



wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 22, 2024 – 10:04 AM EDT

PDB ID : 8T59
Title : Crystal structure of Para.09 bound to TREM2
Authors : Wallweber, H.; Hsu, P.L.
Deposited on : 2023-06-12
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.37.1
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) : 2.37.1

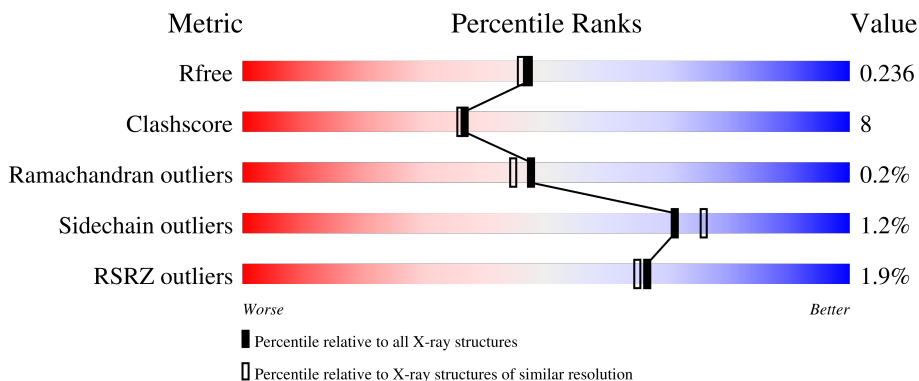
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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.



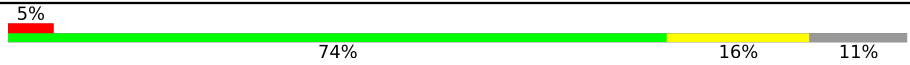
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	225	 3% 80% 12% 7%
1	C	225	 83% 12% . .
2	B	219	 2% 83% 16%
2	D	219	 % 86% 13% .
3	E	19	 74% 5% 21%

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Mol	Chain	Length	Quality of chain
3	F	19	

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	GOL	B	305	-	X	-	-
4	GOL	C	302	-	X	-	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7624 atoms, of which 90 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 Para.09 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	210	Total	C	N	O	S	0	1	0
			1587	1008	261	313	5			
1	C	216	Total	C	N	O	S	0	5	0
			1658	1051	273	329	5			

- Molecule 2 is a protein called Para.09 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	218	Total	C	N	O	S	0	2	0
			1691	1068	280	337	6			
2	D	219	Total	C	N	O	S	0	1	0
			1691	1067	280	337	7			

- Molecule 3 is a protein called Triggering receptor expressed on myeloid cells 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	E	15	Total	C	N	O	0	0	0
			116	70	22	24			
3	F	17	Total	C	N	O	0	0	0
			131	78	24	29			

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



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

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

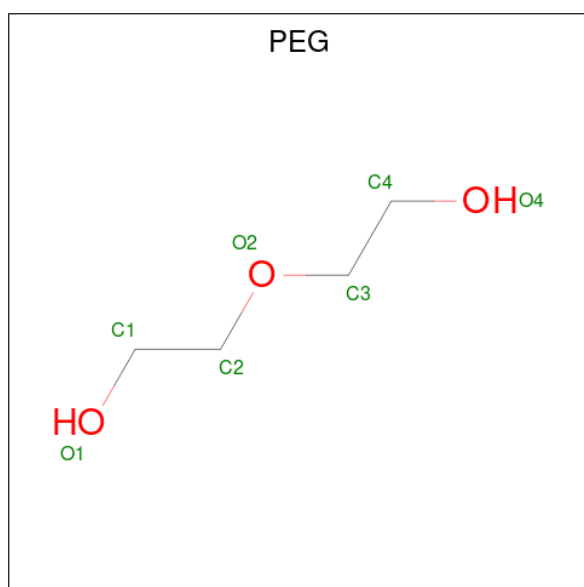
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	3	Total	Zn	0	0
			3	3		
5	D	2	Total	Zn	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	E	1	Total	Zn	0	0
			1	1		
5	F	1	Total	Zn	0	0
			1	1		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	C	1	Total	C	H	O	0	0
			17	4	10	3		

