



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:12 AM GMT

PDB ID : 2W8S
Title : CRYSTAL STRUCTURE OF A CATALYTICALLY PROMISCUOUS
PHOSPHONATE MONOESTER HYDROLASE FROM BURKHOLDERIA
CARYOPHYLLI
Authors : Jonas, S.; Van Loo, B.; Hyvonen, M.; Hollfelder, F.
Deposited on : 2009-01-19
Resolution : 2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

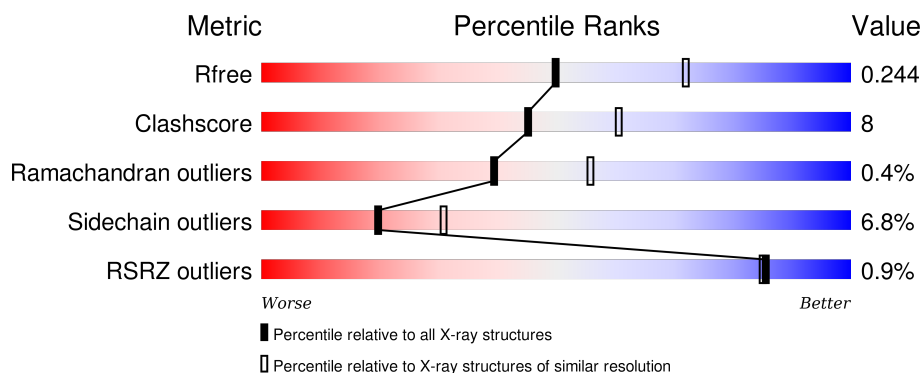
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

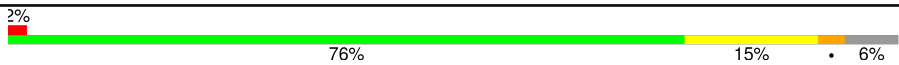



The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	544	 2% 76% 15% • 6%
1	B	544	 78% 15% • 6%
1	C	544	 % 75% 16% • 6%
1	D	544	 % 74% 17% • 6%

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
5	GOL	D	1522	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 17251 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 PHOSPHONATE MONOESTER HYDROLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	512	Total	C	N	O	S	0	1	0
			4074	2582	716	759	17			
1	B	513	Total	C	N	O	S	0	1	0
			4096	2593	721	765	17			
1	C	513	Total	C	N	O	S	0	2	0
			4109	2601	726	765	17			
1	D	513	Total	C	N	O	S	0	1	0
			4087	2589	720	761	17			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-28	MET	-	EXPRESSION TAG	UNP Q45087
A	-27	ALA	-	EXPRESSION TAG	UNP Q45087
A	-26	SER	-	EXPRESSION TAG	UNP Q45087
A	-25	TRP	-	EXPRESSION TAG	UNP Q45087
A	-24	SER	-	EXPRESSION TAG	UNP Q45087
A	-23	HIS	-	EXPRESSION TAG	UNP Q45087
A	-22	PRO	-	EXPRESSION TAG	UNP Q45087
A	-21	GLN	-	EXPRESSION TAG	UNP Q45087
A	-20	PHE	-	EXPRESSION TAG	UNP Q45087
A	-19	GLU	-	EXPRESSION TAG	UNP Q45087
A	-18	LYS	-	EXPRESSION TAG	UNP Q45087
A	-17	GLY	-	EXPRESSION TAG	UNP Q45087
A	-16	ALA	-	EXPRESSION TAG	UNP Q45087
A	-15	GLU	-	EXPRESSION TAG	UNP Q45087
A	-14	THR	-	EXPRESSION TAG	UNP Q45087
A	-13	ALA	-	EXPRESSION TAG	UNP Q45087
A	-12	VAL	-	EXPRESSION TAG	UNP Q45087
A	-11	PRO	-	EXPRESSION TAG	UNP Q45087
A	-10	ASN	-	EXPRESSION TAG	UNP Q45087
A	-9	SER	-	EXPRESSION TAG	UNP Q45087
A	-8	SER	-	EXPRESSION TAG	UNP Q45087

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	SER	-	EXPRESSION TAG	UNP Q45087
A	-6	VAL	-	EXPRESSION TAG	UNP Q45087
A	-5	PRO	-	EXPRESSION TAG	UNP Q45087
A	-4	GLY	-	EXPRESSION TAG	UNP Q45087
A	-3	ASP	-	EXPRESSION TAG	UNP Q45087
A	-2	PRO	-	EXPRESSION TAG	UNP Q45087
A	-1	SER	-	EXPRESSION TAG	UNP Q45087
A	0	SER	-	EXPRESSION TAG	UNP Q45087
A	57	FGL	CYS	MICROHETEROGENEITY	UNP Q45087
B	-28	MET	-	EXPRESSION TAG	UNP Q45087
B	-27	ALA	-	EXPRESSION TAG	UNP Q45087
B	-26	SER	-	EXPRESSION TAG	UNP Q45087
B	-25	TRP	-	EXPRESSION TAG	UNP Q45087
B	-24	SER	-	EXPRESSION TAG	UNP Q45087
B	-23	HIS	-	EXPRESSION TAG	UNP Q45087
B	-22	PRO	-	EXPRESSION TAG	UNP Q45087
B	-21	GLN	-	EXPRESSION TAG	UNP Q45087
B	-20	PHE	-	EXPRESSION TAG	UNP Q45087
B	-19	GLU	-	EXPRESSION TAG	UNP Q45087
B	-18	LYS	-	EXPRESSION TAG	UNP Q45087
B	-17	GLY	-	EXPRESSION TAG	UNP Q45087
B	-16	ALA	-	EXPRESSION TAG	UNP Q45087
B	-15	GLU	-	EXPRESSION TAG	UNP Q45087
B	-14	THR	-	EXPRESSION TAG	UNP Q45087
B	-13	ALA	-	EXPRESSION TAG	UNP Q45087
B	-12	VAL	-	EXPRESSION TAG	UNP Q45087
B	-11	PRO	-	EXPRESSION TAG	UNP Q45087
B	-10	ASN	-	EXPRESSION TAG	UNP Q45087
B	-9	SER	-	EXPRESSION TAG	UNP Q45087
B	-8	SER	-	EXPRESSION TAG	UNP Q45087
B	-7	SER	-	EXPRESSION TAG	UNP Q45087
B	-6	VAL	-	EXPRESSION TAG	UNP Q45087
B	-5	PRO	-	EXPRESSION TAG	UNP Q45087
B	-4	GLY	-	EXPRESSION TAG	UNP Q45087
B	-3	ASP	-	EXPRESSION TAG	UNP Q45087
B	-2	PRO	-	EXPRESSION TAG	UNP Q45087
B	-1	SER	-	EXPRESSION TAG	UNP Q45087
B	0	SER	-	EXPRESSION TAG	UNP Q45087
B	57	FGL	CYS	MICROHETEROGENEITY	UNP Q45087
C	-28	MET	-	EXPRESSION TAG	UNP Q45087
C	-27	ALA	-	EXPRESSION TAG	UNP Q45087
C	-26	SER	-	EXPRESSION TAG	UNP Q45087

