



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:47 AM UTC

PDB ID : 7QRF / pdb_00007qrf
Title : Structure of the dimeric complex between precursor membrane ectodomain (prM) and envelope protein ectodomain (E) from tick-borne encephalitis virus
Authors : Vaney, M.C.; Rouvinski, A.; Rey, F.A.
Deposited on : 2022-01-11
Resolution : 2.28 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

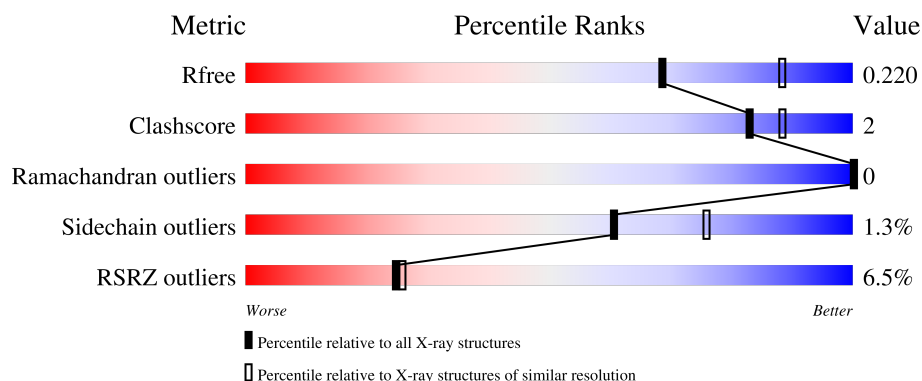
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.28 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	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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	443	7% 79% 7% 14%
2	C	5	100%
3	D	138	% 57% . 42%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3689 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 Envelope protein E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	382	Total	C	N	O	S	0	0	1
			2931	1845	515	550	21			

There are 43 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP P14336
A	-2	GLY	-	expression tag	UNP P14336
A	-1	GLY	-	expression tag	UNP P14336
A	0	GLY	-	expression tag	UNP P14336
A	401	GLY	-	expression tag	UNP P14336
A	402	PRO	-	expression tag	UNP P14336
A	403	PHE	-	expression tag	UNP P14336
A	404	GLU	-	expression tag	UNP P14336
A	405	ASP	-	expression tag	UNP P14336
A	406	ASP	-	expression tag	UNP P14336
A	407	ASP	-	expression tag	UNP P14336
A	408	ASP	-	expression tag	UNP P14336
A	409	LYS	-	expression tag	UNP P14336
A	410	ALA	-	expression tag	UNP P14336
A	411	GLY	-	expression tag	UNP P14336
A	412	TRP	-	expression tag	UNP P14336
A	413	SER	-	expression tag	UNP P14336
A	414	HIS	-	expression tag	UNP P14336
A	415	PRO	-	expression tag	UNP P14336
A	416	GLN	-	expression tag	UNP P14336
A	417	PHE	-	expression tag	UNP P14336
A	418	GLU	-	expression tag	UNP P14336
A	419	LYS	-	expression tag	UNP P14336
A	420	GLY	-	expression tag	UNP P14336
A	421	GLY	-	expression tag	UNP P14336
A	422	GLY	-	expression tag	UNP P14336
A	423	SER	-	expression tag	UNP P14336

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Chain	Residue	Modelled	Actual	Comment	Reference
A	424	GLY	-	expression tag	UNP P14336
A	425	GLY	-	expression tag	UNP P14336
A	426	GLY	-	expression tag	UNP P14336
A	427	SER	-	expression tag	UNP P14336
A	428	GLY	-	expression tag	UNP P14336
A	429	GLY	-	expression tag	UNP P14336
A	430	GLY	-	expression tag	UNP P14336
A	431	SER	-	expression tag	UNP P14336
A	432	TRP	-	expression tag	UNP P14336
A	433	SER	-	expression tag	UNP P14336
A	434	HIS	-	expression tag	UNP P14336
A	435	PRO	-	expression tag	UNP P14336
A	436	GLN	-	expression tag	UNP P14336
A	437	PHE	-	expression tag	UNP P14336
A	438	GLU	-	expression tag	UNP P14336
A	439	LYS	-	expression tag	UNP P14336