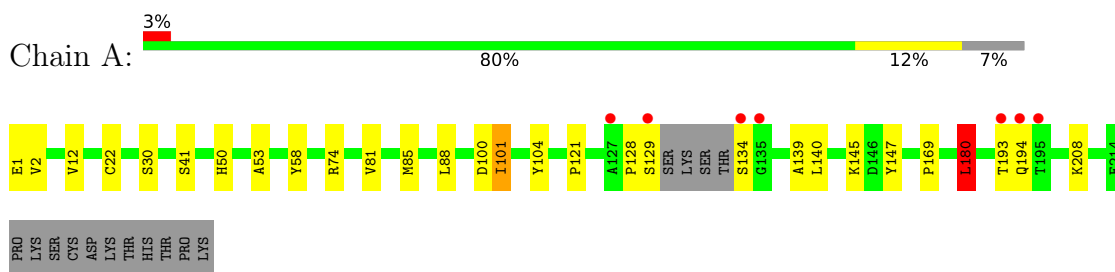
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	116	Total	O	0	1
			117	117		
7	B	114	Total	O	0	2
			116	116		
7	C	154	Total	O	0	6
			160	160		
7	D	159	Total	O	0	3
			162	162		
7	E	14	Total	O	0	2
			16	16		
7	F	15	Total	O	0	0
			15	15		

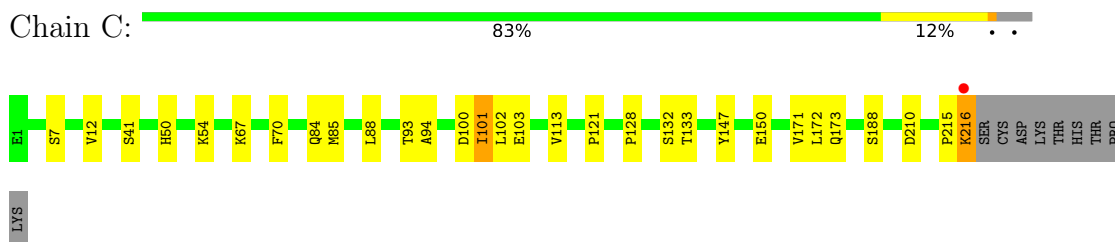
3 Residue-property plots [i](#)

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.

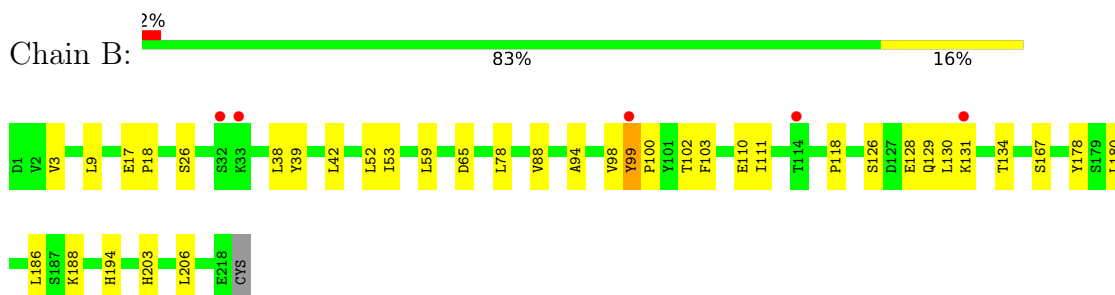
- Molecule 1: Para.09 heavy chain



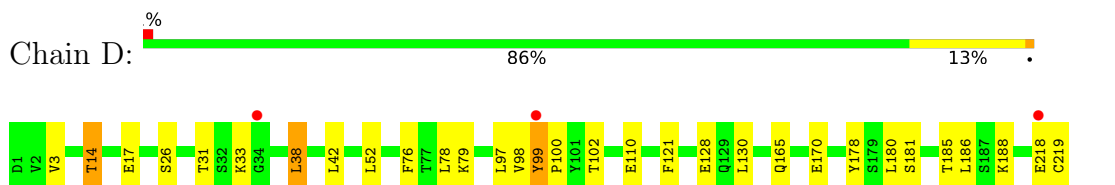
- Molecule 1: Para.09 heavy chain



- Molecule 2: Para.09 light chain

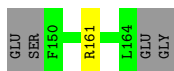


- Molecule 2: Para.09 light chain




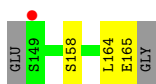
- Molecule 3: Triggering receptor expressed on myeloid cells 2