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-25	TRP	-	EXPRESSION TAG	UNP Q45087
C	-24	SER	-	EXPRESSION TAG	UNP Q45087
C	-23	HIS	-	EXPRESSION TAG	UNP Q45087
C	-22	PRO	-	EXPRESSION TAG	UNP Q45087
C	-21	GLN	-	EXPRESSION TAG	UNP Q45087
C	-20	PHE	-	EXPRESSION TAG	UNP Q45087
C	-19	GLU	-	EXPRESSION TAG	UNP Q45087
C	-18	LYS	-	EXPRESSION TAG	UNP Q45087
C	-17	GLY	-	EXPRESSION TAG	UNP Q45087
C	-16	ALA	-	EXPRESSION TAG	UNP Q45087
C	-15	GLU	-	EXPRESSION TAG	UNP Q45087
C	-14	THR	-	EXPRESSION TAG	UNP Q45087
C	-13	ALA	-	EXPRESSION TAG	UNP Q45087
C	-12	VAL	-	EXPRESSION TAG	UNP Q45087
C	-11	PRO	-	EXPRESSION TAG	UNP Q45087
C	-10	ASN	-	EXPRESSION TAG	UNP Q45087
C	-9	SER	-	EXPRESSION TAG	UNP Q45087
C	-8	SER	-	EXPRESSION TAG	UNP Q45087
C	-7	SER	-	EXPRESSION TAG	UNP Q45087
C	-6	VAL	-	EXPRESSION TAG	UNP Q45087
C	-5	PRO	-	EXPRESSION TAG	UNP Q45087
C	-4	GLY	-	EXPRESSION TAG	UNP Q45087
C	-3	ASP	-	EXPRESSION TAG	UNP Q45087
C	-2	PRO	-	EXPRESSION TAG	UNP Q45087
C	-1	SER	-	EXPRESSION TAG	UNP Q45087
C	0	SER	-	EXPRESSION TAG	UNP Q45087
C	57	FGL	CYS	MICROHETEROGENEITY	UNP Q45087
D	-28	MET	-	EXPRESSION TAG	UNP Q45087
D	-27	ALA	-	EXPRESSION TAG	UNP Q45087
D	-26	SER	-	EXPRESSION TAG	UNP Q45087
D	-25	TRP	-	EXPRESSION TAG	UNP Q45087
D	-24	SER	-	EXPRESSION TAG	UNP Q45087
D	-23	HIS	-	EXPRESSION TAG	UNP Q45087
D	-22	PRO	-	EXPRESSION TAG	UNP Q45087
D	-21	GLN	-	EXPRESSION TAG	UNP Q45087
D	-20	PHE	-	EXPRESSION TAG	UNP Q45087
D	-19	GLU	-	EXPRESSION TAG	UNP Q45087
D	-18	LYS	-	EXPRESSION TAG	UNP Q45087
D	-17	GLY	-	EXPRESSION TAG	UNP Q45087
D	-16	ALA	-	EXPRESSION TAG	UNP Q45087
D	-15	GLU	-	EXPRESSION TAG	UNP Q45087
D	-14	THR	-	EXPRESSION TAG	UNP Q45087

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-13	ALA	-	EXPRESSION TAG	UNP Q45087
D	-12	VAL	-	EXPRESSION TAG	UNP Q45087
D	-11	PRO	-	EXPRESSION TAG	UNP Q45087
D	-10	ASN	-	EXPRESSION TAG	UNP Q45087
D	-9	SER	-	EXPRESSION TAG	UNP Q45087
D	-8	SER	-	EXPRESSION TAG	UNP Q45087
D	-7	SER	-	EXPRESSION TAG	UNP Q45087
D	-6	VAL	-	EXPRESSION TAG	UNP Q45087
D	-5	PRO	-	EXPRESSION TAG	UNP Q45087
D	-4	GLY	-	EXPRESSION TAG	UNP Q45087
D	-3	ASP	-	EXPRESSION TAG	UNP Q45087
D	-2	PRO	-	EXPRESSION TAG	UNP Q45087
D	-1	SER	-	EXPRESSION TAG	UNP Q45087
D	0	SER	-	EXPRESSION TAG	UNP Q45087
D	57	FGL	CYS	MICROHETEROGENEITY	UNP Q45087

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0

- Molecule 3 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Fe 1 1	0	0
3	A	1	Total Fe 1 1	0	0
3	D	1	Total Fe 1 1	0	0
3	C	1	Total Fe 1 1	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

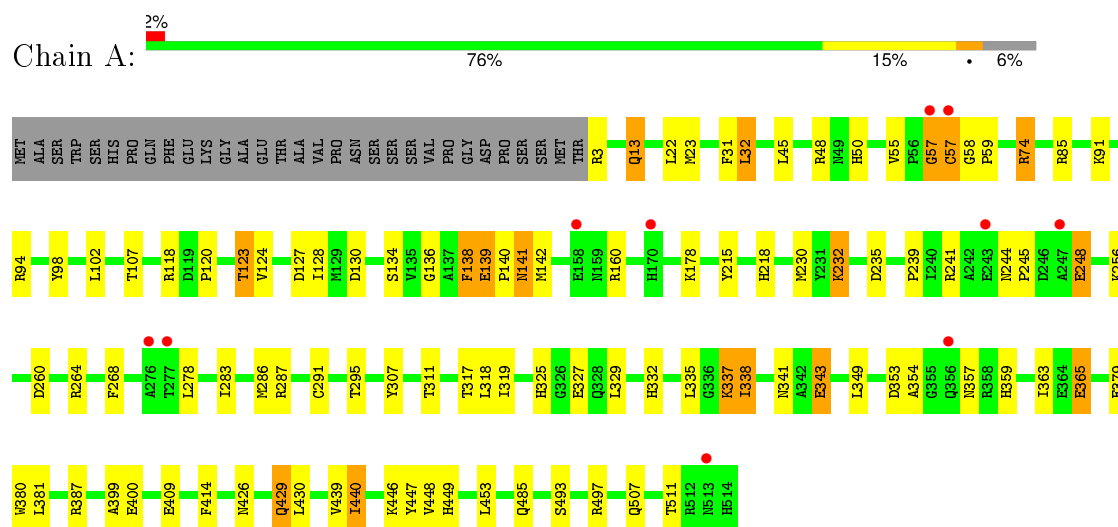
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	158	Total	O	0	0
			158	158		
6	B	204	Total	O	0	0
			204	204		
6	C	249	Total	O	0	0
			249	249		
6	D	207	Total	O	0	0
			207	207		

