



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 09:25 PM GMT

PDB ID : 2OOG
Title : Crystal structure of glycerophosphoryl diester phosphodiesterase from *Staphylococcus aureus*
Authors : Patskovsky, Y.; Fedorov, E.; Toro, R.; Sauder, J.M.; Smith, D.; Freeman, J.; Maletic, M.; Powell, A.; Gheyi, T.; Wasserman, S.R.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2007-01-25
Resolution : 2.20 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

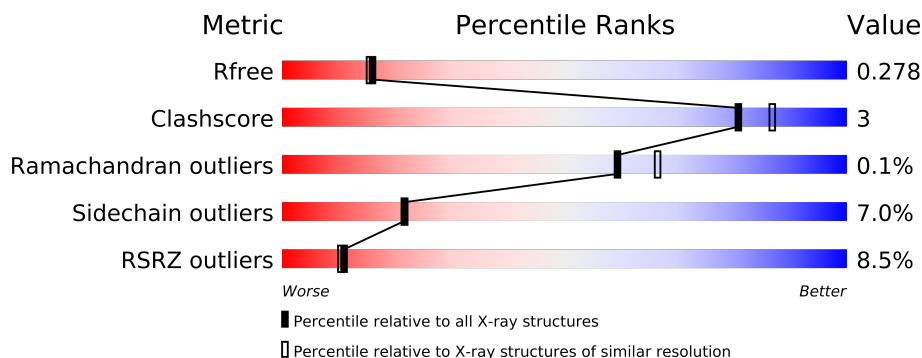
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.20 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}	66092	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	287	
1	B	287	
1	C	287	
1	D	287	
1	E	287	
1	F	287	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	SO4	A	441	-	X
3	SO4	A	445	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
3	SO4	B	443	-	X
4	GOL	A	470	-	X
4	GOL	A	476	-	X
4	GOL	A	487	-	X
4	GOL	A	489	-	X
4	GOL	B	469	-	X
4	GOL	B	472	-	X
4	GOL	B	473	-	X
4	GOL	B	478	-	X
4	GOL	B	479	-	X
4	GOL	B	480	-	X
4	GOL	C	482	-	X
4	GOL	D	463	-	X
4	GOL	D	466	-	X
4	GOL	D	471	-	X
4	GOL	D	483	-	X
4	GOL	E	454	-	X
4	GOL	E	467	-	X
4	GOL	F	457	-	X
4	GOL	F	464	-	X
4	GOL	F	486	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14474 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Glycerophosphoryl diester phosphodiesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	267	Total	C	N	O	S	0	10	0
			2238	1418	392	424	4			
1	B	267	Total	C	N	O	S	0	9	0
			2233	1413	392	424	4			
1	C	267	Total	C	N	O	S	0	5	0
			2216	1400	393	419	4			
1	D	268	Total	C	N	O	S	0	6	0
			2223	1406	392	421	4			
1	E	267	Total	C	N	O	S	0	3	0
			2200	1392	386	418	4			
1	F	267	Total	C	N	O	S	0	3	0
			2203	1392	389	418	4			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	310	GLU	-	EXPRESSION TAG	UNP Q7A6H7
A	311	GLY	-	EXPRESSION TAG	UNP Q7A6H7
A	312	HIS	-	EXPRESSION TAG	UNP Q7A6H7
A	313	HIS	-	EXPRESSION TAG	UNP Q7A6H7
A	314	HIS	-	EXPRESSION TAG	UNP Q7A6H7
A	315	HIS	-	EXPRESSION TAG	UNP Q7A6H7
A	316	HIS	-	EXPRESSION TAG	UNP Q7A6H7
A	317	HIS	-	EXPRESSION TAG	UNP Q7A6H7
B	310	GLU	-	EXPRESSION TAG	UNP Q7A6H7
B	311	GLY	-	EXPRESSION TAG	UNP Q7A6H7
B	312	HIS	-	EXPRESSION TAG	UNP Q7A6H7
B	313	HIS	-	EXPRESSION TAG	UNP Q7A6H7
B	314	HIS	-	EXPRESSION TAG	UNP Q7A6H7
B	315	HIS	-	EXPRESSION TAG	UNP Q7A6H7
B	316	HIS	-	EXPRESSION TAG	UNP Q7A6H7
B	317	HIS	-	EXPRESSION TAG	UNP Q7A6H7
C	310	GLU	-	EXPRESSION TAG	UNP Q7A6H7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	311	GLY	-	EXPRESSION TAG	UNP Q7A6H7
C	312	HIS	-	EXPRESSION TAG	UNP Q7A6H7
C	313	HIS	-	EXPRESSION TAG	UNP Q7A6H7
C	314	HIS	-	EXPRESSION TAG	UNP Q7A6H7
C	315	HIS	-	EXPRESSION TAG	UNP Q7A6H7
C	316	HIS	-	EXPRESSION TAG	UNP Q7A6H7
C	317	HIS	-	EXPRESSION TAG	UNP Q7A6H7
D	310	GLU	-	EXPRESSION TAG	UNP Q7A6H7
D	311	GLY	-	EXPRESSION TAG	UNP Q7A6H7
D	312	HIS	-	EXPRESSION TAG	UNP Q7A6H7
D	313	HIS	-	EXPRESSION TAG	UNP Q7A6H7
D	314	HIS	-	EXPRESSION TAG	UNP Q7A6H7
D	315	HIS	-	EXPRESSION TAG	UNP Q7A6H7
D	316	HIS	-	EXPRESSION TAG	UNP Q7A6H7
D	317	HIS	-	EXPRESSION TAG	UNP Q7A6H7
E	310	GLU	-	EXPRESSION TAG	UNP Q7A6H7
E	311	GLY	-	EXPRESSION TAG	UNP Q7A6H7
E	312	HIS	-	EXPRESSION TAG	UNP Q7A6H7
E	313	HIS	-	EXPRESSION TAG	UNP Q7A6H7
E	314	HIS	-	EXPRESSION TAG	UNP Q7A6H7
E	315	HIS	-	EXPRESSION TAG	UNP Q7A6H7
E	316	HIS	-	EXPRESSION TAG	UNP Q7A6H7
E	317	HIS	-	EXPRESSION TAG	UNP Q7A6H7
F	310	GLU	-	EXPRESSION TAG	UNP Q7A6H7
F	311	GLY	-	EXPRESSION TAG	UNP Q7A6H7
F	312	HIS	-	EXPRESSION TAG	UNP Q7A6H7
F	313	HIS	-	EXPRESSION TAG	UNP Q7A6H7
F	314	HIS	-	EXPRESSION TAG	UNP Q7A6H7
F	315	HIS	-	EXPRESSION TAG	UNP Q7A6H7
F	316	HIS	-	EXPRESSION TAG	UNP Q7A6H7
F	317	HIS	-	EXPRESSION TAG	UNP Q7A6H7

