fraction	0.365 for H, K, L 0.232 for -K, -H, -L 0.221 for -h,-k,l 0.182 for K, H, -L	Depositor
Outliers	0 of 42683 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4911	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.22% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SF4

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	2.03	28/1267 (2.2%)	1.42	24/1711 (1.4%)
1	B	1.78	7/1223 (0.6%)	1.46	25/1653 (1.5%)
1	C	1.91	27/1273 (2.1%)	1.54	21/1717 (1.2%)
1	D	1.68	8/1238 (0.6%)	1.42	24/1675 (1.4%)
All	All	1.85	70/5001 (1.4%)	1.46	94/6756 (1.4%)

All (70) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	348	ASN	CA-C	7.42	1.61	1.52
1	A	447	PHE	C-O	-7.10	1.15	1.24
1	D	304	GLY	C-O	-6.93	1.16	1.23
1	C	443	HIS	C-O	-6.85	1.16	1.24
1	A	417	GLY	C-O	-6.84	1.16	1.23
1	C	422	VAL	C-O	-6.84	1.16	1.24
1	A	414	LEU	C-O	-6.77	1.16	1.24
1	C	384	CYS	C-O	-6.69	1.16	1.24
1	A	440[A]	SER	C-O	-6.53	1.16	1.24
1	A	440[B]	SER	C-O	-6.53	1.16	1.24
1	D	319	THR	CA-C	-6.52	1.45	1.52
1	A	374	ASN	CA-C	-6.49	1.49	1.53
1	A	442	ASN	C-O	-6.49	1.17	1.24
1	C	435	ASP	C-O	-6.38	1.16	1.24
1	A	319	THR	C-O	-6.30	1.16	1.23
1	A	311	LEU	C-O	-6.20	1.16	1.24
1	D	347	PHE	C-O	-6.16	1.16	1.24
1	A	304	GLY	C-O	-5.96	1.17	1.24
1	D	445	ASN	C-O	-5.88	1.16	1.24
1	C	446	GLN	C-O	-5.87	1.17	1.24
1	C	288	MET	C-O	-5.86	1.16	1.24
1	A	302	ARG	C-O	-5.86	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	454	ILE	C-O	-5.81	1.17	1.24
1	A	411	ILE	C-O	-5.79	1.17	1.24
1	C	306	ARG	C-O	-5.75	1.17	1.24
1	B	313	LEU	C-O	-5.71	1.17	1.24
1	C	349	ILE	C-O	-5.70	1.18	1.24
1	C	324	LEU	CA-C	5.69	1.60	1.53
1	C	412	LEU	C-O	-5.67	1.16	1.24
1	B	451	SER	N-CA	-5.67	1.39	1.46
1	C	439	PHE	C-O	-5.67	1.17	1.23
1	A	452	GLN	C-O	-5.66	1.17	1.24
1	A	375	PRO	C-O	-5.50	1.20	1.25
1	C	442	ASN	C-O	-5.50	1.17	1.24
1	D	318	LEU	C-O	-5.47	1.17	1.23
1	C	291	LEU	C-O	-5.46	1.17	1.24
1	D	308	GLN	C-O	-5.46	1.17	1.24
1	A	301	LEU	CA-C	-5.43	1.45	1.52
1	C	413	ASP	C-O	-5.39	1.17	1.24
1	B	426	LYS	C-O	-5.38	1.18	1.24
1	C	441	LEU	C-O	-5.38	1.17	1.24
1	A	443	HIS	C-O	-5.37	1.16	1.25
1	B	442	ASN	C-O	-5.35	1.17	1.24
1	B	385	PRO	N-CA	-5.34	1.40	1.47
1	C	319	THR	C-O	-5.28	1.17	1.24
1	A	308	GLN	C-O	-5.27	1.18	1.24
1	C	421	GLN	C-O	-5.26	1.17	1.24
1	A	431	ILE	C-O	-5.24	1.17	1.24
1	D	389	SER	CA-C	-5.22	1.46	1.52
1	D	305	GLY	C-O	-5.20	1.17	1.23
1	C	451	SER	C-O	-5.19	1.18	1.24
1	A	295	LEU	C-O	-5.17	1.17	1.24
1	A	396	GLN	C-O	-5.17	1.17	1.24