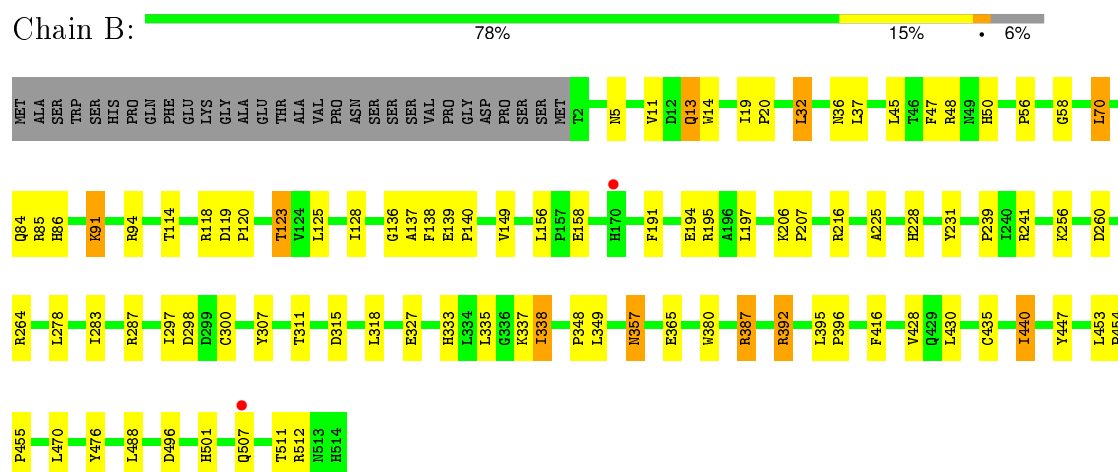
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: PHOSPHONATE MONOESTER HYDROLASE

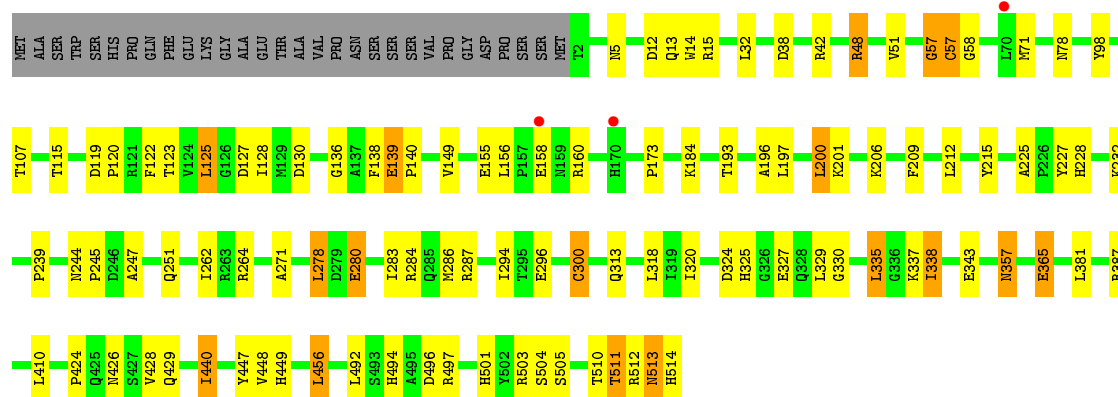


• Molecule 1: PHOSPHONATE MONOESTER HYDROLASE

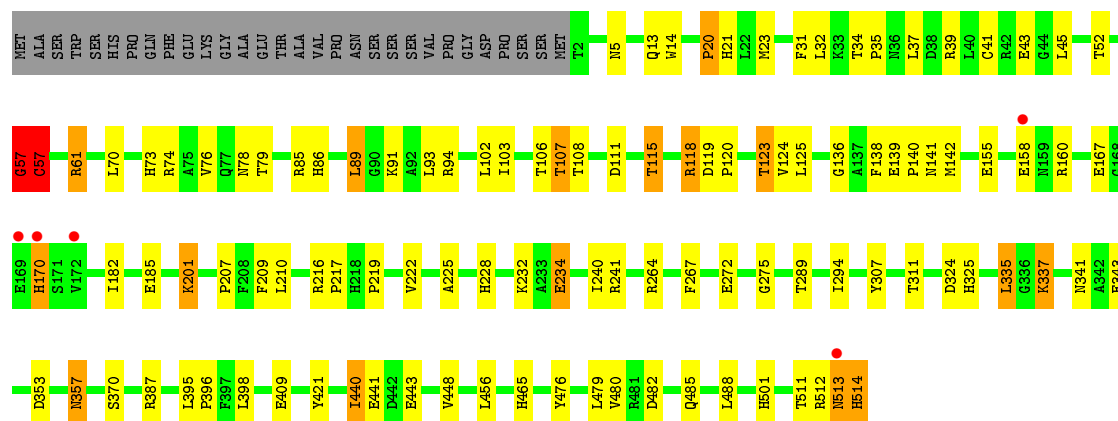
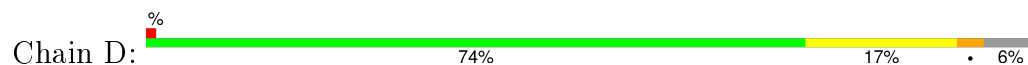


• Molecule 1: PHOSPHONATE MONOESTER HYDROLASE





● Molecule 1: PHOSPHONATE MONOESTER HYDROLASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.70Å 200.10Å 211.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.62 – 2.40 48.68 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.9 (48.62-2.40) 98.9 (48.68-2.40)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0070	Depositor
R, R_{free}	0.182 , 0.239 0.192 , 0.244	Depositor DCC
R_{free} test set	4887 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	34.6	Xtriage
Anisotropy	0.213	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 37.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 95959 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17251	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FGL, GOL, ZN, FE, SO4

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	0.80	1/4184 (0.0%)	0.77	2/5687 (0.0%)
1	B	0.77	1/4206 (0.0%)	0.79	0/5715
1	C	0.77	1/4223 (0.0%)	0.82	2/5737 (0.0%)
1	D	0.75	0/4198	0.81	1/5706 (0.0%)
All	All	0.77	3/16811 (0.0%)	0.80	5/22845 (0.0%)