Chain E:  74% 5% 21%



- Molecule 3: Triggering receptor expressed on myeloid cells 2

Chain F:  5% 74% 16% 11%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.17Å 68.16Å 254.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.78 – 2.00 34.08 – 1.92	Depositor EDS
% Data completeness (in resolution range)	99.9 (33.78-2.00) 92.0 (34.08-1.92)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.78 (at 1.92Å)	Xtrriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.200 , 0.237 0.199 , 0.236	Depositor DCC
R_{free} test set	3629 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	29.0	Xtrriage
Anisotropy	0.086	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7624	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.89% 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: GOL, PEG, ZN

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	0.36	0/1626	0.56	1/2218 (0.0%)
1	C	0.37	0/1699	0.59	0/2318
2	B	0.37	0/1729	0.62	0/2350
2	D	0.37	0/1729	0.62	0/2350
3	E	0.34	0/117	0.52	0/157
3	F	0.34	0/132	0.55	0/177
All	All	0.37	0/7032	0.60	1/9570 (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
2	B	0	1
2	D	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	180	LEU	CA-CB-CG	5.27	127.43	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	98	VAL	Peptide

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Mol	Chain	Res	Type	Group
2	D	98	VAL	Peptide

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	1587	0	1552	26	0
1	C	1658	0	1627	28	0
2	B	1691	0	1667	27	0
2	D	1691	0	1666	32	0
3	E	116	0	106	1	0
3	F	131	0	117	2	0
4	A	12	16	16	2	0
4	B	24	32	32	5	0
4	C	18	24	22	3	0
4	D	6	8	8	0	0
5	B	3	0	0	0	0
5	D	2	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
6	C	7	10	10	0	0
7	A	117	0	0	3	0
7	B	116	0	0	3	0
7	C	160	0	0	5	1
7	D	162	0	0	5	1
7	E	16	0	0	1	0
7	F	15	0	0	0	0
All	All	7534	90	6823	108	1

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.

The worst 5 of 108 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)
2:D:14:THR:HG23	2:D:17:GLU:HG3	1.48	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:203:HIS:HB3	2:B:206:LEU:HD23	1.46	0.95
2:D:218:GLU:OE1	7:D:401:HOH:O	1.84	0.94
1:A:128:PRO:HG3	1:A:140:LEU:HB3	1.54	0.89
1:C:41:SER:HB3	4:C:301:GOL:O2	1.76	0.86

All (1) 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)
7:C:524:HOH:O	7:D:540:HOH:O[3_644]	1.79	0.41

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	207/225 (92%)	199 (96%)	7 (3%)	1 (0%)	29	23
1	C	219/225 (97%)	212 (97%)	6 (3%)	1 (0%)	29	23
2	B	218/219 (100%)	212 (97%)	6 (3%)	0	100	100
2	D	218/219 (100%)	212 (97%)	6 (3%)	0	100	100
3	E	13/19 (68%)	13 (100%)	0	0	100	100
3	F	15/19 (79%)	14 (93%)	1 (7%)	0	100	100
All	All	890/926 (96%)	862 (97%)	26 (3%)	2 (0%)	47	44

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	101	ILE
1	C	101	ILE

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	179/193 (93%)	178 (99%)	1 (1%)	86	90
1	C	189/193 (98%)	187 (99%)	2 (1%)	73	78
2	B	195/194 (100%)	193 (99%)	2 (1%)	76	81
2	D	195/194 (100%)	191 (98%)	4 (2%)	53	57
3	E	13/17 (76%)	13 (100%)	0	100	100
3	F	15/17 (88%)	15 (100%)	0	100	100
All	All	786/808 (97%)	777 (99%)	9 (1%)	71	78

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	97	LEU
2	D	99	TYR
1	C	188	SER
1	C	216	LYS
2	D	14	THR

