



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 07:47 PM UTC

PDB ID : 6YED / pdb_00006yed
Title : E.coli's Putrescine receptor PotF in its open apo state
Authors : Shanmugaratnam, S.; Kroeger, P.; Hocker, B.
Deposited on : 2020-03-24
Resolution : 2.18 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

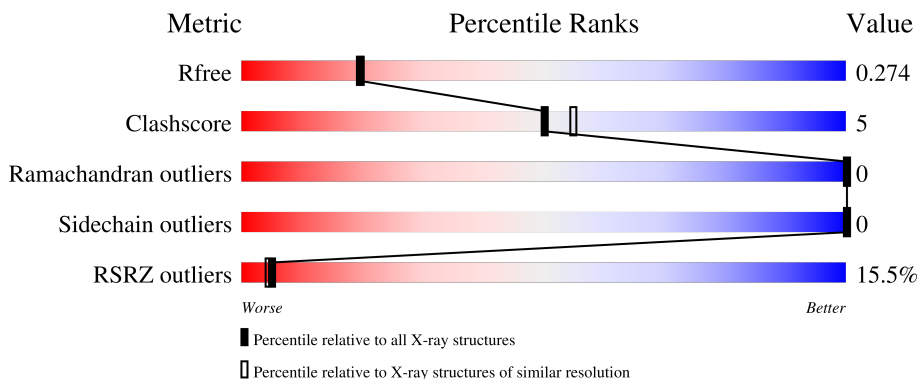
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.18 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	8975 (2.20-2.16)
Clashscore	190562	9786 (2.20-2.16)
Ramachandran outliers	187476	9664 (2.20-2.16)
Sidechain outliers	187428	9664 (2.20-2.16)
RSRZ outliers	180081	8979 (2.20-2.16)

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	352	
1	B	352	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5803 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 Putrescine-binding periplasmic protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	0	4	0
			2695	1733	445	508	9			
1	B	341	Total	C	N	O	S	0	2	0
			2686	1727	445	505	9			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	371	LEU	-	expression tag	UNP P31133
A	372	GLU	-	expression tag	UNP P31133
A	373	HIS	-	expression tag	UNP P31133
A	374	HIS	-	expression tag	UNP P31133
A	375	HIS	-	expression tag	UNP P31133
A	376	HIS	-	expression tag	UNP P31133
A	377	HIS	-	expression tag	UNP P31133
A	378	HIS	-	expression tag	UNP P31133
B	371	LEU	-	expression tag	UNP P31133
B	372	GLU	-	expression tag	UNP P31133
B	373	HIS	-	expression tag	UNP P31133
B	374	HIS	-	expression tag	UNP P31133
B	375	HIS	-	expression tag	UNP P31133
B	376	HIS	-	expression tag	UNP P31133
B	377	HIS	-	expression tag	UNP P31133
B	378	HIS	-	expression tag	UNP P31133

- Molecule 2 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		
3	A	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total Cl 2 2	0	0
5	B	1	Total Cl 1 1	0	0

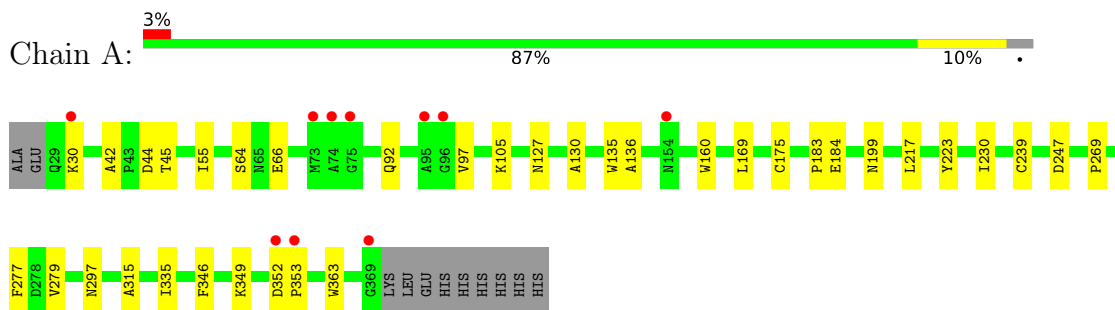
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	199	Total O 199 199	0	0
6	B	108	Total O 108 108	0	0