1	C	302	ARG	C-O	-5.15	1.16	1.23
1	C	390	ASP	C-O	-5.14	1.17	1.23
1	C	434	VAL	C-O	-5.14	1.18	1.24
1	B	296	ARG	N-CA	-5.14	1.40	1.46
1	C	277	ASP	CA-C	-5.14	1.46	1.52
1	C	312	PHE	C-O	-5.14	1.17	1.24
1	C	365	PHE	C-O	-5.14	1.17	1.23
1	C	383	GLY	C-O	-5.12	1.18	1.23
1	A	366	SER	C-O	-5.11	1.17	1.23
1	A	310	GLY	C-O	-5.11	1.17	1.23
1	A	294	ALA	C-O	-5.07	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	446	GLN	C-O	-5.05	1.17	1.24
1	A	371	ILE	C-O	-5.04	1.18	1.24
1	B	300	HIS	C-O	-5.04	1.18	1.23
1	C	350	ARG	C-O	-5.02	1.17	1.23
1	A	411	ILE	N-CA	-5.01	1.40	1.46
1	A	288	MET	C-O	-5.01	1.17	1.24

All (94) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	324	LEU	N-CA-C	20.45	142.85	111.56
1	D	303	HIS	N-CA-C	10.67	123.91	111.11
1	C	324	LEU	CB-CA-C	-9.99	92.34	111.03
1	C	393	LEU	N-CA-C	-9.68	99.78	111.69
1	D	441	LEU	N-CA-C	9.28	123.44	109.25
1	A	282	LYS	N-CA-C	9.19	120.90	111.07
1	B	375	PRO	CB-CA-C	-9.00	99.94	110.92
1	D	433	ASN	N-CA-C	8.99	123.88	111.74
1	B	283	SER	N-CA-C	8.55	124.99	112.94
1	B	286	PRO	CB-CA-C	-8.28	100.14	112.55
1	B	282	LYS	N-CA-C	8.08	119.71	111.07
1	D	425	GLN	N-CA-C	8.01	120.01	111.28
1	B	418	THR	N-CA-C	-8.00	100.32	111.52
1	B	441	LEU	N-CA-C	7.58	121.81	109.76
1	C	323	ALA	CB-CA-C	-7.46	94.23	109.38
1	A	363	THR	N-CA-C	7.34	121.41	109.15
1	A	322	GLN	N-CA-C	7.28	120.79	112.57
1	B	297	GLU	N-CA-C	7.21	121.34	112.54
1	A	303	HIS	N-CA-C	7.15	119.74	111.02
1	B	388	HIS	N-CA-C	7.13	121.81	113.18
1	B	369	LYS	N-CA-C	-7.09	102.60	112.45
1	A	364	PRO	CB-CA-C	-6.96	102.73	111.56
1	A	301	LEU	N-CA-C	-6.92	98.56	109.07
1	C	286	PRO	CA-C-N	6.88	129.50	120.28
1	C	286	PRO	C-N-CA	6.88	129.50	120.28
1	D	296	ARG	N-CA-C	6.76	119.67	111.82
1	D	427	TYR	N-CA-C	-6.76	103.91	111.28
1	C	284	PHE	CB-CA-C	6.65	119.94	109.37
1	D	378	GLN	N-CA-C	-6.58	99.80	110.20
1	B	390	ASP	N-CA-C	-6.53	101.54	109.83
1	B	447	PHE	N-CA-C	-6.50	104.27	111.36
1	D	424	CYS	CA-CB-SG	6.44	129.22	114.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	273	LEU	N-CA-C	6.37	118.22	111.28
1	C	378	GLN	N-CA-C	6.35	120.60	112.34
1	C	284	PHE	N-CA-C	-6.34	101.87	110.36
1	C	276	ILE	N-CA-C	6.33	118.25	112.29
1	D	277	ASP	N-CA-C	6.30	117.94	111.14
1	D	350	ARG	CB-CA-C	6.28	123.96	110.45
1	D	352	SER	N-CA-C	6.26	119.32	111.24
1	C	377	SER	N-CA-C	-6.09	100.92	109.69
1	D	368	LEU	N-CA-C	6.07	119.88	112.23
1	A	440[A]	SER	N-CA-C	-6.04	99.35	109.07
1	A	440[B]	SER	N-CA-C	-6.04	99.35	109.07
1	A	447	PHE	N-CA-C	-5.97	104.77	111.28