- Molecule 2 is a protein called Unknown peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	5	Total	C	N	O	0	0	0
			25	15	5	5			

- Molecule 3 is a protein called Genome polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	80	Total	C	N	O	S	0	0	0
			606	365	105	129	7			

There are 11 discrepancies between the modelled and reference sequences:

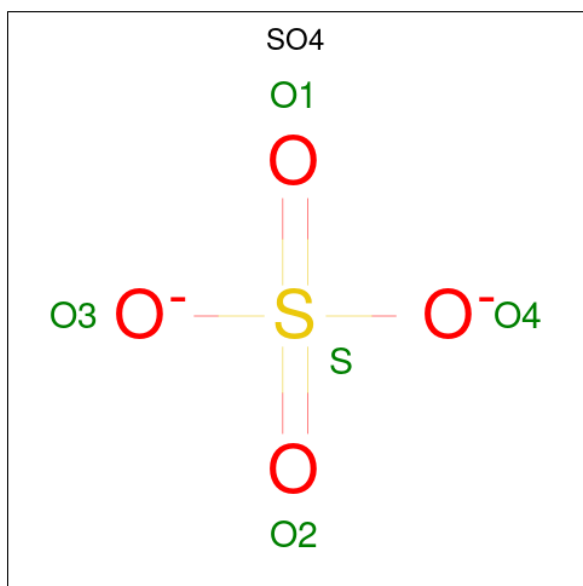
Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	ARG	deletion	UNP P14336
D	129	GLY	-	expression tag	UNP P14336
D	130	GLY	-	expression tag	UNP P14336
D	131	GLY	-	expression tag	UNP P14336
D	132	GLY	-	expression tag	UNP P14336
D	133	GLU	-	expression tag	UNP P14336
D	134	ASN	-	expression tag	UNP P14336
D	135	LEU	-	expression tag	UNP P14336
D	136	TYR	-	expression tag	UNP P14336
D	137	PHE	-	expression tag	UNP P14336

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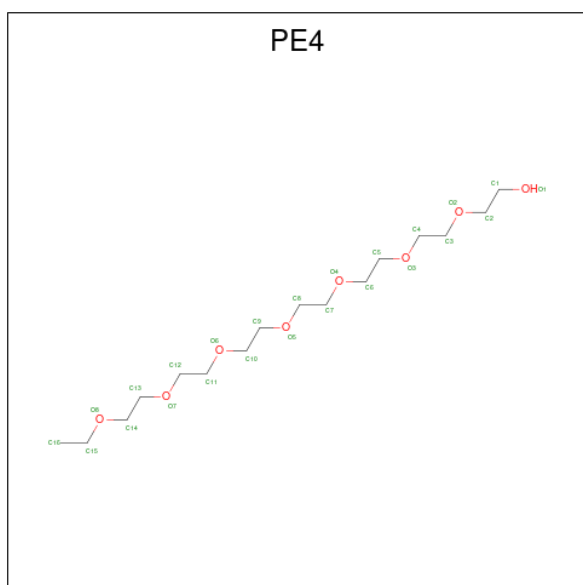
Chain	Residue	Modelled	Actual	Comment	Reference
D	138	GLN	-	expression tag	UNP P14336