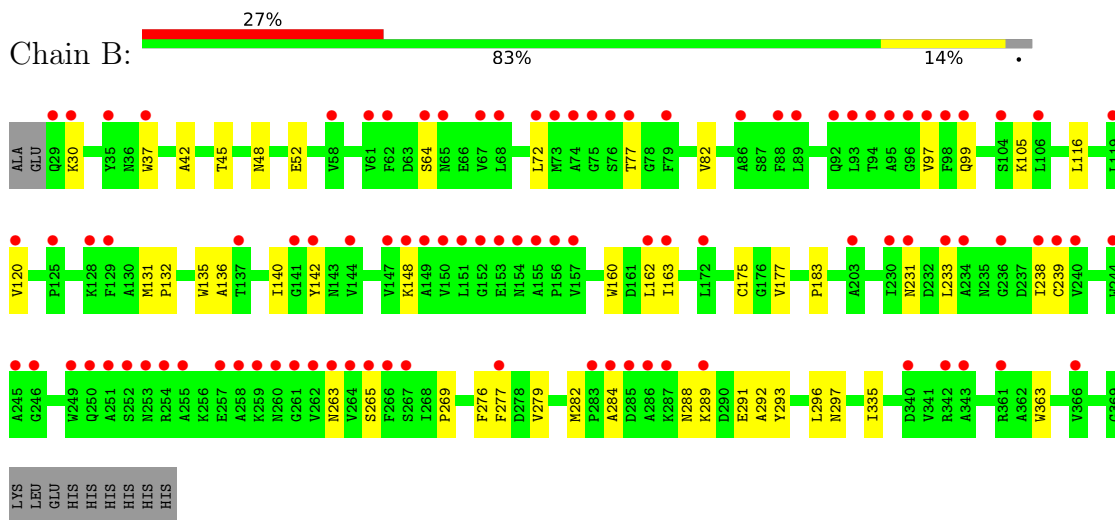
3 Residue-property plots [i](#)

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: Putrescine-binding periplasmic protein



- Molecule 1: Putrescine-binding periplasmic protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	76.22Å 53.45Å 88.13Å 90.00° 111.59° 90.00°	Depositor
Resolution (Å)	45.90 – 2.18 45.90 – 2.18	Depositor EDS
% Data completeness (in resolution range)	99.9 (45.90-2.18) 96.3 (45.90-2.18)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.61 (at 2.18Å)	Xtriage
Refinement program	PHENIX 1.17.1 _3660	Depositor
R, R_{free}	0.228 , 0.273 0.228 , 0.274	Depositor DCC
R_{free} test set	1995 reflections (2.96%)	wwPDB-VP
Wilson B-factor (Å ²)	28.2	Xtriage
Anisotropy	0.325	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 40.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5803	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.14% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PGE, CL, PEG, EDO

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	0.09	0/2775	0.28	0/3776
1	B	0.11	0/2760	0.31	0/3756
All	All	0.10	0/5535	0.29	0/7532

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2695	0	2667	24	0
1	B	2686	0	2656	34	0
2	A	10	0	14	0	0
3	A	14	0	20	1	0
3	B	28	0	40	2	0
4	A	44	0	66	6	0
4	B	16	0	24	3	0
5	A	2	0	0	0	0
5	B	1	0	0	0	0
6	A	199	0	0	1	0
6	B	108	0	0	3	0
All	All	5803	0	5487	58	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 5.