1	B	375	PRO	N-CA-C	5.93	117.93	110.70
1	B	374	ASN	N-CA-C	5.90	122.85	109.81
1	A	382	HIS	N-CA-C	5.89	119.19	109.94
1	B	281	THR	N-CA-C	-5.88	104.50	111.03
1	D	283	SER	N-CA-C	5.87	121.88	114.31
1	D	424	CYS	N-CA-C	-5.87	104.88	111.28
1	C	282	LYS	N-CA-C	5.86	120.71	113.50
1	A	390	ASP	CA-C-N	-5.84	113.73	120.04
1	A	390	ASP	C-N-CA	-5.84	113.73	120.04
1	D	369	LYS	N-CA-C	-5.84	104.99	111.36
1	D	303	HIS	CB-CA-C	-5.75	101.61	110.81
1	B	365	PHE	N-CA-C	5.73	118.88	109.76
1	B	312	PHE	N-CA-C	-5.70	104.68	111.69
1	C	437	CYS	N-CA-C	5.68	119.93	112.89
1	C	388	HIS	N-CA-C	5.66	120.88	113.30
1	A	376	PRO	N-CA-C	5.64	119.74	110.55
1	B	424	CYS	N-CA-C	-5.52	104.48	111.11
1	C	294	ALA	N-CA-C	5.51	116.97	110.97
1	D	415	VAL	CB-CA-C	-5.51	104.65	111.70
1	C	346	SER	N-CA-C	-5.50	100.12	107.88
1	D	428	PHE	N-CA-C	-5.47	105.22	111.07
1	B	377	SER	N-CA-C	-5.44	102.84	110.35
1	B	397	LYS	N-CA-C	-5.42	105.28	111.14
1	C	318	LEU	N-CA-CB	-5.41	102.20	110.85
1	B	367	CYS	N-CA-C	5.41	119.37	112.34
1	A	369	LYS	CB-CA-C	5.40	119.28	110.96
1	D	384	CYS	N-CA-C	-5.37	103.41	110.39
1	A	440[A]	SER	CA-CB-OG	5.34	121.77	111.10
1	A	440[B]	SER	CA-CB-OG	5.34	121.77	111.10
1	A	394	LEU	N-CA-C	-5.33	105.55	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	306	ARG	N-CA-C	-5.33	105.92	112.90
1	B	424	CYS	CA-CB-SG	5.29	126.58	114.40
1	C	408	ILE	N-CA-C	-5.29	105.38	110.72
1	A	283	SER	N-CA-C	5.25	122.18	113.89
1	B	378	GLN	N-CA-C	-5.24	102.72	110.48
1	D	349	ILE	CB-CA-C	-5.24	103.35	110.90
1	C	312	PHE	N-CA-C	-5.21	105.28	111.69
1	A	289	ARG	N-CA-C	-5.20	105.62	111.28
1	D	313	LEU	N-CA-C	-5.19	105.70	112.23
1	A	390	ASP	N-CA-C	-5.18	102.64	109.84
1	D	286	PRO	N-CA-C	5.17	120.63	113.65
1	D	304	GLY	N-CA-C	-5.14	108.93	115.31
1	B	450	GLU	N-CA-C	-5.14	106.97	113.18
1	A	368	LEU	N-CA-C	5.09	116.83	111.28
1	B	438	GLY	N-CA-C	5.09	122.61	115.43
1	B	434	VAL	CB-CA-C	5.08	118.19	110.62
1	C	441	LEU	N-CA-C	5.08	117.52	109.96
1	C	285	PRO	N-CA-C	-5.07	104.52	110.70
1	A	306	ARG	N-CA-C	-5.03	105.46	112.45
1	A	377	SER	N-CA-C	-5.00	103.45	110.35

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1229	0	1164	56	0
1	B	1193	0	1101	46	0
1	C	1236	0	1173	44	0
1	D	1207	0	1088	62	0
2	A	8	0	0	1	0
2	B	8	0	0	1	0
2	C	8	0	0	0	0
2	D	8	0	0	0	0
3	A	4	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	3	0	0	0	0
3	C	5	0	0	0	0
3	D	2	0	0	0	0
All	All	4911	0	4526	198	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 21.