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	1	0
1	D	0	1
All	All	1	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	57[B]	CYS	C-N	26.90	1.81	1.33
1	B	300	CYS	CB-SG	-5.62	1.72	1.81
1	C	300	CYS	CB-SG	-5.33	1.73	1.81

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	57[B]	CYS	O-C-N	-7.29	110.81	123.20
1	C	287	ARG	NE-CZ-NH2	-5.87	117.36	120.30
1	C	57[B]	CYS	O-C-N	-5.36	114.10	123.20
1	A	74	ARG	NE-CZ-NH1	5.26	122.93	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	57[B]	CYS	O-C-N	-5.20	114.37	123.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	169	GLU	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	57[A]	FGL	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	4074	0	3873	74	0
1	B	4096	0	3898	56	0
1	C	4109	0	3917	60	0
1	D	4087	0	3885	72	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
4	C	15	0	0	0	0
4	D	10	0	0	0	0
5	D	24	0	32	3	0
6	A	158	0	0	5	0
6	B	204	0	0	6	0
6	C	249	0	0	2	0
6	D	207	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	17251	0	15605	248	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 8.

All (248) 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:57[A]:FGL:C	1:A:58:GLY:N	1.72	1.52
1:C:57[A]:FGL:C	1:C:58:GLY:N	1.72	1.46
1:D:409:GLU:HG2	1:D:440:ILE:HD11	1.45	0.99
1:D:139:GLU:HB3	1:D:140:PRO:HD2	1.59	0.85
1:A:120:PRO:O	1:A:123:THR:HB	1.79	0.80
1:B:139:GLU:HB3	1:B:140:PRO:HD2	1.71	0.73
1:B:239:PRO:HG3	1:B:283:ILE:HG21	1.71	0.72
1:A:141:ASN:HD22	1:C:206:LYS:NZ	1.88	0.72
1:B:440:ILE:HG22	1:B:447:TYR:HB3	1.73	0.70
1:D:23:MET:CE	1:D:31:PHE:CE2	2.75	0.70
1:A:57[A]:FGL:C	1:A:58:GLY:CA	2.70	0.69
1:D:23:MET:HE2	1:D:31:PHE:CE2	2.28	0.69
1:B:392:ARG:HD2	6:B:2153:HOH:O	1.94	0.67
1:D:170:HIS:ND1	1:D:170:HIS:N	2.41	0.67
1:A:268:PHE:CZ	1:A:286:MET:HE2	2.30	0.67
1:D:139:GLU:HB3	1:D:140:PRO:CD	2.25	0.66
1:B:256:LYS:NZ	1:B:260:ASP:OD2	2.28	0.66
1:A:354:ALA:HB1	6:A:2091:HOH:O	1.96	0.64
1:A:429:GLN:HA	1:A:429:GLN:HE21	1.62	0.64
1:B:120:PRO:O	1:B:123:THR:HB	1.96	0.64
1:C:139:GLU:HB3	1:C:140:PRO:HD2	1.80	0.64
1:A:400:GLU:CD	1:A:400:GLU:H	2.02	0.62
1:D:513:ASN:HD22	1:D:514:HIS:N	1.98	0.61
1:B:149:VAL:HG11	1:B:156:LEU:HD21	1.82	0.61
1:A:32:LEU:HD23	1:A:291:CYS:SG	2.40	0.61
1:D:118:ARG:NH1	6:D:2057:HOH:O	2.34	0.60
1:A:268:PHE:CZ	1:A:286:MET:CE	2.84	0.60
1:C:120:PRO:O	1:C:123:THR:HB	2.02	0.60
1:A:440:ILE:HG22	1:A:447:TYR:HB3	1.84	0.60
1:A:409:GLU:HG2	1:A:440:ILE:HD11	1.85	0.59
1:D:61:ARG:HD3	1:D:106:THR:HA	1.85	0.59
1:C:51:VAL:HG22	1:C:410:LEU:HD22	1.84	0.59
1:D:240:ILE:HD13	1:D:465:HIS:CD2	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:387:ARG:HG2	1:B:501:HIS:CD2	2.38	0.58
1:A:127:ASP:OD1	1:A:128:ILE:HG22	2.03	0.58
1:A:215:TYR:O	1:A:218:HIS:HB2	2.03	0.58
1:A:32:LEU:HD23	1:A:291:CYS:CB	2.33	0.58
1:D:234:GLU:CD	1:D:234:GLU:H	2.06	0.58
1:C:15:ARG:HD2	1:C:327:GLU:O	2.04	0.58
1:C:14:TRP:CH2	1:C:294:ILE:HG23	2.39	0.58
1:A:107:THR:O	1:A:107:THR:HG22	2.02	0.57
1:B:119:ASP:OD2	1:D:94:ARG:HD3	2.04	0.57
1:D:23:MET:HE2	1:D:31:PHE:HE2	1.68	0.57
1:D:108:THR:HG21	5:D:1522:GOL:H11	1.87	0.57
1:A:139:GLU:HG3	1:A:140:PRO:CD	2.34	0.57
1:D:23:MET:HE1	1:D:31:PHE:CE2	2.39	0.57
1:C:262:ILE:HD13	1:C:335:LEU:O	2.05	0.57
1:B:70:LEU:C	1:B:70:LEU:HD23	2.25	0.56
1:C:448:VAL:HB	1:C:456:LEU:HB2	1.88	0.56
1:D:225:ALA:HA	1:D:228:HIS:HD2	1.71	0.56
1:C:78:ASN:HB3	1:C:125:LEU:HD13	1.87	0.56
1:A:22:LEU:HD23	1:A:363:ILE:HD13	1.88	0.56
1:A:23:MET:CE	1:A:31:PHE:CE2	2.88	0.56
1:D:357:ASN:HD22	1:D:357:ASN:N	2.03	0.56
1:B:428:VAL:CG1	1:B:453:LEU:HD11	2.36	0.56
1:B:139:GLU:HB3	1:B:140:PRO:CD	2.35	0.55
1:C:440:ILE:HG22	1:C:447:TYR:HB3	1.89	0.55
1:A:23:MET:HE2	1:A:31:PHE:CE2	2.42	0.55
1:A:268:PHE:HZ	1:A:286:MET:CE	2.19	0.55
1:A:94:ARG:HD3	1:C:119:ASP:OD2	2.07	0.55
1:A:98:TYR:CZ	1:A:381:LEU:HD22	2.41	0.55
1:C:511:THR:O	1:C:511:THR:HG22	2.07	0.55
1:D:14:TRP:CH2	1:D:294:ILE:HG23	2.41	0.55
1:C:57[A]:FGL:C	1:C:58:GLY:CA	2.79	0.54
1:B:318:LEU:HD22	1:B:380:TRP:CD2	2.43	0.54
1:A:439:VAL:HG11	1:A:446:LYS:HE3	1.90	0.54
1:C:38:ASP:O	1:C:42[B]:ARG:HG3	2.08	0.54
1:B:50:HIS:CE1	1:B:349:LEU:HD22	2.43	0.54
