



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 4, 2024 – 11:49 am GMT

PDB ID : 4X8E
Title : Ergothioneine-biosynthetic sulfoxide synthase EgtB in complex with N,N,N-t
rimethyl-histidine
Authors : Vit, A.; Goncharenko, K.V.; Blankenfeldt, W.; Seebeck, F.P.
Deposited on : 2014-12-10
Resolution : 1.60 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

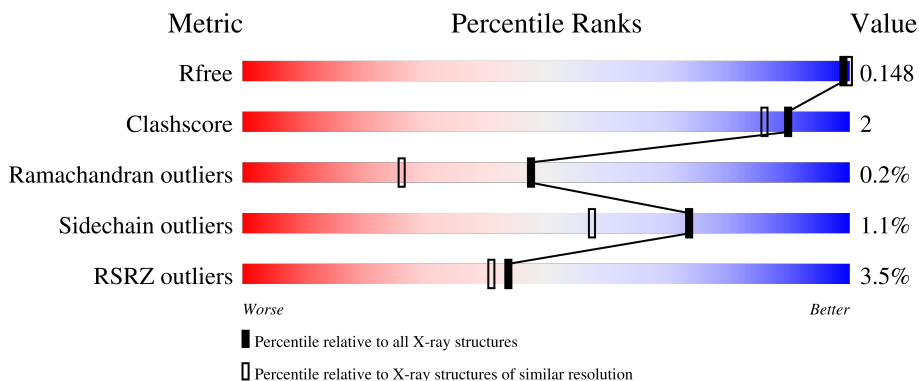
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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}	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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	447	
1	B	447	

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
4	CL	A	512	-	-	X	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 14685 atoms, of which 6657 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.

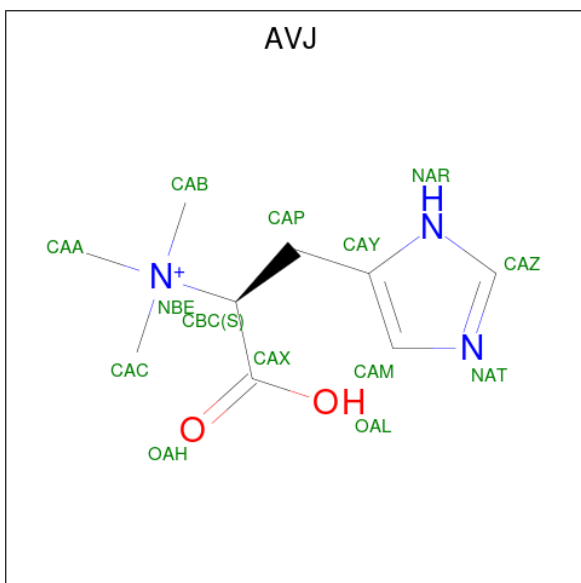
- Molecule 1 is a protein called Sulfoxide synthase EgtB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	428	Total 6759	C 2188	H 3314	N 635	O 612	S 10	0	14	0
1	B	426	Total 6583	C 2138	H 3219	N 615	O 601	S 10	0	3	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP G7CFI3
A	1	HIS	-	expression tag	UNP G7CFI3
A	2	MET	-	expression tag	UNP G7CFI3
B	0	GLY	-	expression tag	UNP G7CFI3
B	1	HIS	-	expression tag	UNP G7CFI3
B	2	MET	-	expression tag	UNP G7CFI3

- Molecule 2 is N,N,N-trimethyl-histidine (three-letter code: AVJ) (formula: C₉H₁₆N₃O₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	0	0
			29	9	15	3	2		
2	B	1	Total	C	H	N	O	0	0
			29	9	15	3	2		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			13	3	7	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			13	3	7	3		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	5	Total	Cl	0	0
			5	5		
4	B	2	Total	Cl	0	0
			2	2		

- Molecule 5 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Fe	0	0
			1	1		
5	B	1	Total	Fe	0	0
			1	1		

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Ca	0	0
			1	1		
6	B	1	Total	Ca	0	0
			1	1		

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Mg	0	0
			1	1		
7	B	1	Total	Mg	0	0
			1	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	671	Total	O	0	0
			671	671		

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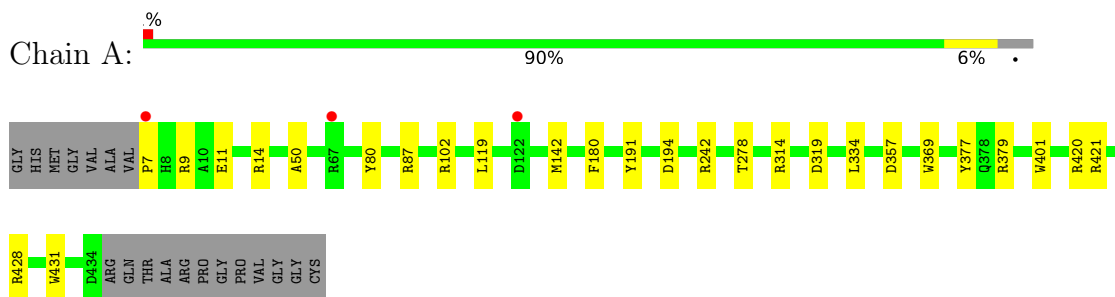
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	435	Total 435	O 435	0	0