All (198) 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:A:449:CYS:SG	1:B:449:CYS:SG	1.35	1.33
1:B:301:LEU:O	1:B:306:ARG:NH1	1.76	1.17
1:D:295:LEU:HD13	1:D:301:LEU:HD12	1.35	1.03
1:B:367:CYS:O	1:B:371:ILE:HD12	1.59	0.99
1:B:286:PRO:HD2	2:B:501:SF4:S3	2.07	0.94
1:A:274:ASP:HA	1:A:277:ASP:OD1	1.68	0.93
1:B:286:PRO:O	1:B:290:GLN:HG2	1.68	0.92
1:C:321:GLU:HG3	1:C:322:GLN:H	1.34	0.92
1:C:286:PRO:HB2	1:C:385:PRO:HG2	1.51	0.92
1:D:273:LEU:HD21	1:D:295:LEU:HD23	1.53	0.89
1:D:417:GLY:O	1:D:418:THR:HG23	1.77	0.84
1:D:417:GLY:C	1:D:418:THR:HG23	2.02	0.84
1:D:274:ASP:HA	1:D:277:ASP:OD2	1.81	0.80
1:D:424:CYS:SG	1:D:441:LEU:CD2	2.70	0.79
1:A:286:PRO:HG2	1:A:386:PHE:CE2	2.18	0.78
1:A:453:ARG:HD2	1:B:446:GLN:CD	2.08	0.77
1:C:426:LYS:HD3	1:C:429:GLU:OE1	1.85	0.76
1:C:322:GLN:HB2	1:C:346:SER:O	1.86	0.75
1:D:309:TYR:O	1:D:313:LEU:HG	1.87	0.75
1:B:274:ASP:HB3	1:B:296:ARG:NH2	2.03	0.74
1:A:277:ASP:OD1	1:A:296:ARG:NE	2.20	0.74
1:C:321:GLU:HG3	1:C:322:GLN:N	1.99	0.73
1:C:437:CYS:HB2	1:C:439:PHE:CE1	2.25	0.72
1:D:439:PHE:HE2	1:D:441:LEU:HB2	1.55	0.71
1:A:449:CYS:SG	1:B:449:CYS:CB	2.77	0.71
1:B:274:ASP:HB3	1:B:296:ARG:CZ	2.22	0.70
1:C:397:LYS:HE3	1:C:401:TYR:CZ	2.26	0.70
1:D:424:CYS:SG	1:D:441:LEU:HD21	2.32	0.69
1:B:395:LYS:HG2	1:B:399:GLN:OE1	1.93	0.68
1:C:346:SER:O	1:C:347:PHE:CD1	2.46	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:390:ASP:HB3	1:C:393:LEU:HD12	1.75	0.67
1:C:404:SER:O	1:C:408:ILE:HG13	1.95	0.67
1:D:324:LEU:HD12	1:D:325:GLN:O	1.94	0.67
1:D:387:ARG:O	1:D:387:ARG:HD2	1.95	0.66
1:A:285:PRO:HD2	1:A:288:MET:HB2	1.78	0.66
1:D:309:TYR:CE2	1:D:313:LEU:HD11	2.32	0.64
1:A:285:PRO:HG2	1:A:288:MET:HG2	1.79	0.64
1:D:295:LEU:HD13	1:D:301:LEU:CD1	2.22	0.64
1:D:309:TYR:CZ	1:D:313:LEU:HD21	2.32	0.63
1:B:418:THR:O	1:B:418:THR:HG22	1.97	0.62
1:C:288:MET:HE3	1:C:312:PHE:HB2	1.81	0.62
1:D:287:CYS:O	1:D:290:GLN:HG2	1.99	0.62
1:D:439:PHE:CE2	1:D:441:LEU:HB2	2.35	0.62
1:C:322:GLN:CB	1:C:346:SER:O	2.48	0.61
1:D:300:HIS:CG	1:D:301:LEU:N	2.68	0.61
1:C:321:GLU:O	1:C:348:ASN:N	2.34	0.61
1:A:286:PRO:HG2	1:A:386:PHE:HE2	1.62	0.60
1:B:377:SER:O	1:B:380:ASP:HB2	2.02	0.60
1:A:321:GLU:N	1:A:348:ASN:O	2.31	0.60