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

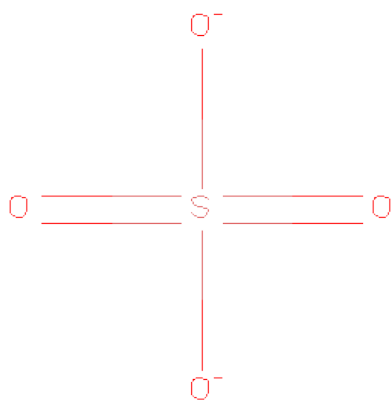
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total Zn 1 1	0	0
2	E	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	F	1	Total	Zn	0	0
			1	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		

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

- Molecule 5 is water.

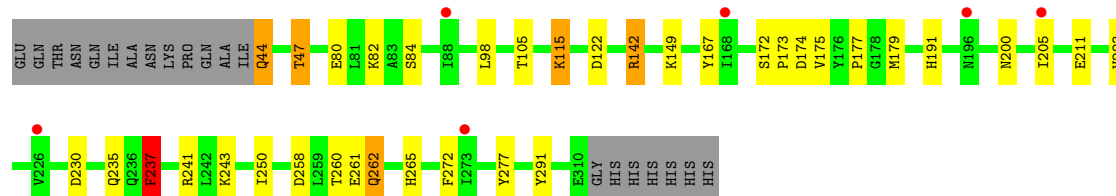
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	198	Total	O	0	0
			198	198		
5	B	211	Total	O	0	0
			211	211		
5	C	87	Total	O	0	0
			87	87		
5	D	193	Total	O	0	0
			193	193		
5	E	92	Total	O	0	0
			92	92		
5	F	110	Total	O	0	0
			110	110		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

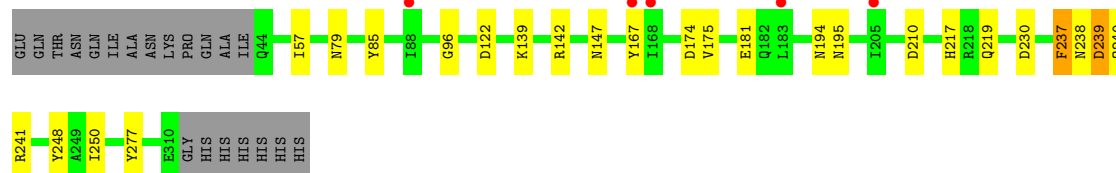
- Molecule 1: Glycerophosphoryl diester phosphodiesterase

Chain A: 



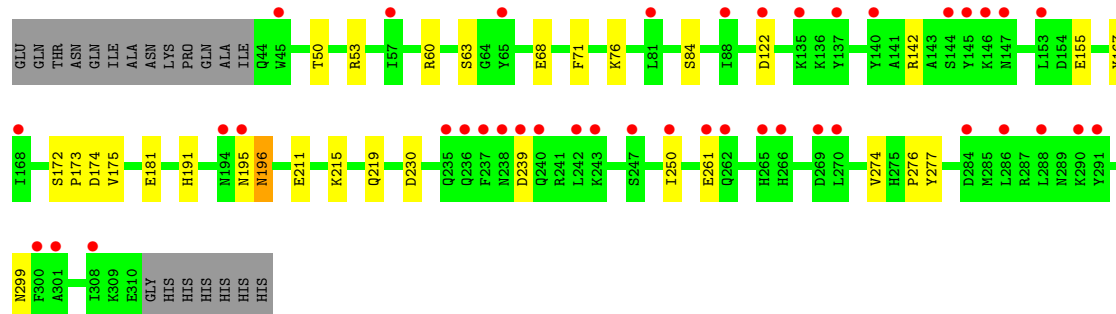
- Molecule 1: Glycerophosphoryl diester phosphodiesterase

Chain B: 



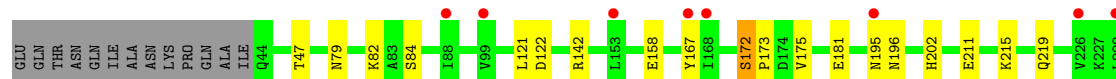
- Molecule 1: Glycerophosphoryl diester phosphodiesterase

Chain C: 