1:C:338:ILE:N	1:C:338:ILE:HD13	2.23	0.53
1:B:137:ALA:HB3	1:B:139:GLU:HG2	1.89	0.53
1:B:216:ARG:HB2	1:B:297:ILE:HD11	1.90	0.53
1:C:511:THR:O	1:C:511:THR:CG2	2.54	0.53
1:A:307:TYR:CZ	1:A:311:THR:HG21	2.44	0.53
1:D:240:ILE:HD13	1:D:465:HIS:NE2	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:283:ILE:HD13	1:C:330:GLY:HA3	1.90	0.53
1:D:216:ARG:HB3	1:D:217:PRO:HA	1.89	0.53
1:B:206:LYS:NZ	1:D:141:ASN:ND2	2.57	0.53
1:A:230:MET:SD	1:A:295:THR:HG21	2.49	0.53
1:A:440:ILE:O	1:A:440:ILE:CG2	2.57	0.53
1:B:395:LEU:N	1:B:396:PRO:CD	2.73	0.52
1:C:107:THR:HG22	1:C:107:THR:O	2.08	0.52
1:B:318:LEU:HD22	1:B:380:TRP:CG	2.45	0.52
1:C:48:ARG:HD3	1:C:365:GLU:OE1	2.09	0.52
1:B:338:ILE:N	1:B:338:ILE:HD13	2.25	0.51
1:A:359:HIS:NE2	1:A:399:ALA:O	2.33	0.51
1:D:5:ASN:OD1	1:D:207:PRO:HA	2.11	0.51
1:C:71:MET:HE2	1:C:494:HIS:O	2.10	0.51
1:B:11:VAL:HG21	1:B:14:TRP:CE3	2.45	0.51
1:A:48:ARG:HD3	1:A:365:GLU:OE1	2.11	0.51
1:D:125:LEU:HD11	1:D:421:TYR:CE2	2.45	0.51
1:B:118:ARG:HD2	6:B:2051:HOH:O	2.09	0.51
1:A:268:PHE:HZ	1:A:286:MET:HE3	1.75	0.51
1:D:111:ASP:O	1:D:115:THR:CG2	2.59	0.51
1:B:94:ARG:HD3	1:D:119:ASP:OD2	2.11	0.51
1:A:325:HIS:CE1	1:A:337:LYS:HD2	2.46	0.51
1:C:503:ARG:HB2	1:C:510:THR:CG2	2.41	0.50
1:C:280:GLU:HG3	1:C:284:ARG:HH11	1.76	0.50
1:A:138:PHE:O	1:A:142:MET:HA	2.11	0.50
1:C:357:ASN:N	1:C:357:ASN:HD22	2.10	0.50
1:B:19:ILE:HD12	1:B:37:LEU:HD21	1.93	0.50
1:C:513:ASN:HD22	1:C:514:HIS:HB3	1.77	0.50
1:D:264:ARG:HD2	1:D:272:GLU:O	2.11	0.50
1:C:196:ALA:HB2	1:C:212:LEU:HD13	1.94	0.50
1:C:280:GLU:HG3	1:C:284:ARG:NH1	2.26	0.49
1:A:13:GLN:HG2	1:A:327:GLU:HB2	1.93	0.49
1:C:123:THR:O	1:C:123:THR:CG2	2.61	0.49
1:A:239:PRO:HG3	1:A:283:ILE:HG21	1.94	0.49
1:D:107:THR:O	1:D:107:THR:HG22	2.12	0.49
1:A:139:GLU:HG3	1:A:140:PRO:HD3	1.93	0.49
1:D:275:GLY:HA3	1:D:335:LEU:HD22	1.94	0.49
1:A:3:ARG:HA	6:A:2002:HOH:O	2.12	0.49
1:B:194:GLU:HB2	6:B:2077:HOH:O	2.13	0.49
1:A:141:ASN:ND2	1:C:206:LYS:NZ	2.59	0.49
1:D:103:ILE:HD12	1:D:210:LEU:HD11	1.95	0.49
1:A:50:HIS:CE1	1:A:349:LEU:HD22	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:428:VAL:HG13	1:B:453:LEU:HD11	1.95	0.48
1:C:239:PRO:HG3	1:C:283:ILE:HG21	1.93	0.48
1:A:256:LYS:NZ	1:A:260:ASP:OD2	2.32	0.48
1:B:128:ILE:HG23	1:B:128:ILE:O	2.12	0.48
1:A:178:LYS:NZ	6:A:2062:HOH:O	2.42	0.48
1:C:156:LEU:HD13	1:C:160:ARG:HG2	1.94	0.48
1:D:39:ARG:O	1:D:43:GLU:HG3	2.13	0.48
1:D:140:PRO:O	1:D:141:ASN:HB2	2.13	0.48
1:A:353:ASP:OD1	1:A:354:ALA:N	2.46	0.48
1:D:222:VAL:HB	6:D:2092:HOH:O	2.13	0.48
1:C:496:ASP:HB3	1:D:74:ARG:HG3	1.95	0.48
1:D:440:ILE:C	1:D:440:ILE:HD13	2.34	0.48
1:A:23:MET:HE1	1:A:31:PHE:CE2	2.49	0.48
1:B:91:LYS:NZ	6:B:2039:HOH:O	2.43	0.48
1:A:449:HIS:CG	1:B:488:LEU:HD23	2.48	0.48
1:A:264:ARG:CZ	1:A:278:LEU:HD23	2.44	0.48
1:C:209:PHE:C	1:C:209:PHE:CD2	2.87	0.48
1:B:137:ALA:CB	1:B:139:GLU:HG2	2.44	0.47
1:B:47:PHE:HB2	1:B:349:LEU:HB3	1.96	0.47
1:D:78:ASN:C	1:D:79:THR:HG23	2.34	0.47
1:C:12:ASP:HB3	1:C:215:TYR:O	2.14	0.47
1:D:70:LEU:HD11	1:D:76:VAL:HA	1.96	0.47
1:C:504:SER:HB3	1:D:79:THR:HB	1.97	0.47
1:C:264:ARG:CZ	1:C:278:LEU:HD13	2.45	0.47
1:D:73:HIS:HA	1:D:86:HIS:CE1	2.50	0.47
1:C:193:THR:OG1	1:C:300:CYS:HB3	2.15	0.47
1:A:48:ARG:CD	1:A:365:GLU:OE1	2.63	0.47
1:B:86:HIS:HD2	6:B:2035:HOH:O	1.98	0.47
1:D:141:ASN:O	1:D:142:MET:HB2	2.15	0.46
1:A:55:VAL:HG23	1:A:414:PHE:CD2	2.50	0.46
1:A:127:ASP:OD1	1:A:128:ILE:N	2.48	0.46
1:D:324:ASP:CG	1:D:325:HIS:CD2	2.88	0.46
1:B:36:ASN:ND2	1:B:298:ASP:O	2.47	0.46
1:B:357:ASN:N	1:B:357:ASN:HD22	2.13	0.46
1:C:504:SER:OG	1:D:124:VAL:O	2.33	0.46
1:D:209:PHE:C	1:D:209:PHE:CD2	2.88	0.46
1:A:283:ILE:O	1:A:287:ARG:HG3	2.15	0.46
1:C:503:ARG:HB2	1:C:510:THR:HG22	1.96	0.46
1:C:449:HIS:CG	1:D:488:LEU:HD23	2.51	0.46
1:D:482:ASP:HA	1:D:485:GLN:HE21	1.80	0.46
1:C:98:TYR:CZ	1:C:381:LEU:HD22	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:307:TYR:CZ	1:D:311:THR:HG21	2.50	0.46
1:A:439:VAL:HG22	1:A:448:VAL:HG22	1.97	0.46
1:A:118:ARG:HD2	6:A:2040:HOH:O	2.16	0.46
1:D:111:ASP:O	1:D:115:THR:HG23	2.15	0.46
1:A:58:GLY:N	1:A:59:PRO:CD	2.79	0.45