1:D:324:LEU:HD12	1:D:324:LEU:C	2.27	0.59
1:B:300:HIS:CG	1:B:301:LEU:N	2.71	0.58
1:B:280:SER:HA	1:B:284:PHE:CG	2.39	0.58
1:B:300:HIS:O	1:B:301:LEU:HD23	2.04	0.58
1:A:429:GLU:HA	1:A:434:VAL:CG2	2.35	0.57
1:A:396:GLN:HA	1:A:399:GLN:OE1	2.05	0.56
1:D:300:HIS:CD2	1:D:301:LEU:H	2.23	0.56
1:D:324:LEU:HD12	1:D:324:LEU:O	2.06	0.56
1:A:401:TYR:O	1:A:402:LYS:CB	2.51	0.56
1:A:306:ARG:O	1:A:310:GLY:N	2.33	0.55
1:B:302:ARG:O	1:B:306:ARG:HG3	2.07	0.54
1:A:351:HIS:CE1	1:B:318:LEU:HD21	2.42	0.54
1:C:285:PRO:HD2	1:C:288:MET:HB2	1.89	0.54
1:C:417:GLY:O	1:C:418:THR:OG1	2.22	0.54
1:A:426:LYS:O	1:A:430:MET:HG2	2.07	0.54
1:B:272:SER:HB2	1:B:274:ASP:OD1	2.07	0.54
1:A:322:GLN:CB	1:A:347:PHE:CE1	2.91	0.54
1:C:374:ASN:O	1:C:382:HIS:NE2	2.39	0.54
1:A:286:PRO:HD2	2:A:501:SF4:S2	2.48	0.54
1:D:287:CYS:HB3	1:D:384:CYS:HA	1.90	0.54
1:C:288:MET:HG3	1:C:312:PHE:CD2	2.43	0.53
1:C:346:SER:O	1:C:347:PHE:CG	2.60	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:417:GLY:O	1:D:418:THR:CG2	2.53	0.53
1:D:319:THR:O	1:D:349:ILE:HA	2.09	0.53
1:A:386:PHE:CE2	1:A:424:CYS:HB2	2.44	0.53
1:D:417:GLY:C	1:D:418:THR:CG2	2.73	0.53
1:A:322:GLN:CB	1:A:347:PHE:HE1	2.22	0.53
1:B:287:CYS:HA	1:B:290:GLN:NE2	2.24	0.53
1:A:453:ARG:HD2	1:B:446:GLN:NE2	2.23	0.52
1:C:346:SER:C	1:C:347:PHE:CD1	2.87	0.52
1:A:395:LYS:O	1:A:399:GLN:OE1	2.27	0.52
1:D:318:LEU:C	1:D:352:SER:OG	2.53	0.52
1:C:321:GLU:O	1:C:347:PHE:HA	2.09	0.51
1:A:453:ARG:NH2	3:A:601:HOH:O	2.42	0.51
1:C:311:LEU:HD13	1:C:363:THR:O	2.10	0.51
1:C:390:ASP:CG	1:C:391:PRO:HD2	2.36	0.51
1:A:404:SER:HB2	1:A:405:PRO:HD2	1.92	0.51
1:A:277:ASP:CG	1:A:296:ARG:HE	2.13	0.51
1:D:300:HIS:CG	1:D:301:LEU:H	2.29	0.51
1:D:286:PRO:HG3	1:D:427:TYR:CE2	2.46	0.50
1:D:444:PRO:O	1:D:447:PHE:HB3	2.12	0.50
1:D:309:TYR:CE1	1:D:313:LEU:HD21	2.46	0.50
1:C:437:CYS:HB2	1:C:439:PHE:HE1	1.74	0.50
1:D:284:PHE:CD1	1:D:284:PHE:N	2.79	0.50
1:C:441:LEU:CD1	1:C:447:PHE:HD2	2.24	0.49
1:C:288:MET:HG3	1:C:312:PHE:CG	2.47	0.49
1:B:433:ASN:CG	1:B:433:ASN:O	2.56	0.49
1:D:287:CYS:HB3	1:D:385:PRO:HD3	1.95	0.49
1:A:353:PHE:HB3	1:B:279:LEU:HD13	1.94	0.48
1:A:353:PHE:CD1	1:A:353:PHE:C	2.91	0.48