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



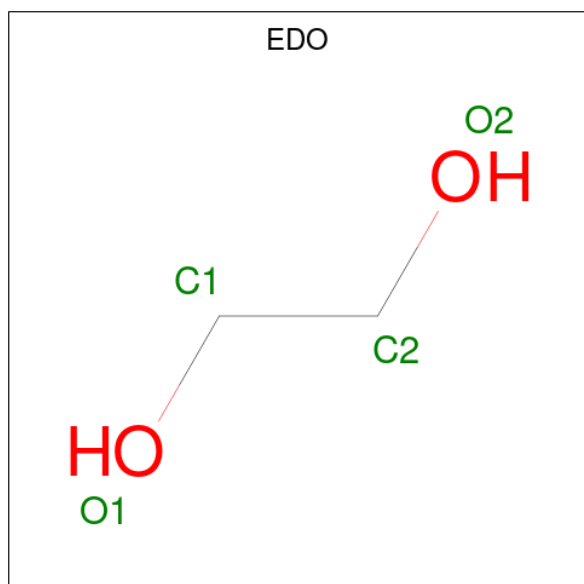
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is 2-{2-[2-(2-{2-[2-(2-ETHOXY-ETHOXY)-ETHOXY]-ETHOXY}-ETHOXY)-ETHOXY]-ETHOXY}-ETHANOL (CCD ID: PE4) (formula: C₁₆H₃₄O₈).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			16	10	6		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	65	Total	O	0	0
			65	65		

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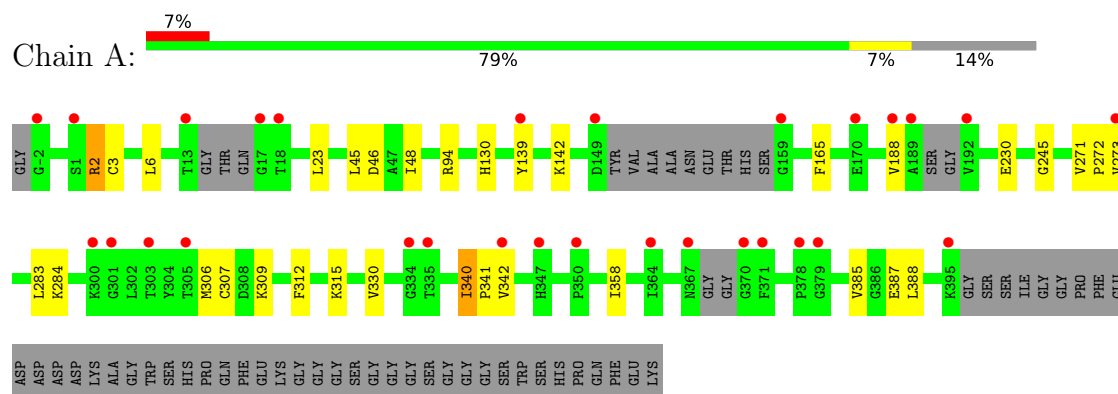
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	D	9	Total	O	0	0
			9	9		

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: Envelope protein E

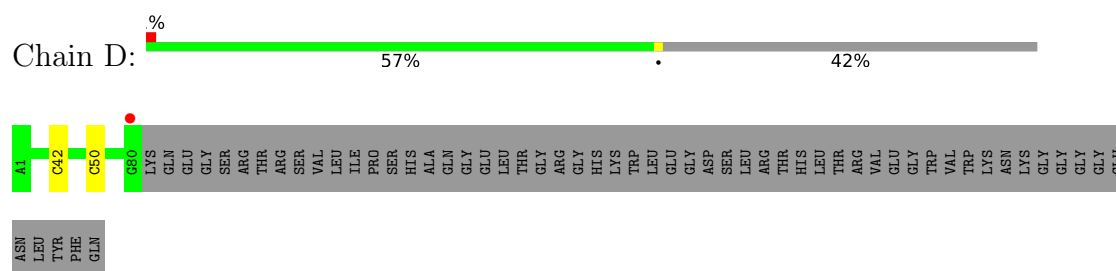


• Molecule 2: Unknown peptide



There are no outlier residues recorded for this chain.