- Molecule 1: Glycerophosphoryl diester phosphodiesterase

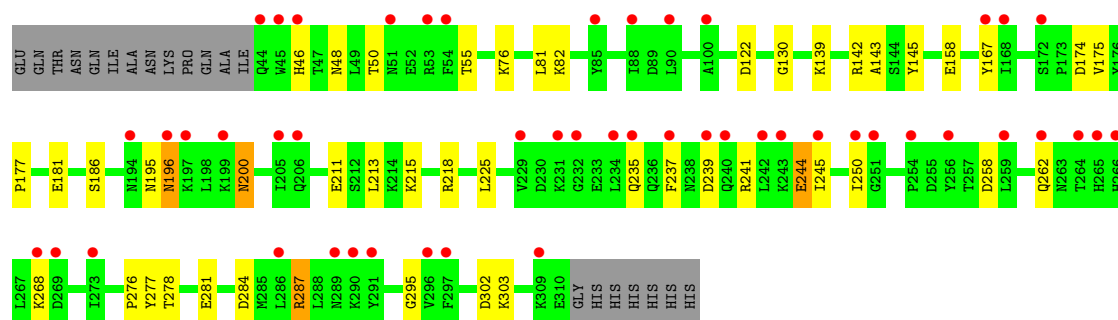
Chain D: 





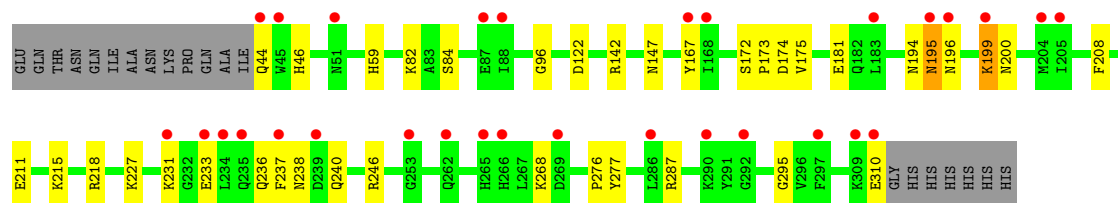
- Molecule 1: Glycerophosphoryl diester phosphodiesterase

Chain E:



- Molecule 1: Glycerophosphoryl diester phosphodiesterase

Chain F:



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	156.31Å 183.55Å 176.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 35.23 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.2 (20.00-2.20) 97.1 (35.23-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.95 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.235 , 0.280 0.232 , 0.278	Depositor DCC
R_{free} test set	3743 reflections (3.11%)	DCC
Wilson B-factor (Å ²)	45.7	Xtriage
Anisotropy	0.231	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 47.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 124052 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14474	wwPDB-VP
Average B, all atoms (Å ²)	56.0	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 26.80 % 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 2.4673e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ZN, 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	0.50	0/2319	0.65	1/3128 (0.0%)
1	B	0.46	0/2311	0.62	0/3119
1	C	0.43	0/2282	0.56	0/3080
1	D	0.42	0/2293	0.57	0/3095
1	E	0.43	0/2260	0.58	0/3052
1	F	0.40	0/2263	0.58	1/3055 (0.0%)
All	All	0.44	0/13728	0.59	2/18529 (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	2
1	B	0	1
1	C	0	1
1	D	0	2
1	E	0	1
1	F	1	3
All	All	2	10

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	237	PHE	N-CA-C	6.03	127.27	111.00
1	F	240	GLN	N-CA-C	5.70	126.38	111.00

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	237	PHE	CA
1	F	240	GLN	CA

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	272	PHE	Peptide
1	A	277	TYR	Peptide
1	B	277	TYR	Peptide
1	C	277	TYR	Peptide
1	D	272	PHE	Peptide
1	D	277	TYR	Peptide
1	E	277	TYR	Peptide
1	F	237	PHE	Peptide
1	F	238	ASN	Peptide
1	F	277	TYR	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2238	0	2216	24	0
1	B	2233	0	2202	13	0
1	C	2216	0	2178	11	0
1	D	2223	0	2183	11	0
1	E	2200	0	2157	20	0
1	F	2203	0	2159	13	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
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	15	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	36	0	48	9	0
4	B	60	0	80	8	0
4	C	12	0	16	0	0
4	D	54	0	72	7	0
4	E	30	0	40	7	0
4	F	42	0	56	3	0
5	A	198	0	0	1	0
5	B	211	0	0	0	0
5	C	87	0	0	3	0
5	D	193	0	0	0	0
5	E	92	0	0	1	0
5	F	110	0	0	2	0
All	All	14474	0	13407	90	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 3.