1:D:290:GLN:OE1	1:D:385:PRO:HG3	2.13	0.48
1:A:320:LEU:HA	1:A:348:ASN:O	2.14	0.48
1:A:273:LEU:HD11	1:A:320:LEU:CD1	2.44	0.48
1:A:273:LEU:HD12	1:A:349:ILE:HG12	1.96	0.48
1:A:287:CYS:HB2	1:A:308:GLN:NE2	2.29	0.48
1:A:298:ASN:O	1:A:299:HIS:HB2	2.14	0.48
1:C:403:ILE:HG22	1:C:404:SER:N	2.29	0.47
1:B:285:PRO:HB2	1:B:287:CYS:SG	2.54	0.47
1:D:273:LEU:HD13	1:D:347:PHE:HB3	1.96	0.47
1:D:284:PHE:N	1:D:284:PHE:HD1	2.12	0.47
1:A:285:PRO:HG3	1:A:444:PRO:HB3	1.96	0.47
1:B:277:ASP:O	1:B:281:THR:HG23	2.14	0.47
1:C:428:PHE:C	1:C:428:PHE:CD1	2.93	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:272:SER:O	1:D:275:GLN:CB	2.62	0.47
1:D:374:ASN:O	1:D:382:HIS:NE2	2.43	0.47
1:B:428:PHE:C	1:B:428:PHE:CD1	2.93	0.47
1:B:387:ARG:HG3	1:B:388:HIS:N	2.29	0.47
1:D:404:SER:C	1:D:406:GLY:H	2.22	0.47
1:A:272:SER:O	1:A:275:GLN:CB	2.63	0.47
1:B:417:GLY:O	1:B:418:THR:HB	2.15	0.47
1:A:367:CYS:SG	1:A:444:PRO:HD3	2.55	0.46
1:C:441:LEU:HD11	1:C:447:PHE:HD2	1.80	0.46
1:C:449:CYS:SG	1:D:449:CYS:C	2.98	0.46
1:A:429:GLU:HA	1:A:434:VAL:HG23	1.96	0.46
1:A:439:PHE:CD1	1:A:439:PHE:N	2.84	0.46
1:D:324:LEU:CD1	1:D:325:GLN:O	2.63	0.46
1:D:367:CYS:N	1:D:444:PRO:HD3	2.30	0.46
1:A:397:LYS:HA	1:A:397:LYS:HD3	1.72	0.46
1:A:371:ILE:HG23	1:A:387:ARG:HG2	1.98	0.45
1:B:295:LEU:HD12	1:B:295:LEU:O	2.17	0.45
1:C:390:ASP:HB3	1:C:393:LEU:CD1	2.42	0.45
1:A:273:LEU:C	1:A:275:GLN:H	2.23	0.45
1:B:300:HIS:CD2	1:B:301:LEU:H	2.34	0.45
1:D:273:LEU:HD11	1:D:320:LEU:CD1	2.47	0.45
1:D:291:LEU:HD11	1:D:308:GLN:NE2	2.31	0.44
1:A:292:HIS:ND1	1:A:309:TYR:OH	2.34	0.44
1:C:397:LYS:HE3	1:C:401:TYR:OH	2.17	0.44
1:A:387:ARG:O	1:A:387:ARG:HD2	2.17	0.44
1:B:364:PRO:HB2	1:B:443:HIS:CE1	2.53	0.44
1:A:288:MET:HE3	1:A:312:PHE:HB2	1.98	0.44
1:A:451:SER:O	1:A:455:LEU:HG	2.18	0.44
1:D:404:SER:O	1:D:408:ILE:HG13	2.18	0.44
1:D:426:LYS:HA	1:D:429:GLU:HB2	1.99	0.44
1:D:447:PHE:C	1:D:447:PHE:CD1	2.96	0.44
1:C:301:LEU:O	1:C:306:ARG:NH1	2.51	0.44
1:A:308:GLN:OE1	1:A:382:HIS:HB2	2.18	0.43
1:C:397:LYS:HE3	1:C:401:TYR:CE1	2.53	0.43
1:C:441:LEU:C	1:C:441:LEU:HD23	2.43	0.43
1:A:413:ASP:O	1:A:416:LYS:HB2	2.17	0.43
1:A:455:LEU:HD23	1:A:455:LEU:N	2.32	0.43
1:B:286:PRO:HB2	1:B:385:PRO:CD	2.49	0.43