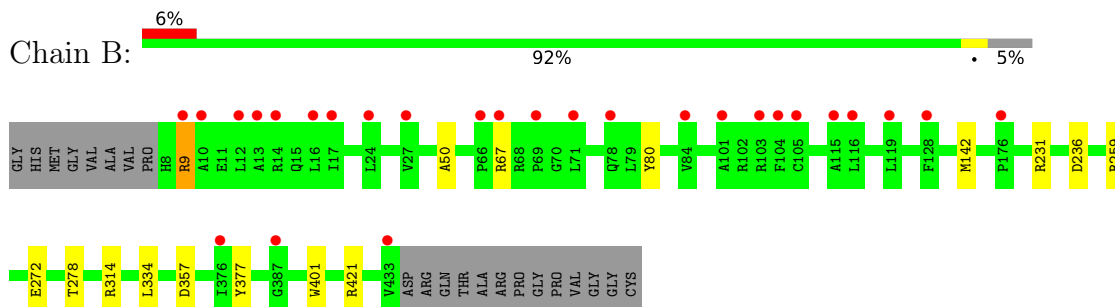
3 Residue-property plots [i](#)

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: Sulfoxide synthase EgtB



- Molecule 1: Sulfoxide synthase EgtB



4 Data and refinement statistics i

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	135.24Å 135.24Å 142.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.97 – 1.60 48.97 – 1.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.97-1.60) 100.0 (48.97-1.60)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 1.60Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.144 , 0.163 0.150 , 0.148	Depositor DCC
R_{free} test set	8755 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	21.5	Xtriage
Anisotropy	0.133	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 51.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.013 for -h,l,k 0.009 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	14685	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.67% 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: CA, MG, FE, CL, AVJ, GOL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.55	0/3602	0.74	9/4924 (0.2%)
1	B	0.44	0/3482	0.59	3/4764 (0.1%)
All	All	0.50	0/7084	0.67	12/9688 (0.1%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	142	MET	CG-SD-CE	-8.33	86.87	100.20
1	B	9	ARG	NE-CZ-NH1	5.93	123.27	120.30
1	A	420	ARG	NE-CZ-NH2	-5.59	117.51	120.30
1	A	319[A]	ASP	CB-CG-OD1	5.36	123.13	118.30
1	A	319[B]	ASP	CB-CG-OD1	5.36	123.13	118.30
1	A	428	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	A	194	ASP	CB-CG-OD1	5.09	122.88	118.30
1	A	428	ARG	NE-CZ-NH1	5.07	122.83	120.30
1	B	67	ARG	NE-CZ-NH1	5.07	122.83	120.30
1	B	142	MET	CG-SD-CE	-5.06	92.11	100.20
1	A	87	ARG	NE-CZ-NH1	5.00	122.80	120.30
1	A	194	ASP	CB-CG-OD2	-5.00	113.80	118.30

There are no chirality outliers.

There are no planarity outliers.

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	3445	3314	3316	11	1
1	B	3364	3219	3220	9	0
2	A	14	15	15	0	0
2	B	14	15	15	0	0
3	A	48	63	63	4	1
3	B	24	31	32	3	0
4	A	5	0	0	2	0
4	B	2	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
8	A	671	0	0	4	1
8	B	435	0	0	3	0
All	All	8028	6657	6661	24	2

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 2.