All (58) 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:99:GLN:HG3	1:B:284:ALA:HA	1.68	0.75
1:A:199:ASN:HB2	1:A:349:LYS:HD2	1.74	0.69
1:A:346:PHE:HB3	3:A:403:PEG:H31	1.77	0.66
1:B:72:LEU:HD23	1:B:77:THR:HG21	1.78	0.66
1:B:136:ALA:HA	4:B:405:EDO:H12	1.80	0.64
1:A:352:ASP:OD1	1:A:353:PRO:HD2	1.99	0.62
1:A:175[B]:CYS:HB3	1:A:239[B]:CYS:SG	2.44	0.58
1:B:263:ASN:ND2	6:B:509:HOH:O	2.38	0.57
1:B:291:GLU:OE2	1:B:291:GLU:N	2.34	0.56
1:B:231:ASN:ND2	6:B:511:HOH:O	2.38	0.56
1:A:183:PRO:HB3	1:A:363:TRP:CG	2.41	0.55
1:B:116:LEU:O	1:B:120:VAL:HG23	2.06	0.55
1:A:223:TYR:HA	4:A:412:EDO:H11	1.90	0.54
1:A:199:ASN:CB	1:A:349:LYS:HD2	2.36	0.54
1:A:64:SER:OG	1:A:66:GLU:OE2	2.24	0.54
1:B:160:TRP:CE2	1:B:269:PRO:HG2	2.43	0.54
1:B:292:ALA:O	1:B:296:LEU:HG	2.08	0.53
1:A:136:ALA:HA	4:A:404:EDO:H22	1.90	0.53
1:B:140:ILE:HG21	1:B:162:LEU:HD23	1.91	0.53
1:A:184[A]:GLU:OE2	6:A:501:HOH:O	2.19	0.52
1:B:30:LYS:HD2	1:B:291:GLU:HG3	1.91	0.52
1:A:160:TRP:CE2	1:A:269:PRO:HG2	2.46	0.51
1:A:105:LYS:O	1:A:297:ASN:ND2	2.44	0.50
1:B:183:PRO:HB3	1:B:363:TRP:CG	2.46	0.50
1:B:289:LYS:HZ3	1:B:293:TYR:HE2	1.59	0.50
1:A:230:ILE:HG12	1:A:247:ASP:HB3	1.93	0.50
1:B:37:TRP:CZ3	1:B:64:SER:HA	2.47	0.50
1:B:276:PHE:HE1	4:B:408:EDO:H22	1.78	0.48
1:A:315:ALA:HB3	4:A:404:EDO:H21	1.94	0.48
1:B:288:ASN:HB3	1:B:291:GLU:CD	2.38	0.48
1:A:169:LEU:HD22	1:A:217:LEU:HD22	1.96	0.47
1:B:131:MET:HE1	1:B:296:LEU:HB3	1.96	0.47
1:B:135:TRP:HB3	1:B:277:PHE:CD1	2.50	0.47
1:A:130:ALA:HB1	1:A:279:VAL:HB	1.97	0.46
1:A:30:LYS:HB2	1:A:55:ILE:HA	1.98	0.46
1:A:127:ASN:OD1	4:A:413:EDO:O2	2.29	0.46
1:B:163:ILE:HD11	1:B:177:VAL:HG13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:GLN:HB3	1:A:97:VAL:HG11	1.97	0.46
1:B:52:GLU:HB2	3:B:403:PEG:H32	1.98	0.45
1:A:44:ASP:OD1	1:A:44:ASP:N	2.50	0.45
1:B:99:GLN:HB2	1:B:282:MET:HG3	1.97	0.45
1:B:233:LEU:HG	1:B:238:ILE:HD11	1.99	0.45
1:B:132:PRO:HA	1:B:279:VAL:HG12	1.99	0.45
1:B:335:ILE:HG23	4:B:405:EDO:H22	1.98	0.45
1:A:135:TRP:HB3	1:A:277:PHE:CD1	2.53	0.44
1:A:277:PHE:H	4:A:407:EDO:H21	1.83	0.44
1:B:148:LYS:HE3	1:B:148:LYS:HB2	1.73	0.44
1:B:97:VAL:O	1:B:284:ALA:N	2.50	0.43
1:B:175[B]:CYS:HB3	1:B:239[B]:CYS:HB2	2.00	0.43
1:B:282:MET:HE1	1:B:289:LYS:HG3	2.01	0.42
1:B:72:LEU:HD11	1:B:82:VAL:HG21	2.01	0.42
1:B:105:LYS:O	1:B:297:ASN:ND2	2.50	0.41
1:A:42:ALA:HB3	1:A:45:THR:OG1	2.20	0.41
1:B:48:ASN:HB3	3:B:403:PEG:H31	2.02	0.41
1:B:77:THR:N	6:B:508:HOH:O	2.37	0.41
1:B:142:TYR:CE1	1:B:265:SER:HB2	2.55	0.40
1:A:335:ILE:HG23	4:A:404:EDO:H12	2.01	0.40