1:D:387:ARG:HD3	1:D:420:TYR:CZ	2.54	0.43
1:C:390:ASP:OD2	1:C:391:PRO:HD2	2.19	0.43
1:D:288:MET:HE1	1:D:308:GLN:HG2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:404:SER:C	1:D:406:GLY:N	2.76	0.43
1:A:270:PRO:HB2	1:A:348:ASN:CB	2.49	0.43
1:A:453:ARG:NE	1:B:442:ASN:OD1	2.50	0.43
1:D:448:PHE:CD1	1:D:448:PHE:C	2.96	0.43
1:D:318:LEU:HD23	1:D:350:ARG:O	2.19	0.42
1:D:307:MET:HB3	1:D:365:PHE:HZ	1.83	0.42
1:B:385:PRO:O	1:B:389:SER:HB2	2.20	0.42
1:C:349:ILE:O	1:C:349:ILE:HG13	2.19	0.42
1:D:285:PRO:HG3	1:D:447:PHE:CG	2.54	0.42
1:D:434:VAL:O	1:D:434:VAL:HG23	2.18	0.42
1:B:287:CYS:HA	1:B:290:GLN:HE21	1.83	0.42
1:C:393:LEU:O	1:C:396:GLN:HB2	2.19	0.42
1:A:370:ILE:HG23	1:A:383:GLY:HA2	2.00	0.42
1:A:429:GLU:HG3	1:A:437:CYS:HB3	2.02	0.42
1:C:311:LEU:HB3	1:C:364:PRO:HA	2.01	0.42
1:A:363:THR:HA	1:A:364:PRO:HD3	1.98	0.42
1:B:286:PRO:CB	1:B:385:PRO:HG2	2.50	0.42
1:D:390:ASP:OD1	1:D:391:PRO:HD2	2.19	0.42
1:B:298:ASN:O	1:B:299:HIS:C	2.62	0.41
1:B:274:ASP:OD1	1:B:274:ASP:N	2.53	0.41
1:A:278:LEU:O	1:A:278:LEU:HG	2.21	0.41
1:C:432:HIS:O	1:C:434:VAL:HG13	2.20	0.41
1:D:307:MET:HB3	1:D:365:PHE:CZ	2.55	0.41
1:D:415:VAL:O	1:D:416:LYS:C	2.63	0.41
1:B:367:CYS:O	1:B:371:ILE:CD1	2.48	0.41
1:B:404:SER:O	1:B:408:ILE:HG13	2.21	0.41
1:B:321:GLU:CD	1:B:350:ARG:HE	2.28	0.41
1:C:291:LEU:HD13	1:C:309:TYR:HB2	2.03	0.41
1:D:317:GLY:C	1:D:318:LEU:HG	2.46	0.41
1:A:424:CYS:SG	1:A:441:LEU:HD22	2.61	0.41
1:A:456:ASN:HB3	1:B:443:HIS:NE2	2.35	0.41
1:B:397:LYS:HG3	1:B:401:TYR:CZ	2.55	0.41
1:C:401:TYR:O	1:C:402:LYS:HB2	2.20	0.41
1:D:401:TYR:O	1:D:402:LYS:HB2	2.20	0.41
1:B:286:PRO:HG2	1:B:386:PHE:CE2	2.56	0.41
1:D:287:CYS:HA	1:D:385:PRO:HD3	2.02	0.41
1:C:446:GLN:HB2	1:D:453:ARG:NH1	2.36	0.40
1:D:417:GLY:O	1:D:418:THR:CB	2.66	0.40
1:A:283:SER:OG	1:A:451:SER:OG	2.39	0.40
1:B:374:ASN:HA	1:B:375:PRO:HD2	1.76	0.40
1:C:300:HIS:CG	1:C:301:LEU:N	2.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:322:GLN:HA	1:C:347:PHE:HA	2.03	0.40
1:B:280:SER:O	1:B:284:PHE:HB2	2.22	0.40
1:B:424:CYS:SG	1:B:441:LEU:HD21	2.61	0.40
1:D:279:LEU:O	1:D:283:SER:N	2.43	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	153/197 (78%)	147 (96%)	6 (4%)	0	100	100