1:B:225:ALA:HA	1:B:228:HIS:HD2	1.81	0.45
1:C:244:ASN:ND2	1:C:247:ALA:H	2.14	0.45
1:D:232:LYS:HB3	1:D:234:GLU:OE2	2.16	0.45
1:A:318:LEU:HB2	1:A:380:TRP:CZ2	2.51	0.45
1:C:227:TYR:CE2	1:C:296:GLU:HG3	2.52	0.45
1:A:400:GLU:CD	1:A:400:GLU:N	2.70	0.45
1:A:341:ASN:HB3	1:A:343:GLU:OE1	2.16	0.45
1:D:108:THR:CG2	5:D:1522:GOL:H11	2.47	0.45
1:C:201:LYS:NZ	6:C:2106:HOH:O	2.38	0.45
1:D:448:VAL:HB	1:D:456:LEU:HB2	1.98	0.45
1:B:315:ASP:HA	6:B:2138:HOH:O	2.17	0.45
1:B:191:PHE:O	1:B:195:ARG:HG2	2.17	0.45
1:B:283:ILE:O	1:B:287:ARG:HG3	2.17	0.45
1:A:430:LEU:HD11	1:A:453:LEU:HG	1.98	0.45
1:B:206:LYS:NZ	1:D:141:ASN:HD21	2.14	0.44
1:B:428:VAL:HG11	1:B:453:LEU:HD11	1.98	0.44
1:D:219:PRO:HB2	6:D:2112:HOH:O	2.18	0.44
1:A:55:VAL:HG23	1:A:414:PHE:CE2	2.52	0.44
1:A:409:GLU:HG2	1:A:440:ILE:CD1	2.46	0.44
1:C:149:VAL:HG11	1:C:156:LEU:HD21	1.99	0.44
1:A:440:ILE:O	1:A:440:ILE:HG23	2.18	0.44
1:B:32:LEU:HA	1:B:231:TYR:CE1	2.53	0.44
1:D:201:LYS:NZ	5:D:1519:GOL:O2	2.51	0.44
1:C:318:LEU:HD21	1:C:320:ILE:HD11	2.00	0.44
1:A:232:LYS:HD3	1:A:235:ASP:OD2	2.17	0.44
1:C:324:ASP:CG	1:C:325:HIS:CD2	2.91	0.44
1:B:470:LEU:HD13	1:B:476:TYR:CZ	2.52	0.44
1:A:248:GLU:OE2	1:A:332:HIS:ND1	2.37	0.44
1:D:395:LEU:N	1:D:396:PRO:CD	2.81	0.43
1:C:196:ALA:O	1:C:200:LEU:HD22	2.18	0.43
1:C:173:PRO:HB2	1:C:271:ALA:HA	2.01	0.43
1:B:416:PHE:CD1	1:B:435:CYS:HB3	2.54	0.43
1:C:505:SER:O	1:D:123:THR:HA	2.19	0.43
1:D:409:GLU:CG	1:D:440:ILE:HD11	2.33	0.43
1:A:128:ILE:HD13	1:A:134:SER:HB2	2.00	0.43
1:B:440:ILE:CG2	1:B:447:TYR:HB3	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:ARG:HG2	1:A:329:LEU:HG	2.01	0.43
1:B:470:LEU:HD13	1:B:476:TYR:CE1	2.54	0.43
1:A:338:ILE:N	1:A:338:ILE:HD13	2.34	0.43
1:B:454:PRO:HA	1:B:455:PRO:HD3	1.88	0.43
1:C:225:ALA:HA	1:C:228:HIS:CD2	2.53	0.43
1:D:219:PRO:HG3	1:D:267:PHE:CD1	2.54	0.42
1:D:185:GLU:CD	1:D:185:GLU:H	2.23	0.42
1:D:479:LEU:HA	1:D:479:LEU:HD23	1.86	0.42
1:D:353:ASP:HB2	1:D:398:LEU:HD13	2.01	0.42
1:A:232:LYS:HD2	1:A:235:ASP:HB2	2.01	0.42
1:D:120:PRO:O	1:D:123:THR:HB	2.20	0.42
1:A:485:GLN:NE2	6:A:2144:HOH:O	2.52	0.42
1:A:102:LEU:HD22	1:A:128:ILE:CD1	2.49	0.42
1:C:115:THR:HG23	1:C:122:PHE:CE2	2.55	0.42
1:B:428:VAL:HG12	1:B:430:LEU:HG	2.01	0.42
1:C:501:HIS:CD2	1:C:501:HIS:H	2.37	0.42
1:A:139:GLU:HG3	1:A:140:PRO:HD2	2.01	0.42
1:D:225:ALA:HA	1:D:228:HIS:CD2	2.51	0.42
1:C:329:LEU:HA	1:C:329:LEU:HD12	1.88	0.42
1:C:5:ASN:HD21	1:C:313:GLN:HE21	1.67	0.42
1:D:325:HIS:CE1	1:D:337:LYS:HD2	2.54	0.42
1:D:341:ASN:HB3	1:D:343:GLU:OE1	2.19	0.42
1:B:84:GLN:CD	1:B:114:THR:HG21	2.40	0.42
1:B:241:ARG:HB2	1:B:333:HIS:CE1	2.54	0.42
1:A:32:LEU:HD23	1:A:291:CYS:HB3	2.01	0.42
1:C:283:ILE:HG23	1:C:286:MET:HE2	2.00	0.42
1:D:21:HIS:CG	1:D:41:CYS:HB3	2.55	0.41
1:D:501:HIS:CD2	1:D:501:HIS:H	2.37	0.41
1:B:13:GLN:HG3	1:B:327:GLU:HB2	2.02	0.41
1:C:424:PRO:O	1:C:428:VAL:HG22	2.21	0.41
1:D:89:LEU:HD22	1:D:93:LEU:CD1	2.51	0.41
1:A:337:LYS:HG2	1:A:337:LYS:O	2.21	0.41
1:A:317:THR:HG22	1:A:319:ILE:HG12	2.03	0.41
1:B:20:PRO:HG3	1:B:32:LEU:HD13	2.02	0.41
1:A:244:ASN:HB2	1:A:245:PRO:HD2	2.03	0.41
1:D:141:ASN:O	1:D:142:MET:CB	2.68	0.41
1:A:74:ARG:HG3	1:B:496:ASP:HB3	2.03	0.41
1:D:52:THR:HA	1:D:370:SER:HB3	2.02	0.41
1:B:128:ILE:CG2	1:B:128:ILE:O	2.69	0.41
1:D:387:ARG:CZ	1:D:501:HIS:HB3	2.51	0.41
1:B:307:TYR:CZ	1:B:311:THR:HG21	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:127:ASP:OD1	1:C:128:ILE:N	2.47	0.41
1:C:426:ASN:O	1:C:429:GLN:NE2	2.54	0.41
1:D:102:LEU:C	1:D:102:LEU:HD23	2.42	0.41
1:D:476:TYR:O	1:D:480:VAL:HG23	2.21	0.41
1:A:123:THR:HG22	1:A:124:VAL:HG13	2.03	0.40
1:D:20:PRO:HG2	1:D:34:THR:OG1	2.21	0.40
1:A:318:LEU:HB2	1:A:380:TRP:CH2	2.57	0.40
1:B:5:ASN:OD1	1:B:207:PRO:HA	2.21	0.40
1:C:251:GLN:HG3	6:C:2218:HOH:O	2.22	0.40
1:B:264:ARG:CZ	1:B:278:LEU:HD23	2.52	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	509/544 (94%)	485 (95%)	22 (4%)	2 (0%)	39	56
1	B	510/544 (94%)	495 (97%)	12 (2%)	3 (1%)	30	43
1	C	511/544 (94%)	490 (96%)	19 (4%)	2 (0%)	39	56
1	D	510/544 (94%)	490 (96%)	19 (4%)	1 (0%)	52	69
All	All	2040/2176 (94%)	1960 (96%)	72 (4%)	8 (0%)	39	56