All (90) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:194:ASN:HB2	4:B:478:GOL:H11	1.02	0.99
1:B:194:ASN:HB2	4:B:478:GOL:C1	1.94	0.97
1:B:194:ASN:CB	4:B:478:GOL:H11	1.96	0.95
1:D:202:HIS:NE2	4:D:463:GOL:H32	1.90	0.86
1:D:79:ASN:O	1:D:82:LYS:HE2	1.81	0.79
1:B:239[A]:ASP:HB2	4:B:473:GOL:H2	1.66	0.77
4:A:476:GOL:H32	5:A:654:HOH:O	1.85	0.76
1:A:191:HIS:NE2	4:A:487:GOL:H32	2.07	0.68
1:E:215:LYS:HD3	4:E:467:GOL:H32	1.81	0.63
1:F:46:HIS:O	1:F:268:LYS:NZ	2.31	0.62
1:A:191:HIS:CD2	4:A:487:GOL:H32	2.35	0.62
1:F:195:ASN:O	1:F:199:LYS:HG2	2.01	0.61
1:F:173:PRO:HA	5:F:522:HOH:O	2.01	0.60
1:E:218:ARG:NH2	4:E:467:GOL:H2	2.18	0.59
1:F:194:ASN:HB2	4:F:460:GOL:O2	2.04	0.57
1:A:237:PHE:HB2	1:A:241:ARG:HG2	1.85	0.57
1:E:281:GLU:OE1	4:E:474:GOL:H2	2.06	0.56
1:D:181:GLU:HG3	1:D:219[B]:GLN:HE22	1.71	0.55
1:D:219[A]:GLN:NE2	4:D:481:GOL:H32	2.21	0.55
1:D:219[A]:GLN:HE21	4:D:481:GOL:H32	1.70	0.55
1:E:276:PRO:HD2	1:E:295:GLY:O	2.06	0.55
1:B:217:HIS:CE1	4:B:480:GOL:H32	2.42	0.55
1:A:47:THR:HG21	1:C:53[B]:ARG:HD3	1.89	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:191:HIS:ND1	5:C:514:HOH:O	2.34	0.54
1:E:46:HIS:O	1:E:268:LYS:NZ	2.40	0.54
1:D:202:HIS:CD2	4:D:463:GOL:H32	2.43	0.53
1:C:181:GLU:OE2	1:C:215:LYS:HE3	2.08	0.53
1:B:238:ASN:HB3	4:B:472:GOL:H32	1.91	0.52
1:A:142:ARG:NH1	4:A:476:GOL:H2	2.23	0.52
1:E:284:ASP:OD1	1:E:287:ARG:NH2	2.42	0.52
1:E:181:GLU:HB3	1:F:181:GLU:HB3	1.92	0.52
1:D:121:LEU:HD21	4:D:468:GOL:H11	1.90	0.52
1:E:241:ARG:HG3	1:E:241:ARG:O	2.11	0.51
1:E:48:ASN:HB3	5:E:558:HOH:O	2.12	0.50
1:C:181:GLU:HG3	1:C:219:GLN:HE22	1.77	0.50
1:E:303:LYS:HD3	4:E:474:GOL:H11	1.94	0.49
1:E:81:LEU:HD22	1:E:302:ASP:HB3	1.94	0.49
1:F:276:PRO:HD2	1:F:295:GLY:O	2.13	0.49
1:F:287:ARG:NH1	5:F:540:HOH:O	2.45	0.48
1:E:177:PRO:HB3	1:F:96:GLY:HA3	1.95	0.48
1:A:142:ARG:NH1	4:A:476:GOL:C3	2.77	0.48
1:A:191:HIS:NE2	4:A:487:GOL:C3	2.76	0.48
1:E:218:ARG:HD2	4:E:467:GOL:O1	2.13	0.48
1:B:210:ASP:OD1	1:B:248:TYR:OH	2.32	0.48
1:E:213:LEU:HD22	1:E:225:LEU:HB3	1.95	0.47
1:C:60:ARG:NH1	1:C:68:GLU:OE1	2.43	0.47
1:A:237:PHE:CB	1:A:241:ARG:HG2	2.45	0.47
1:A:172:SER:HA	1:A:173:PRO:HD3	1.61	0.47
1:E:130:GLY:HA3	1:E:145:TYR:O	2.14	0.47
1:A:142:ARG:HH11	4:A:476:GOL:C3	2.28	0.47
1:A:177:PRO:HB3	1:B:96:GLY:HA2	1.95	0.47
1:A:205:ILE:HD12	1:A:223:VAL:HG11	1.97	0.47
1:D:215:LYS:O	1:D:219[A]:GLN:HG3	2.15	0.46
1:B:237:PHE:HB2	1:B:241:ARG:HG2	1.97	0.46
1:B:79:ASN:HD21	4:B:458:GOL:H31	1.80	0.46
1:C:71:PHE:HZ	1:C:155:GLU:HB3	1.81	0.45
1:D:202:HIS:NE2	4:D:463:GOL:C3	2.72	0.45
1:A:44:GLN:HB2	1:A:44:GLN:HE21	1.58	0.45
1:C:63:SER:OG	1:C:299:ASN:OD1	2.35	0.45
1:A:142:ARG:NH1	4:A:476:GOL:C2	2.80	0.45
1:A:235:GLN:HE22	1:A:258:ASP:HB3	1.82	0.44
1:E:218:ARG:HH21	4:E:467:GOL:H2	1.82	0.44
1:A:105:THR:HA	1:A:115:LYS:HA	2.00	0.44
1:F:218:ARG:HH21	4:F:459:GOL:H31	1.83	0.44
1:A:260:THR:OG1	1:A:262:GLN:NE2	2.51	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:274:VAL:HG12	1:C:276:PRO:HD3	2.00	0.43
1:F:215:LYS:HD3	4:F:459:GOL:H12	2.01	0.43
1:B:57:ILE:HA	1:B:85:TYR:HB2	2.00	0.43
1:C:196[A]:ASN:HD22	1:C:196[A]:ASN:HA	1.63	0.43
1:F:208:PHE:O	1:F:227:LYS:NZ	2.46	0.43
1:E:196:ASN:O	1:E:200:ASN:ND2	2.52	0.43
1:A:98:LEU:HD22	1:A:179:MET:HE2	2.01	0.43
1:F:172:SER:HA	1:F:173:PRO:HD3	1.85	0.43
1:A:265:HIS:CE1	1:A:291:TYR:O	2.72	0.43
1:A:142:ARG:NH1	4:A:476:GOL:H32	2.34	0.43
1:C:172:SER:HA	1:C:173:PRO:HD3	1.90	0.43
1:E:235:GLN:HE22	1:E:258:ASP:HB3	1.84	0.42
1:A:261:GLU:O	1:A:265:HIS:ND1	2.52	0.42
5:C:548:HOH:O	4:D:481:GOL:H31	2.19	0.42
1:C:76:LYS:NZ	5:C:529:HOH:O	2.52	0.42
1:D:172:SER:HA	1:D:173:PRO:HD3	1.91	0.42
1:E:143:ALA:H	4:E:485:GOL:H11	1.83	0.42
1:D:276:PRO:HD2	1:D:295:GLY:O	2.20	0.41
1:A:149[B]:LYS:HA	1:A:149[B]:LYS:HD3	1.77	0.41
1:A:262:GLN:H	1:A:262:GLN:HG3	1.37	0.41
1:E:244[A]:GLU:CG	1:E:245:ILE:N	2.84	0.41
1:B:238:ASN:HB2	4:B:473:GOL:H12	2.02	0.41
1:A:250:ILE:O	1:A:250:ILE:HG13	2.21	0.40
1:B:181:GLU:HG3	1:B:219[B]:GLN:HE22	1.87	0.40
1:F:246:ARG:HA	1:F:246:ARG:HD2	1.97	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	275/287 (96%)	267 (97%)	8 (3%)	0	100	100
1	B	274/287 (96%)	268 (98%)	4 (2%)	2 (1%)	30	28
1	C	270/287 (94%)	263 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	272/287 (95%)	265 (97%)	7 (3%)	0	100	100
1	E	268/287 (93%)	259 (97%)	9 (3%)	0	100	100
1	F	268/287 (93%)	260 (97%)	7 (3%)	1 (0%)	43	45
All	All	1627/1722 (94%)	1582 (97%)	42 (3%)	3 (0%)	59	62