1:B:42:ALA:HB3	1:B:45:THR:OG1	2.21	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	343/352 (97%)	337 (98%)	6 (2%)	0	100	100
1	B	341/352 (97%)	331 (97%)	10 (3%)	0	100	100
All	All	684/704 (97%)	668 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	292/298 (98%)	292 (100%)	0	100	100
1	B	290/298 (97%)	290 (100%)	0	100	100
All	All	582/596 (98%)	582 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	GLN
1	A	294	GLN
1	A	297	ASN
1	B	65	ASN
1	B	127	ASN
1	B	263	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 25 ligands modelled in this entry, 3 are monoatomic - leaving 22 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	EDO	A	407	-	3,3,3	0.42	0	2,2,2	0.38	0
3	PEG	B	401	-	6,6,6	0.50	0	5,5,5	0.27	0
4	EDO	B	405	-	3,3,3	0.42	0	2,2,2	0.36	0
4	EDO	A	406	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	A	408	-	3,3,3	0.42	0	2,2,2	0.38	0
4	EDO	A	410	-	3,3,3	0.43	0	2,2,2	0.37	0
4	EDO	B	407	-	3,3,3	0.42	0	2,2,2	0.36	0
4	EDO	A	409	-	3,3,3	0.43	0	2,2,2	0.37	0
4	EDO	B	408	-	3,3,3	0.42	0	2,2,2	0.36	0
3	PEG	B	404	-	6,6,6	0.50	0	5,5,5	0.27	0
3	PEG	A	403	-	6,6,6	0.50	0	5,5,5	0.25	0
4	EDO	A	411	-	3,3,3	0.42	0	2,2,2	0.37	0
3	PEG	B	403	-	6,6,6	0.50	0	5,5,5	0.29	0
4	EDO	A	414	-	3,3,3	0.43	0	2,2,2	0.39	0
4	EDO	B	406	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	A	404	-	3,3,3	0.42	0	2,2,2	0.36	0
4	EDO	A	412	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	A	413	-	3,3,3	0.42	0	2,2,2	0.36	0
3	PEG	A	402	-	6,6,6	0.50	0	5,5,5	0.27	0
4	EDO	A	405	-	3,3,3	0.42	0	2,2,2	0.38	0
3	PEG	B	402	-	6,6,6	0.50	0	5,5,5	0.28	0
2	PGE	A	401	-	9,9,9	0.31	0	8,8,8	0.32	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	EDO	A	407	-	-	0/1/1/1	-
3	PEG	B	401	-	-	0/4/4/4	-
4	EDO	B	405	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	A	406	-	-	0/1/1/1	-
4	EDO	A	408	-	-	0/1/1/1	-
4	EDO	A	410	-	-	0/1/1/1	-
4	EDO	B	407	-	-	0/1/1/1	-
4	EDO	A	409	-	-	0/1/1/1	-
4	EDO	B	408	-	-	0/1/1/1	-
3	PEG	B	404	-	-	0/4/4/4	-
3	PEG	A	403	-	-	2/4/4/4	-
4	EDO	A	411	-	-	0/1/1/1	-
3	PEG	B	403	-	-	0/4/4/4	-
4	EDO	A	414	-	-	0/1/1/1	-
4	EDO	B	406	-	-	0/1/1/1	-
4	EDO	A	404	-	-	0/1/1/1	-
4	EDO	A	412	-	-	0/1/1/1	-
4	EDO	A	413	-	-	0/1/1/1	-
3	PEG	A	402	-	-	1/4/4/4	-
4	EDO	A	405	-	-	0/1/1/1	-
3	PEG	B	402	-	-	2/4/4/4	-
2	PGE	A	401	-	-	3/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	PGE	O2-C3-C4-O3
3	A	403	PEG	C1-C2-O2-C3
3	A	402	PEG	C1-C2-O2-C3
2	A	401	PGE	O1-C1-C2-O2
3	A	403	PEG	O1-C1-C2-O2
3	B	402	PEG	C1-C2-O2-C3
3	B	402	PEG	O1-C1-C2-O2
2	A	401	PGE	C3-C4-O3-C5