All (24) 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:B:272[B]:GLU:OE2	8:B:601:HOH:O	2.05	0.73
1:A:119:LEU:O	8:A:601:HOH:O	2.14	0.65
1:A:379[A]:ARG:NH2	3:A:506:GOL:O2	2.30	0.65
3:A:508:GOL:O3	8:A:602:HOH:O	2.15	0.64
1:B:259:ARG:NH1	1:B:272[B]:GLU:OE2	2.33	0.61
1:B:231:ARG:NH2	1:B:236:ASP:OD1	2.34	0.60
1:B:314:ARG:NH2	8:B:604:HOH:O	2.36	0.57
1:A:7:PRO:HD3	1:A:191:TYR:OH	2.06	0.56
3:A:507:GOL:C3	4:A:512:CL:CL	2.93	0.54
1:A:7:PRO:CD	1:A:191:TYR:OH	2.55	0.54
1:A:314:ARG:NH2	8:A:607:HOH:O	2.43	0.52
1:B:421:ARG:HE	3:B:505:GOL:H31	1.75	0.51
3:B:505:GOL:H32	8:B:680:HOH:O	2.10	0.51
1:B:334:LEU:HA	1:B:401:TRP:CZ3	2.46	0.50
1:B:421:ARG:NE	3:B:505:GOL:H31	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:ALA:HB3	1:B:80:TYR:CE1	2.49	0.48
3:A:507:GOL:H31	4:A:512:CL:CL	2.51	0.47
1:B:278:THR:HG23	1:B:421:ARG:HD3	1.98	0.46
1:A:11:GLU:OE2	1:A:14[A]:ARG:NH2	2.50	0.44
1:A:278:THR:HG23	1:A:421:ARG:HD3	1.99	0.44
1:A:50:ALA:HB3	1:A:80:TYR:CE1	2.53	0.43
1:A:102[A]:ARG:HD3	8:A:1095:HOH:O	2.18	0.42
1:A:334:LEU:HA	1:A:401:TRP:CZ3	2.55	0.41
1:A:7:PRO:HD3	1:A:191:TYR:HH	1.86	0.41

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:431:TRP:HE1	3:A:503:GOL:HO2[8_665]	1.12	0.48
8:A:1164:HOH:O	8:A:1164:HOH:O[8_665]	2.14	0.06

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	441/447 (99%)	436 (99%)	4 (1%)	1 (0%)	47	26
1	B	427/447 (96%)	423 (99%)	3 (1%)	1 (0%)	47	26
All	All	868/894 (97%)	859 (99%)	7 (1%)	2 (0%)	47	26

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	357	ASP
1	B	357	ASP

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	347/348 (100%)	342 (99%)	5 (1%)	67	47
1	B	334/348 (96%)	332 (99%)	2 (1%)	86	77
All	All	681/696 (98%)	674 (99%)	7 (1%)	73	61

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ARG
1	A	180	PHE
1	A	242	ARG
1	A	369	TRP
1	A	377	TYR
1	B	9	ARG
1	B	377	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 27 ligands modelled in this entry, 13 are monoatomic - leaving 14 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	GOL	A	502	-	5,5,5	0.41	0	5,5,5	0.38	0
3	GOL	B	504	-	5,5,5	0.40	0	5,5,5	0.28	0
3	GOL	A	503	-	5,5,5	0.33	0	5,5,5	0.23	0
3	GOL	B	505	-	5,5,5	0.76	0	5,5,5	2.36	3 (60%)
3	GOL	B	503	-	5,5,5	0.37	0	5,5,5	0.44	0
3	GOL	A	507	-	5,5,5	0.48	0	5,5,5	0.55	0
3	GOL	A	506	-	5,5,5	0.54	0	5,5,5	0.38	0
3	GOL	A	509	-	5,5,5	0.31	0	5,5,5	0.64	0
3	GOL	B	502	-	5,5,5	0.36	0	5,5,5	0.32	0
3	GOL	A	505	-	5,5,5	0.33	0	5,5,5	0.71	0
2	AVJ	B	501	5	9,14,14	1.38	0	11,20,20	1.43	2 (18%)
3	GOL	A	508	-	5,5,5	1.02	1 (20%)	5,5,5	1.22	1 (20%)
3	GOL	A	504	-	5,5,5	0.34	0	5,5,5	0.29	0
2	AVJ	A	501	5	9,14,14	1.34	1 (11%)	11,20,20	1.76	2 (18%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	502	-	-	0/4/4/4	-
3	GOL	B	504	-	-	0/4/4/4	-
3	GOL	A	503	-	-	0/4/4/4	-
3	GOL	B	505	-	-	0/4/4/4	-
3	GOL	B	503	-	-	0/4/4/4	-
3	GOL	A	507	-	-	2/4/4/4	-
3	GOL	A	506	-	-	4/4/4/4	-
3	GOL	A	509	-	-	2/4/4/4	-
3	GOL	B	502	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	505	-	-	2/4/4/4	-
2	AVJ	B	501	5	-	1/14/14/14	0/1/1/1
3	GOL	A	508	-	-	2/4/4/4	-
3	GOL	A	504	-	-	0/4/4/4	-
2	AVJ	A	501	5	-	1/14/14/14	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	AVJ	CBC-CAX	-2.28	1.49	1.53
3	A	508	GOL	O3-C3	-2.05	1.33	1.42

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	AVJ	OAL-CAX-CBC	4.02	121.40	111.87
3	B	505	GOL	O2-C2-C3	-3.61	93.21	109.12
2	B	501	AVJ	OAL-CAX-CBC	3.30	119.69	111.87
2	A	501	AVJ	CAM-NAT-CAZ	2.84	110.22	105.78
3	B	505	GOL	O3-C3-C2	-2.77	96.93	110.20
3	A	508	GOL	C3-C2-C1	-2.42	102.29	111.70
3	B	505	GOL	O2-C2-C1	2.27	119.14	109.12
2	B	501	AVJ	OAL-CAX-OAH	-2.17	119.16	124.09