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	147[A]	ASN
1	B	147[B]	ASN
1	F	59	HIS

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	247/254 (97%)	229 (93%)	18 (7%)	20	20
1	B	246/254 (97%)	231 (94%)	15 (6%)	26	28
1	C	242/254 (95%)	227 (94%)	15 (6%)	26	27
1	D	243/254 (96%)	228 (94%)	15 (6%)	26	27
1	E	240/254 (94%)	216 (90%)	24 (10%)	11	10
1	F	240/254 (94%)	221 (92%)	19 (8%)	18	17
All	All	1458/1524 (96%)	1352 (93%)	106 (7%)	21	20

All (106) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	GLN
1	A	47	THR
1	A	80	GLU
1	A	82	LYS
1	A	84	SER
1	A	115	LYS
1	A	122	ASP

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Mol	Chain	Res	Type
1	A	142	ARG
1	A	167	TYR
1	A	174	ASP
1	A	175	VAL
1	A	200[A]	ASN
1	A	200[B]	ASN
1	A	211	GLU
1	A	230	ASP
1	A	237	PHE
1	A	243	LYS
1	A	262	GLN
1	B	122	ASP
1	B	139[A]	LYS
1	B	139[B]	LYS
1	B	142	ARG
1	B	167	TYR
1	B	174[A]	ASP
1	B	174[B]	ASP
1	B	175	VAL
1	B	195	ASN
1	B	230	ASP
1	B	237	PHE
1	B	239[A]	ASP
1	B	239[B]	ASP
1	B	240	GLN
1	B	250	ILE
1	C	50	THR
1	C	84	SER
1	C	122	ASP
1	C	142	ARG
1	C	167	TYR
1	C	174	ASP
1	C	175	VAL
1	C	195	ASN
1	C	196[A]	ASN
1	C	196[B]	ASN
1	C	211	GLU
1	C	230	ASP
1	C	239	ASP
1	C	250	ILE
1	C	261	GLU
1	D	47	THR

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Mol	Chain	Res	Type
1	D	84	SER
1	D	122	ASP
1	D	142	ARG
1	D	158	GLU
1	D	167	TYR
1	D	172	SER
1	D	175	VAL
1	D	195	ASN
1	D	196	ASN
1	D	211	GLU
1	D	237	PHE
1	D	239	ASP
1	D	250	ILE
1	D	262	GLN
1	E	50	THR
1	E	55	THR
1	E	76	LYS
1	E	82	LYS
1	E	122	ASP
1	E	139	LYS
1	E	142	ARG
1	E	158	GLU
1	E	167	TYR
1	E	174	ASP
1	E	175	VAL
1	E	186	SER
1	E	195	ASN
1	E	196	ASN
1	E	200	ASN
1	E	211	GLU
1	E	237	PHE
1	E	239	ASP
1	E	244[A]	GLU
1	E	244[B]	GLU
1	E	250	ILE
1	E	262	GLN
1	E	278	THR
1	E	287	ARG
1	F	44	GLN
1	F	82	LYS
1	F	84	SER
1	F	122	ASP

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Mol	Chain	Res	Type
1	F	142	ARG
1	F	147	ASN
1	F	167	TYR
1	F	174	ASP
1	F	175	VAL
1	F	195	ASN
1	F	196	ASN
1	F	199	LYS
1	F	200	ASN
1	F	211	GLU
1	F	231	LYS
1	F	233[A]	GLU
1	F	233[B]	GLU
1	F	236	GLN
1	F	310	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	GLN
1	A	79	ASN
1	A	195	ASN
1	A	262	GLN
1	A	289	ASN
1	B	113	HIS
1	B	194	ASN
1	B	289	ASN
1	C	79	ASN
1	C	91	GLN
1	C	194	ASN
1	C	219	GLN
1	C	240	GLN
1	C	289	ASN
1	D	79	ASN
1	D	194	ASN
1	D	289	ASN
1	E	79	ASN
1	E	102	HIS
1	E	200	ASN
1	E	235	GLN
1	E	289	ASN
1	F	195	ASN