There are no ring outliers.

8 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	407	EDO	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	405	EDO	2	0
4	B	408	EDO	1	0
3	A	403	PEG	1	0
3	B	403	PEG	2	0
4	A	404	EDO	3	0
4	A	412	EDO	1	0
4	A	413	EDO	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	341/352 (96%)	0.28	10 (2%) 53 53	16, 31, 54, 83	4 (1%)
1	B	341/352 (96%)	1.48	96 (28%) 1 1	35, 49, 77, 97	2 (0%)
All	All	682/704 (96%)	0.88	106 (15%) 5 4	16, 41, 73, 97	6 (0%)

All (106) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	74	ALA	4.9
1	B	258	ALA	4.7
1	B	264	VAL	4.4
1	B	259	LYS	4.3
1	B	73	MET	4.2
1	B	149	ALA	4.2
1	B	93	LEU	4.2
1	B	97	VAL	4.2
1	B	266	PHE	4.0
1	B	162	LEU	4.0
1	B	88	PHE	3.9
1	B	234	ALA	3.8
1	B	95	ALA	3.7
1	B	151	LEU	3.6
1	B	286	ALA	3.6
1	B	152	GLY	3.6
1	B	79	PHE	3.6
1	B	67	VAL	3.5
1	B	285	ASP	3.4
1	B	250	GLN	3.3
1	B	65	ASN	3.3
1	B	163	ILE	3.3
1	B	98	PHE	3.3
1	B	262	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	72	LEU	3.2
1	B	155	ALA	3.2
1	B	251	ALA	3.2
1	B	148	LYS	3.2
1	B	154	ASN	3.2
1	A	352	ASP	3.1
1	B	231	ASN	3.1
1	B	77	THR	3.1
1	B	129	PHE	3.1
1	B	61	VAL	3.0
1	A	353	PRO	3.0
1	B	255	ALA	3.0
1	B	246	GLY	3.0
1	B	147	VAL	2.9
1	B	157	VAL	2.9
1	B	29	GLN	2.9
1	B	125	PRO	2.9
1	B	144	VAL	2.8
1	B	89	LEU	2.8
1	B	260	ASN	2.8
1	B	257	GLU	2.8
1	B	64	SER	2.8
1	B	96	GLY	2.7
1	B	62	PHE	2.7
1	B	68	LEU	2.7
1	B	156	PRO	2.7
1	B	150	VAL	2.7
1	B	265	SER	2.7
1	B	203	ALA	2.6
1	B	340	ASP	2.6
1	A	369	GLY	2.6
1	B	236	GLY	2.6
1	B	99	GLN	2.6
1	B	128	LYS	2.6
1	B	142	TYR	2.5
1	B	366	VAL	2.5
1	B	153	GLU	2.5
1	B	283	PRO	2.5
1	B	342	ARG	2.5
1	A	73	MET	2.4
1	B	37	TRP	2.4
1	B	252	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	137	THR	2.4
1	B	75	GLY	2.3
1	B	94	THR	2.3
1	B	284	ALA	2.3
1	B	106	LEU	2.3
1	B	172	LEU	2.3
1	B	261	GLY	2.3
1	B	58	VAL	2.3
1	B	120	VAL	2.3
1	A	75	GLY	2.3
1	B	35	TYR	2.3
1	B	267	SER	2.2
1	A	95	ALA	2.2
1	B	244	TRP	2.2
1	B	254	ARG	2.2
1	A	154	ASN	2.2
1	B	30	LYS	2.2
1	B	230	ILE	2.2
1	B	240	VAL	2.2
1	B	287	LYS	2.2
1	B	86	ALA	2.2
1	B	245	ALA	2.2
1	B	104	SER	2.2
1	A	30	LYS	2.2
1	B	238	ILE	2.2
1	B	343	ALA	2.2
1	B	119	LEU	2.1
1	B	253	ASN	2.1
1	B	92	GLN	2.1
1	A	96	GLY	2.1
1	B	239[A]	CYS	2.1
1	B	263	ASN	2.1
1	A	74	ALA	2.1
1	B	233	LEU	2.1
1	B	277	PHE	2.1
1	B	141	GLY	2.0
1	B	76	SER	2.0
1	B	249	TRP	2.0
1	B	361	ARG	2.0
1	B	289	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	PEG	B	402	7/7	0.51	0.21	70,70,71,72	0
4	EDO	B	405	4/4	0.56	0.34	76,76,78,78	0
4	EDO	A	412	4/4	0.60	0.23	54,56,57,58	0
3	PEG	B	403	7/7	0.65	0.24	68,69,71,71	0
4	EDO	A	409	4/4	0.65	0.24	64,64,65,65	0
3	PEG	A	402	7/7	0.68	0.20	65,66,67,68	0
4	EDO	B	408	4/4	0.70	0.21	64,64,66,67	0
3	PEG	A	403	7/7	0.74	0.19	58,59,60,60	0
4	EDO	A	406	4/4	0.74	0.24	61,62,62,62	0
4	EDO	A	414	4/4	0.75	0.17	56,56,57,57	0
3	PEG	B	404	7/7	0.75	0.16	54,57,59,60	0
3	PEG	B	401	7/7	0.75	0.15	67,67,68,69	0
4	EDO	A	413	4/4	0.76	0.17	56,57,57,57	0
2	PGE	A	401	10/10	0.79	0.14	51,52,53,53	0
5	CL	B	409	1/1	0.81	0.22	105,105,105,105	0
4	EDO	A	407	4/4	0.83	0.15	34,37,40,42	0
4	EDO	A	405	4/4	0.83	0.29	66,66,67,67	0
4	EDO	A	411	4/4	0.83	0.20	48,49,51,52	0
4	EDO	B	406	4/4	0.84	0.13	55,55,56,56	0
4	EDO	B	407	4/4	0.85	0.16	44,44,44,45	0
4	EDO	A	408	4/4	0.86	0.15	52,53,53,54	0
4	EDO	A	410	4/4	0.87	0.16	53,53,53,53	0
4	EDO	A	404	4/4	0.88	0.15	29,31,31,32	0
5	CL	A	416	1/1	0.91	0.23	84,84,84,84	0
5	CL	A	415	1/1	0.94	0.12	53,53,53,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.