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	505	GOL	C1-C2-C3-O3
3	A	506	GOL	C1-C2-C3-O3
3	A	507	GOL	O1-C1-C2-C3
3	A	508	GOL	O1-C1-C2-C3
3	A	509	GOL	C1-C2-C3-O3
3	A	505	GOL	O2-C2-C3-O3
3	A	506	GOL	O2-C2-C3-O3
3	A	507	GOL	O1-C1-C2-O2
3	A	509	GOL	O2-C2-C3-O3
3	A	506	GOL	O1-C1-C2-O2
3	A	506	GOL	O1-C1-C2-C3
3	A	508	GOL	O1-C1-C2-O2
2	B	501	AVJ	OAL-CAX-CBC-NBE

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Mol	Chain	Res	Type	Atoms
2	A	501	AVJ	OAL-CAX-CBC-NBE

There are no ring outliers.

5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	503	GOL	0	1
3	B	505	GOL	3	0
3	A	507	GOL	2	0
3	A	506	GOL	1	0
3	A	508	GOL	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	428/447 (95%)	-0.22	3 (0%) 87 87	14, 22, 40, 63	0
1	B	426/447 (95%)	0.19	27 (6%) 20 18	22, 36, 57, 72	0
All	All	854/894 (95%)	-0.02	30 (3%) 44 41	14, 28, 53, 72	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	9	ARG	4.9
1	B	12	LEU	4.5
1	B	69	PRO	4.2
1	B	17	ILE	3.9
1	A	67	ARG	3.9
1	B	10	ALA	3.7
1	B	119	LEU	3.7
1	B	67	ARG	3.4
1	B	116	LEU	3.1
1	B	115	ALA	2.9
1	B	128	PHE	2.8
1	B	433	VAL	2.8
1	B	24	LEU	2.8
1	B	14	ARG	2.7
1	B	13	ALA	2.6
1	B	387	GLY	2.6
1	B	104	PHE	2.6
1	A	7	PRO	2.6
1	B	27	VAL	2.5
1	B	84	VAL	2.5
1	B	103	ARG	2.5
1	B	105	CYS	2.3
1	B	78	GLN	2.2
1	B	16	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	101	ALA	2.2
1	B	176	PRO	2.2
1	B	71	LEU	2.2
1	B	376	ILE	2.1
1	A	122	ASP	2.1
1	B	66	PRO	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 monosaccharides 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(Å ²)	Q<0.9
7	MG	A	517	1/1	0.27	0.29	102,102,102,102	0
3	GOL	A	509	6/6	0.73	0.38	37,58,70,70	0
3	GOL	A	507	6/6	0.84	0.23	32,55,63,66	0
3	GOL	A	505	6/6	0.85	0.18	22,31,56,56	0
3	GOL	B	503	6/6	0.85	0.15	48,58,68,71	0
3	GOL	A	508	6/6	0.85	0.17	35,46,66,77	0
3	GOL	B	502	6/6	0.88	0.16	41,58,66,69	0
3	GOL	A	506	6/6	0.90	0.22	34,51,61,72	0
3	GOL	B	505	6/6	0.91	0.14	26,57,71,74	0
3	GOL	B	504	6/6	0.92	0.22	32,55,70,70	0
2	AVJ	B	501	14/14	0.94	0.08	25,31,33,33	0
4	CL	A	513	1/1	0.94	0.14	51,51,51,51	0
3	GOL	A	502	6/6	0.94	0.13	21,43,56,56	0
7	MG	B	510	1/1	0.95	0.07	50,50,50,50	0
2	AVJ	A	501	14/14	0.96	0.08	15,19,21,23	0
4	CL	A	514	1/1	0.96	0.08	36,36,36,36	0
3	GOL	A	504	6/6	0.97	0.13	29,37,43,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	GOL	A	503	6/6	0.97	0.10	18,22,24,24	0
4	CL	B	507	1/1	0.98	0.12	38,38,38,38	0
4	CL	A	512	1/1	0.98	0.10	44,44,44,44	0
4	CL	B	506	1/1	0.98	0.06	41,41,41,41	0
5	FE	B	508	1/1	0.99	0.05	24,24,24,24	0
6	CA	A	516	1/1	0.99	0.14	17,17,17,17	0
6	CA	B	509	1/1	0.99	0.08	27,27,27,27	0
4	CL	A	511	1/1	0.99	0.08	29,29,29,29	0
4	CL	A	510	1/1	0.99	0.05	24,24,24,24	0
5	FE	A	515	1/1	1.00	0.13	15,15,15,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.