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	58	GLY
1	A	136	GLY
1	B	56	PRO
1	B	136	GLY
1	A	139	GLU

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Mol	Chain	Res	Type
1	D	136	GLY
1	C	136	GLY
1	C	139	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	426/458 (93%)	398 (93%)	28 (7%)	21	32
1	B	430/458 (94%)	406 (94%)	24 (6%)	26	41
1	C	432/458 (94%)	403 (93%)	29 (7%)	20	31
1	D	428/458 (93%)	392 (92%)	36 (8%)	14	20
All	All	1716/1832 (94%)	1599 (93%)	117 (7%)	20	31

All (117) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	32	LEU
1	A	45	LEU
1	A	85	ARG
1	A	91	LYS
1	A	123	THR
1	A	130	ASP
1	A	138	PHE
1	A	141	ASN
1	A	160	ARG
1	A	232	LYS
1	A	241	ARG
1	A	248	GLU
1	A	335	LEU
1	A	337	LYS
1	A	338	ILE
1	A	343	GLU
1	A	357	ASN

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Mol	Chain	Res	Type
1	A	365	GLU
1	A	379	GLU
1	A	387	ARG
1	A	426	ASN
1	A	429	GLN
1	A	440	ILE
1	A	493	SER
1	A	497	ARG
1	A	507	GLN
1	A	511	THR
1	B	13	GLN
1	B	32	LEU
1	B	45	LEU
1	B	48	ARG
1	B	70	LEU
1	B	85	ARG
1	B	91	LYS
1	B	123	THR
1	B	125	LEU
1	B	138	PHE
1	B	158	GLU
1	B	197	LEU
1	B	335	LEU
1	B	337	LYS
1	B	338	ILE
1	B	348	PRO
1	B	357	ASN
1	B	365	GLU
1	B	387	ARG
1	B	392	ARG
1	B	440	ILE
1	B	507	GLN
1	B	511	THR
1	B	512	ARG
1	C	13	GLN
1	C	32	LEU
1	C	48	ARG
1	C	125	LEU
1	C	130	ASP
1	C	138	PHE
1	C	155	GLU
1	C	158	GLU

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Mol	Chain	Res	Type
1	C	184	LYS
1	C	197	LEU
1	C	200	LEU
1	C	232	LYS
1	C	245	PRO
1	C	278	LEU
1	C	280	GLU
1	C	335	LEU
1	C	337	LYS
1	C	338	ILE
1	C	343	GLU
1	C	357	ASN
1	C	365	GLU
1	C	387	ARG
1	C	440	ILE
1	C	456	LEU
1	C	492	LEU
1	C	497	ARG
1	C	511	THR
1	C	512	ARG
1	C	513	ASN
1	D	13	GLN
1	D	20	PRO
1	D	32	LEU
1	D	35	PRO
1	D	37	LEU
1	D	45	LEU
1	D	57[B]	CYS
1	D	61	ARG
1	D	85	ARG
1	D	89	LEU
1	D	91	LYS
1	D	107	THR
1	D	115	THR
1	D	118	ARG
1	D	123	THR
1	D	138	PHE
1	D	155	GLU
1	D	158	GLU
1	D	160	ARG
1	D	167	GLU
1	D	170	HIS

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Mol	Chain	Res	Type
1	D	182	ILE
1	D	201	LYS
1	D	234	GLU
1	D	241	ARG
1	D	289	THR
1	D	335	LEU
1	D	337	LYS
1	D	357	ASN
1	D	440	ILE
1	D	441	GLU
1	D	443	GLU
1	D	511	THR
1	D	512	ARG
1	D	513	ASN
1	D	514	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	86	HIS
1	A	141	ASN
1	A	159	ASN
1	A	228	HIS
1	A	426	ASN
1	A	429	GLN
1	A	485	GLN
1	A	501	HIS
1	A	507	GLN
1	B	84	GLN
1	B	86	HIS
1	B	313	GLN
1	B	501	HIS
1	B	507	GLN
1	C	86	HIS
1	C	228	HIS
1	C	244	ASN
1	C	313	GLN
1	C	429	GLN
1	C	501	HIS
1	C	513	ASN
1	D	84	GLN
1	D	86	HIS