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 18 ligands modelled in this entry, 7 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	GOL	A	301	-	5,5,5	0.76	0	5,5,5	1.20	0
4	GOL	D	301	-	5,5,5	0.92	0	5,5,5	1.44	1 (20%)
4	GOL	B	305	-	5,5,5	1.38	1 (20%)	5,5,5	1.44	1 (20%)
6	PEG	C	304	-	6,6,6	0.48	0	5,5,5	0.28	0
4	GOL	B	301	-	5,5,5	1.22	0	5,5,5	1.42	1 (20%)
4	GOL	C	302	-	5,5,5	1.20	1 (20%)	5,5,5	1.47	1 (20%)
4	GOL	C	301	-	5,5,5	0.91	0	5,5,5	1.33	1 (20%)
4	GOL	C	303	-	5,5,5	1.34	1 (20%)	5,5,5	1.46	1 (20%)
4	GOL	B	306	-	5,5,5	1.17	1 (20%)	5,5,5	1.43	1 (20%)
4	GOL	B	302	-	5,5,5	0.90	0	5,5,5	1.14	1 (20%)
4	GOL	A	302	-	5,5,5	0.89	0	5,5,5	1.01	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	GOL	A	301	-	-	2/4/4/4	-
4	GOL	D	301	-	-	2/4/4/4	-
4	GOL	B	305	-	-	4/4/4/4	-
6	PEG	C	304	-	-	2/4/4/4	-
4	GOL	B	301	-	-	0/4/4/4	-
4	GOL	C	302	-	-	4/4/4/4	-
4	GOL	C	301	-	-	0/4/4/4	-
4	GOL	C	303	-	-	2/4/4/4	-
4	GOL	B	306	-	-	1/4/4/4	-
4	GOL	B	302	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	A	302	-	-	2/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	302	GOL	O2-C2	-2.63	1.35	1.43
4	C	303	GOL	O2-C2	-2.43	1.36	1.43
4	B	305	GOL	O2-C2	-2.15	1.37	1.43
4	B	306	GOL	O2-C2	-2.01	1.37	1.43

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	303	GOL	C3-C2-C1	-3.00	100.03	111.70
4	B	305	GOL	C3-C2-C1	-2.84	100.68	111.70
4	B	301	GOL	C3-C2-C1	-2.73	101.07	111.70
4	B	306	GOL	C3-C2-C1	-2.69	101.26	111.70
4	C	301	GOL	C3-C2-C1	-2.47	102.09	111.70

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	301	GOL	C1-C2-C3-O3
4	A	302	GOL	O1-C1-C2-O2
4	B	305	GOL	O1-C1-C2-O2
4	B	305	GOL	O1-C1-C2-C3
4	B	305	GOL	C1-C2-C3-O3

There are no ring outliers.

5 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	305	GOL	2	0
4	C	302	GOL	2	0
4	C	301	GOL	1	0
4	B	306	GOL	3	0
4	A	302	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 [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	210/225 (93%)	-0.15	7 (3%) 46 45	27, 36, 55, 84	0
1	C	216/225 (96%)	-0.38	1 (0%) 91 90	23, 30, 48, 82	0
2	B	218/219 (99%)	-0.20	5 (2%) 60 59	27, 35, 54, 81	0
2	D	219/219 (100%)	-0.42	3 (1%) 75 74	24, 32, 44, 98	0
3	E	15/19 (78%)	-0.16	0 100 100	33, 37, 64, 65	0
3	F	17/19 (89%)	0.33	1 (5%) 22 21	28, 33, 81, 88	0
All	All	895/926 (96%)	-0.27	17 (1%) 66 65	23, 33, 53, 98	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	149	SER	5.7
2	B	32	SER	3.3
2	D	34	GLY	3.2
2	B	99	TYR	3.1
1	C	216	LYS	3.0

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
4	GOL	C	301	6/6	0.68	0.26	59,72,85,90	0
4	GOL	B	305	6/6	0.78	0.24	49,70,85,90	0
4	GOL	C	303	6/6	0.79	0.25	53,70,84,87	0
4	GOL	C	302	6/6	0.80	0.20	39,63,75,86	0
4	GOL	B	306	6/6	0.88	0.24	40,62,78,82	0
4	GOL	A	302	6/6	0.88	0.39	54,68,80,85	0
4	GOL	A	301	6/6	0.89	0.23	43,55,77,84	0
6	PEG	C	304	7/7	0.89	0.29	50,61,74,82	0
4	GOL	B	301	6/6	0.91	0.20	30,39,43,47	0
4	GOL	D	301	6/6	0.93	0.14	31,47,57,57	0
4	GOL	B	302	6/6	0.94	0.10	43,52,54,54	0
5	ZN	E	201	1/1	0.98	0.04	50,50,50,50	0
5	ZN	B	307	1/1	0.99	0.05	36,36,36,36	0
5	ZN	D	302	1/1	0.99	0.04	37,37,37,37	0
5	ZN	D	303	1/1	0.99	0.04	33,33,33,33	0
5	ZN	B	303	1/1	0.99	0.06	32,32,32,32	0
5	ZN	F	201	1/1	0.99	0.03	42,42,42,42	0
5	ZN	B	304	1/1	0.99	0.05	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.