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Mol	Chain	Res	Type
1	F	200	ASN
1	F	262	GLN
1	F	289	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 51 ligands modelled in this entry, 6 are monoatomic - leaving 45 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	$\# Z > 2$
3	SO4	A	441	-	4,4,4	0.17	0	6,6,6	0.07	0
3	SO4	A	442	-	4,4,4	0.19	0	6,6,6	0.07	0
3	SO4	A	445	-	4,4,4	0.18	0	6,6,6	0.13	0
4	GOL	A	455	2	5,5,5	0.19	0	5,5,5	0.58	0
4	GOL	A	470	-	5,5,5	0.30	0	5,5,5	0.42	0
4	GOL	A	475	-	5,5,5	0.34	0	5,5,5	0.25	0
4	GOL	A	476	-	5,5,5	0.57	0	5,5,5	0.18	0
4	GOL	A	487	-	5,5,5	0.64	0	5,5,5	0.23	0
4	GOL	A	489	-	5,5,5	0.32	0	5,5,5	0.32	0
3	SO4	B	443	-	4,4,4	0.21	0	6,6,6	0.20	0
4	GOL	B	452	2	5,5,5	0.20	0	5,5,5	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GOL	B	458	-	5,5,5	0.37	0	5,5,5	0.63	0
4	GOL	B	461	-	5,5,5	0.36	0	5,5,5	0.61	0
4	GOL	B	469	-	5,5,5	0.34	0	5,5,5	0.25	0
4	GOL	B	472	-	5,5,5	0.33	0	5,5,5	0.16	0
4	GOL	B	473	-	5,5,5	0.47	0	5,5,5	0.43	0
4	GOL	B	477	-	5,5,5	0.41	0	5,5,5	0.36	0
4	GOL	B	478	-	5,5,5	0.34	0	5,5,5	0.25	0
4	GOL	B	479	-	5,5,5	0.32	0	5,5,5	0.34	0
4	GOL	B	480	-	5,5,5	0.84	0	5,5,5	0.75	0
3	SO4	C	446	-	4,4,4	0.17	0	6,6,6	0.11	0
4	GOL	C	451	2	5,5,5	0.33	0	5,5,5	0.42	0
4	GOL	C	482	-	5,5,5	0.49	0	5,5,5	0.24	0
3	SO4	D	444	-	4,4,4	0.18	0	6,6,6	0.14	0
4	GOL	D	453	2	5,5,5	0.33	0	5,5,5	0.27	0
4	GOL	D	462	-	5,5,5	0.36	0	5,5,5	0.27	0
4	GOL	D	463	-	5,5,5	0.33	0	5,5,5	0.25	0
4	GOL	D	466	-	5,5,5	0.32	0	5,5,5	0.21	0
4	GOL	D	468	-	5,5,5	0.32	0	5,5,5	0.45	0
4	GOL	D	471	-	5,5,5	0.30	0	5,5,5	0.38	0
4	GOL	D	481	-	5,5,5	0.69	0	5,5,5	0.80	0
4	GOL	D	483	-	5,5,5	0.33	0	5,5,5	0.25	0
4	GOL	D	484	-	5,5,5	0.33	0	5,5,5	0.41	0
4	GOL	E	454	2	5,5,5	0.29	0	5,5,5	0.33	0
4	GOL	E	465	-	5,5,5	0.31	0	5,5,5	0.26	0
4	GOL	E	467	-	5,5,5	0.35	0	5,5,5	0.26	0
4	GOL	E	474	-	5,5,5	0.32	0	5,5,5	0.31	0
4	GOL	E	485	-	5,5,5	0.23	0	5,5,5	0.47	0
4	GOL	F	456	2	5,5,5	0.41	0	5,5,5	0.41	0
4	GOL	F	457	-	5,5,5	0.36	0	5,5,5	0.32	0
4	GOL	F	459	-	5,5,5	0.33	0	5,5,5	0.32	0
4	GOL	F	460	-	5,5,5	0.32	0	5,5,5	0.28	0
4	GOL	F	464	-	5,5,5	0.33	0	5,5,5	0.32	0
4	GOL	F	486	-	5,5,5	0.30	0	5,5,5	0.29	0
4	GOL	F	488	-	5,5,5	0.33	0	5,5,5	0.36	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
3	SO4	A	441	-	-	0/0/0/0	0/0/0/0
3	SO4	A	442	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	A	445	-	-	0/0/0/0	0/0/0/0
4	GOL	A	455	2	-	0/4/4/4	0/0/0/0
4	GOL	A	470	-	-	0/4/4/4	0/0/0/0
4	GOL	A	475	-	-	0/4/4/4	0/0/0/0
4	GOL	A	476	-	-	0/4/4/4	0/0/0/0
4	GOL	A	487	-	-	0/4/4/4	0/0/0/0
4	GOL	A	489	-	-	0/4/4/4	0/0/0/0
3	SO4	B	443	-	-	0/0/0/0	0/0/0/0
4	GOL	B	452	2	-	0/4/4/4	0/0/0/0
4	GOL	B	458	-	-	0/4/4/4	0/0/0/0
4	GOL	B	461	-	-	0/4/4/4	0/0/0/0
4	GOL	B	469	-	-	0/4/4/4	0/0/0/0
4	GOL	B	472	-	-	0/4/4/4	0/0/0/0
4	GOL	B	473	-	-	0/4/4/4	0/0/0/0
4	GOL	B	477	-	-	0/4/4/4	0/0/0/0
4	GOL	B	478	-	-	0/4/4/4	0/0/0/0
4	GOL	B	479	-	-	0/4/4/4	0/0/0/0
4	GOL	B	480	-	-	0/4/4/4	0/0/0/0
3	SO4	C	446	-	-	0/0/0/0	0/0/0/0
4	GOL	C	451	2	-	0/4/4/4	0/0/0/0
4	GOL	C	482	-	-	0/4/4/4	0/0/0/0
3	SO4	D	444	-	-	0/0/0/0	0/0/0/0
4	GOL	D	453	2	-	0/4/4/4	0/0/0/0
4	GOL	D	462	-	-	0/4/4/4	0/0/0/0
4	GOL	D	463	-	-	0/4/4/4	0/0/0/0
4	GOL	D	466	-	-	0/4/4/4	0/0/0/0
4	GOL	D	468	-	-	0/4/4/4	0/0/0/0
4	GOL	D	471	-	-	0/4/4/4	0/0/0/0
4	GOL	D	481	-	-	0/4/4/4	0/0/0/0
4	GOL	D	483	-	-	0/4/4/4	0/0/0/0
4	GOL	D	484	-	-	0/4/4/4	0/0/0/0
4	GOL	E	454	2	-	0/4/4/4	0/0/0/0
4	GOL	E	465	-	-	0/4/4/4	0/0/0/0
4	GOL	E	467	-	-	0/4/4/4	0/0/0/0
4	GOL	E	474	-	-	0/4/4/4	0/0/0/0
4	GOL	E	485	-	-	0/4/4/4	0/0/0/0
4	GOL	F	456	2	-	0/4/4/4	0/0/0/0
4	GOL	F	457	-	-	0/4/4/4	0/0/0/0
4	GOL	F	459	-	-	0/4/4/4	0/0/0/0
4	GOL	F	460	-	-	0/4/4/4	0/0/0/0
4	GOL	F	464	-	-	0/4/4/4	0/0/0/0
4	GOL	F	486	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	F	488	-	-	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.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	267/287 (93%)	-0.11	6 (2%) 59 59	29, 43, 73, 125	0
1	B	267/287 (93%)	-0.18	5 (1%) 64 64	25, 37, 65, 113	0
1	C	267/287 (93%)	0.82	41 (15%) 3 3	42, 64, 99, 151	0
1	D	268/287 (93%)	0.02	9 (3%) 43 43	29, 46, 77, 124	0
1	E	267/287 (93%)	0.87	49 (18%) 2 2	36, 66, 100, 145	0
1	F	267/287 (93%)	0.52	30 (11%) 6 5	35, 56, 86, 135	0
All	All	1603/1722 (93%)	0.32	140 (8%) 11 10	25, 52, 92, 151	0