1	B	148/197 (75%)	140 (95%)	8 (5%)	0	100	100
1	C	153/197 (78%)	148 (97%)	5 (3%)	0	100	100
1	D	153/197 (78%)	145 (95%)	8 (5%)	0	100	100
All	All	607/788 (77%)	580 (96%)	27 (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	131/176 (74%)	124 (95%)	7 (5%)	20	30
1	B	127/176 (72%)	124 (98%)	3 (2%)	43	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	133/176 (76%)	129 (97%)	4 (3%)	36	53
1	D	124/176 (70%)	122 (98%)	2 (2%)	55	73
All	All	515/704 (73%)	499 (97%)	16 (3%)	35	52

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	277	ASP
1	A	279	LEU
1	A	290	GLN
1	A	422	VAL
1	A	424	CYS
1	A	426	LYS
1	A	441	LEU
1	B	384	CYS
1	B	454	ILE
1	B	456	ASN
1	C	287	CYS
1	C	416	LYS
1	C	431	ILE
1	C	449	CYS
1	D	384	CYS
1	D	418	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	348	ASN
1	B	456	ASN
1	C	322	GLN
1	C	374	ASN
1	C	445	ASN
1	C	452	GLN
1	D	299	HIS
1	D	300	HIS

5.3.3 RNA ⓘ

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](#)

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SF4	C	501	1	0,12,12	-	-	-		
2	SF4	B	501	1	0,12,12	-	-	-		
2	SF4	A	501	1	0,12,12	-	-	-		
2	SF4	D	501	1	0,12,12	-	-	-		

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SF4	C	501	1	-	-	0/6/5/5
2	SF4	B	501	1	-	-	0/6/5/5
2	SF4	A	501	1	-	-	0/6/5/5
2	SF4	D	501	1	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	SF4	1	0
2	A	501	SF4	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	158/197 (80%)	-0.60	0	100 100	33, 50, 65, 83	6 (3%)
1	B	154/197 (78%)	-0.53	0	100 100	36, 55, 72, 78	4 (2%)
1	C	158/197 (80%)	-0.62	1 (0%)	85 86	32, 53, 69, 83	4 (2%)
1	D	159/197 (80%)	-0.47	1 (0%)	85 86	33, 56, 71, 92	3 (1%)
All	All	629/788 (79%)	-0.55	2 (0%)	90 90	32, 54, 71, 92	17 (2%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	353	PHE	2.6
1	C	379	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no 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
2	SF4	B	501	8/8	0.99	0.03	51,59,63,63	0
2	SF4	C	501	8/8	0.99	0.02	44,57,58,60	0
2	SF4	D	501	8/8	0.99	0.02	53,58,64,67	0
2	SF4	A	501	8/8	1.00	0.02	51,57,67,77	0

6.5 Other polymers [i](#)

There are no such residues in this entry.