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Mol	Chain	Res	Type
1	D	141	ASN
1	D	313	GLN
1	D	485	GLN
1	D	501	HIS
1	D	513	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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
1	FGL	A	57[A]	-	2,6,7	0.92	0	1,7,9	0.16	0
1	FGL	B	57[A]	-	2,6,7	0.89	0	1,7,9	0.18	0
1	FGL	C	57[A]	-	2,6,7	0.89	0	1,7,9	0.19	0
1	FGL	D	57[A]	-	2,6,7	0.91	0	1,7,9	0.17	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	FGL	A	57[A]	-	-	0/0/6/8	0/0/0/0
1	FGL	B	57[A]	-	-	0/0/6/8	0/0/0/0
1	FGL	C	57[A]	-	-	0/0/6/8	0/0/0/0
1	FGL	D	57[A]	-	-	0/0/6/8	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	57[A]	FGL	2	0
1	C	57[A]	FGL	2	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 8 are monoatomic - leaving 11 for Mogul analysis.

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	$\# Z > 2$
4	SO4	A	1517	-	4,4,4	0.20	0	6,6,6	0.54	0
4	SO4	B	1517	-	4,4,4	0.26	0	6,6,6	0.27	0
4	SO4	C	1517	-	4,4,4	0.41	0	6,6,6	0.39	0
4	SO4	C	1518	-	4,4,4	0.16	0	6,6,6	0.23	0
4	SO4	C	1519	-	4,4,4	0.12	0	6,6,6	0.09	0
4	SO4	D	1517	-	4,4,4	0.44	0	6,6,6	0.57	0
4	SO4	D	1518	-	4,4,4	0.22	0	6,6,6	0.14	0
5	GOL	D	1519	-	5,5,5	0.62	0	5,5,5	0.47	0
5	GOL	D	1520	-	5,5,5	0.82	0	5,5,5	0.43	0
5	GOL	D	1521	-	5,5,5	0.47	0	5,5,5	0.72	0
5	GOL	D	1522	-	5,5,5	0.75	0	5,5,5	0.82	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SO4	A	1517	-	-	0/0/0/0	0/0/0/0
4	SO4	B	1517	-	-	0/0/0/0	0/0/0/0
4	SO4	C	1517	-	-	0/0/0/0	0/0/0/0
4	SO4	C	1518	-	-	0/0/0/0	0/0/0/0
4	SO4	C	1519	-	-	0/0/0/0	0/0/0/0
4	SO4	D	1517	-	-	0/0/0/0	0/0/0/0
4	SO4	D	1518	-	-	0/0/0/0	0/0/0/0
5	GOL	D	1519	-	-	0/4/4/4	0/0/0/0
5	GOL	D	1520	-	-	0/4/4/4	0/0/0/0
5	GOL	D	1521	-	-	0/4/4/4	0/0/0/0
5	GOL	D	1522	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	1519	GOL	1	0
5	D	1522	GOL	2	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	511/544 (93%)	-0.13	8 (1%) 74 74	13, 26, 41, 52	0
1	B	512/544 (94%)	-0.39	2 (0%) 93 93	14, 25, 38, 56	0
1	C	512/544 (94%)	-0.33	3 (0%) 90 90	14, 24, 35, 48	0
1	D	512/544 (94%)	-0.37	5 (0%) 84 83	11, 24, 36, 53	0
All	All	2047/2176 (94%)	-0.31	18 (0%) 85 85	11, 25, 39, 56	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	172	VAL	3.1
1	D	170	HIS	3.0
1	A	170	HIS	2.8
1	A	277	THR	2.8
1	D	169	GLU	2.8
1	A	243	GLU	2.7
1	B	170	HIS	2.5
1	D	513	ASN	2.5
1	C	170	HIS	2.4
1	A	247	ALA	2.3
1	C	158	GLU	2.2
1	D	158	GLU	2.2
1	A	276	ALA	2.2
1	A	513	ASN	2.2
1	B	507	GLN	2.2
1	C	70	LEU	2.2
1	A	356	GLN	2.1
1	A	158	GLU	2.1

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
1	FGL	D	57[A]	7/8	0.91	0.21	-	27,28,28,28	7
1	FGL	C	57[A]	7/8	0.93	0.23	-	35,35,36,36	7
1	FGL	B	57[A]	7/8	0.91	0.19	-	39,39,39,40	7
1	FGL	A	57[A]	7/8	0.87	0.29	-	31,32,32,32	7

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	GOL	D	1522	6/6	0.91	0.19	2.52	44,48,49,49	0
5	GOL	D	1521	6/6	0.94	0.19	1.83	42,45,47,50	0
5	GOL	D	1519	6/6	0.82	0.17	1.50	47,50,52,52	0
4	SO4	D	1517	5/5	0.95	0.14	0.25	52,55,57,59	0
4	SO4	C	1517	5/5	0.96	0.13	-0.56	53,54,55,56	0
4	SO4	B	1517	5/5	0.96	0.09	-1.85	49,49,51,52	0
3	FE	B	1516	1/1	0.99	0.11	-2.01	29,29,29,29	1
2	ZN	B	1515	1/1	0.99	0.11	-2.01	30,30,30,30	1
2	ZN	D	1515	1/1	0.98	0.10	-2.29	28,28,28,28	1
3	FE	D	1516	1/1	0.98	0.10	-2.29	28,28,28,28	1
3	FE	C	1516	1/1	0.99	0.10	-2.78	19,19,19,19	1
2	ZN	C	1515	1/1	0.99	0.10	-2.78	20,20,20,20	1
2	ZN	A	1515	1/1	0.99	0.03	-4.14	28,28,28,28	1
3	FE	A	1516	1/1	0.99	0.03	-4.14	27,27,27,27	1
4	SO4	C	1519	5/5	0.92	0.24	-	90,91,91,91	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	SO4	A	1517	5/5	0.96	0.08	-	73,73,74,76	0
4	SO4	C	1518	5/5	0.94	0.15	-	73,73,74,74	0
5	GOL	D	1520	6/6	0.91	0.12	-	53,53,54,54	0
4	SO4	D	1518	5/5	0.97	0.12	-	70,72,73,73	0

6.5 Other polymers [i](#)

There are no such residues in this entry.