All (140) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	54	PHE	7.5
1	E	242	LEU	7.3
1	E	45	TRP	7.0
1	F	239	ASP	6.2
1	F	45	TRP	6.2
1	E	286	LEU	6.0
1	E	239	ASP	5.7
1	C	236	GLN	5.5
1	E	235	GLN	5.5
1	E	237	PHE	5.4
1	E	269	ASP	5.2
1	C	270	LEU	5.1
1	F	269	ASP	4.9
1	E	265	HIS	4.7
1	E	167	TYR	4.7
1	C	308	ILE	4.7
1	E	231	LYS	4.6
1	E	256	TYR	4.3
1	C	266	HIS	4.3

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Mol	Chain	Res	Type	RSRZ
1	D	168	ILE	4.3
1	F	235	GLN	4.2
1	C	45	TRP	4.2
1	C	239	ASP	4.1
1	C	240	GLN	4.0
1	E	262	GLN	4.0
1	F	167	TYR	4.0
1	E	44	GLN	3.9
1	E	268	LYS	3.8
1	F	237	PHE	3.6
1	E	259	LEU	3.6
1	C	247	SER	3.5
1	C	300	PHE	3.5
1	B	168	ILE	3.5
1	C	147	ASN	3.4
1	E	290	LYS	3.4
1	E	289	ASN	3.4
1	F	195	ASN	3.4
1	E	232	GLY	3.4
1	C	146	LYS	3.3
1	D	195	ASN	3.2
1	E	88	ILE	3.2
1	E	243	LYS	3.2
1	C	137	TYR	3.2
1	E	168	ILE	3.1
1	E	264	THR	3.1
1	E	234	LEU	3.1
1	C	286	LEU	3.0
1	F	262	GLN	3.0
1	A	88	ILE	3.0
1	E	309	LYS	2.9
1	D	88	ILE	2.9
1	F	286	LEU	2.9
1	F	309	LYS	2.9
1	F	88	ILE	2.8
1	F	51	ASN	2.8
1	A	168	ILE	2.8
1	F	253	GLY	2.8
1	B	88	ILE	2.8
1	A	196	ASN	2.7
1	E	197	LYS	2.7
1	E	266	HIS	2.7

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Mol	Chain	Res	Type	RSRZ
1	E	297	PHE	2.7
1	E	53	ARG	2.7
1	F	199	LYS	2.7
1	F	205	ILE	2.7
1	C	88	ILE	2.7
1	D	153	LEU	2.7
1	C	144	SER	2.7
1	E	273	ILE	2.7
1	F	168	ILE	2.7
1	C	135	LYS	2.7
1	F	183	LEU	2.6
1	C	250	ILE	2.6
1	C	265	HIS	2.6
1	F	290	LYS	2.6
1	E	250	ILE	2.6
1	E	199	LYS	2.6
1	B	205	ILE	2.6
1	F	292	GLY	2.6
1	C	81	LEU	2.6
1	F	310	GLU	2.5
1	E	196	ASN	2.5
1	C	168	ILE	2.5
1	E	245	ILE	2.5
1	C	140	TYR	2.5
1	C	269	ASP	2.5
1	C	195	ASN	2.5
1	D	167	TYR	2.5
1	E	206	GLN	2.5
1	E	240	GLN	2.5
1	A	273	ILE	2.5
1	B	183	LEU	2.4
1	E	229	VAL	2.4
1	A	226	VAL	2.4
1	C	57	ILE	2.4
1	F	44	GLN	2.4
1	E	172	SER	2.4
1	D	226	VAL	2.4
1	E	296	VAL	2.4
1	F	233[A]	GLU	2.4
1	D	238	ASN	2.4
1	C	237	PHE	2.4
1	C	261	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	235	GLN	2.4
1	E	51	ASN	2.3
1	C	288	LEU	2.3
1	C	262	GLN	2.3
1	B	167	TYR	2.3
1	C	243	LYS	2.3
1	F	297	PHE	2.3
1	F	87	GLU	2.3
1	C	238	ASN	2.2
1	E	254	PRO	2.2
1	C	242	LEU	2.2
1	F	234	LEU	2.2
1	C	145	TYR	2.2
1	E	46	HIS	2.2
1	E	90	LEU	2.2
1	E	100	ALA	2.2
1	C	284	ASP	2.2
1	C	65	TYR	2.2
1	E	194	ASN	2.2
1	F	231	LYS	2.1
1	C	291	TYR	2.1
1	E	85	TYR	2.1
1	E	291	TYR	2.1
1	C	290	LYS	2.1
1	C	153	LEU	2.1
1	E	251	GLY	2.1
1	F	196	ASN	2.1
1	D	228	LEU	2.1
1	A	205	ILE	2.1
1	F	265	HIS	2.1
1	C	194	ASN	2.1
1	E	205[A]	ILE	2.1
1	C	301	ALA	2.1
1	F	204	MET	2.0
1	F	266	HIS	2.0
1	C	122	ASP	2.0
1	D	99	VAL	2.0

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	GOL	B	472	6/6	0.40	24.34	78,93,99,105	0
4	GOL	B	469	6/6	0.43	18.66	60,77,98,113	0
4	GOL	A	489	6/6	0.28	10.19	94,102,108,108	0
4	GOL	B	479	6/6	0.18	9.30	68,90,106,107	0
4	GOL	A	487	6/6	0.27	5.20	80,87,93,107	0
3	SO4	A	441	5/5	0.23	5.12	95,100,125,131	0
4	GOL	A	470	6/6	0.13	5.00	56,70,80,88	0
4	GOL	B	473	6/6	0.35	4.45	105,114,121,126	0
4	GOL	D	463	6/6	0.30	4.12	45,63,89,106	0
3	SO4	A	445	5/5	0.26	4.09	77,85,104,112	0
4	GOL	F	457	6/6	0.22	3.90	39,62,84,84	0
4	GOL	D	471	6/6	0.24	3.81	52,65,80,81	0
4	GOL	F	486	6/6	0.29	3.58	78,91,111,116	0
4	GOL	B	480	6/6	0.20	3.36	69,95,105,118	0
4	GOL	E	467	6/6	0.32	2.97	70,102,105,118	0
4	GOL	E	454	6/6	0.39	2.90	54,65,77,87	0
4	GOL	F	464	6/6	0.17	2.88	63,82,88,93	0
4	GOL	A	476	6/6	0.20	2.88	92,108,116,117	0
4	GOL	D	483	6/6	0.22	2.55	89,93,102,105	0
3	SO4	B	443	5/5	0.18	2.44	73,83,96,114	0
4	GOL	D	466	6/6	0.26	2.42	58,95,100,116	0
4	GOL	C	482	6/6	0.16	2.40	70,95,99,99	0
4	GOL	B	478	6/6	0.24	2.06	79,98,125,136	0
3	SO4	C	446	5/5	0.16	1.89	77,80,103,109	0
4	GOL	B	458	6/6	0.17	1.77	46,64,70,88	0
4	GOL	C	451	6/6	0.24	1.66	58,67,89,90	0
4	GOL	B	477	6/6	0.23	1.66	36,64,80,87	0
4	GOL	F	460	6/6	0.21	1.61	97,117,121,121	0
4	GOL	F	459	6/6	0.15	1.41	52,71,84,99	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	GOL	D	468	6/6	0.17	1.17	49,82,87,89	0
4	GOL	F	456	6/6	0.27	1.10	43,53,53,54	0
4	GOL	B	452	6/6	0.20	1.08	19,25,34,36	0
4	GOL	A	475	6/6	0.14	1.06	67,90,96,98	0
4	GOL	D	462	6/6	0.16	0.97	44,59,87,92	0
4	GOL	E	485	6/6	0.14	0.93	55,60,70,84	0
4	GOL	A	455	6/6	0.18	0.61	30,36,45,50	0
4	GOL	B	461	6/6	0.15	0.39	57,75,86,86	0
4	GOL	E	465	6/6	0.12	0.32	43,84,89,98	0
4	GOL	D	481	6/6	0.13	0.00	64,76,84,92	0
4	GOL	D	484	6/6	0.14	-0.03	57,79,86,87	0
3	SO4	D	444	5/5	0.10	-0.58	73,79,104,107	0
4	GOL	D	453	6/6	0.14	-0.92	34,37,43,49	0
3	SO4	A	442	5/5	0.07	-1.05	57,72,80,81	0
4	GOL	E	474	6/6	0.17	-1.14	101,111,119,121	0
2	ZN	E	404	1/1	0.12	-1.65	73,73,73,73	0
4	GOL	F	488	6/6	0.10	-1.88	56,79,94,94	0
2	ZN	C	406	1/1	0.08	-1.92	76,76,76,76	0
2	ZN	A	403	1/1	0.08	-2.58	53,53,53,53	0
2	ZN	F	402	1/1	0.11	-3.20	76,76,76,76	0
2	ZN	D	405	1/1	0.07	-3.42	60,60,60,60	0
2	ZN	B	401	1/1	0.06	-4.31	46,46,46,46	0

6.5 Other polymers ⓘ

There are no such residues in this entry.