• Molecule 3: Genome polypeptide



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	155.73Å 155.73Å 161.88Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.42 – 2.28 28.42 – 2.28	Depositor EDS
% Data completeness (in resolution range)	84.0 (28.42-2.28) 84.2 (28.42-2.28)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.86 (at 2.29Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.181 , 0.213 0.190 , 0.220	Depositor DCC
R_{free} test set	1487 reflections (3.89%)	wwPDB-VP
Wilson B-factor (Å ²)	66.2	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 60.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3689	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.06% 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: SO4, EDO, PE4

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	0.85	0/2993	1.17	6/4057 (0.1%)
3	D	0.74	0/612	1.19	4/828 (0.5%)
All	All	0.83	0/3605	1.17	10/4885 (0.2%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	50	CYS	CA-C-N	6.98	130.88	120.69
3	D	50	CYS	C-N-CA	6.98	130.88	120.69
3	D	42	CYS	CA-C-N	6.76	129.34	120.28
3	D	42	CYS	C-N-CA	6.76	129.34	120.28
1	A	315	LYS	N-CA-C	-5.97	104.15	112.45
1	A	340	ILE	N-CA-C	5.72	114.56	108.95
1	A	273	VAL	N-CA-CB	5.70	116.75	110.53
1	A	2	ARG	CA-C-N	5.45	127.58	120.28
1	A	2	ARG	C-N-CA	5.45	127.58	120.28
1	A	358	ILE	N-CA-C	-5.08	105.19	112.35

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	2931	0	2895	17	0
2	C	25	0	9	0	0
3	D	606	0	565	0	0
4	A	5	0	0	0	0
5	A	16	0	21	0	0
6	A	24	0	36	3	0
6	D	8	0	12	0	0
7	A	65	0	0	1	0
7	D	9	0	0	0	0
All	All	3689	0	3538	17	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 2.

All (17) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:272:PRO:HB2	1:A:284:LYS:HG2	1.77	0.65
1:A:340:ILE:HG22	1:A:342:VAL:HG13	1.81	0.61
1:A:307:CYS:HB2	1:A:341:PRO:HD3	1.84	0.59
1:A:130:HIS:HD2	7:A:604:HOH:O	1.88	0.55
1:A:309:LYS:HB3	1:A:387:GLU:HG3	1.91	0.52
1:A:330:VAL:HG11	1:A:385:VAL:HG11	1.93	0.51
1:A:245:GLY:HA2	6:A:505:EDO:H11	1.94	0.49
1:A:271:VAL:HG13	1:A:272:PRO:HD2	1.96	0.48
1:A:139:TYR:CE2	1:A:165:PHE:HB2	2.49	0.47
1:A:2:ARG:NH2	1:A:6:LEU:HD11	2.30	0.47
1:A:45:LEU:HD21	1:A:48:ILE:HD11	1.99	0.44
1:A:230:GLU:HG3	6:A:506:EDO:H21	1.99	0.44
1:A:48:ILE:CG2	1:A:283:LEU:HD12	2.49	0.42
1:A:48:ILE:HG21	1:A:283:LEU:HD12	2.02	0.42
1:A:245:GLY:CA	6:A:505:EDO:H11	2.49	0.42
1:A:46:ASP:CG	1:A:142:LYS:HE2	2.45	0.42
1:A:312:PHE:HB3	1:A:388:LEU:HD22	2.04	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	372/443 (84%)	360 (97%)	12 (3%)	0	100	100
3	D	78/138 (56%)	78 (100%)	0	0	100	100
All	All	450/581 (78%)	438 (97%)	12 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	317/357 (89%)	312 (98%)	5 (2%)	55	71
3	D	67/114 (59%)	67 (100%)	0	100	100
All	All	384/471 (82%)	379 (99%)	5 (1%)	61	76

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	CYS
1	A	23	LEU
1	A	94	ARG
1	A	188	VAL
1	A	306	MET

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	52	ASN
1	A	196	GLN
1	A	221	ASN
1	A	282	HIS
1	A	366	ASN
1	A	375	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

10 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	EDO	A	504	-	3,3,3	0.42	0	2,2,2	0.52	0
6	EDO	A	503	-	3,3,3	0.56	0	2,2,2	0.58	0
6	EDO	A	505	-	3,3,3	0.58	0	2,2,2	0.14	0
6	EDO	A	507	-	3,3,3	0.54	0	2,2,2	0.37	0
6	EDO	D	201	-	3,3,3	0.50	0	2,2,2	0.38	0
6	EDO	A	508	-	3,3,3	0.53	0	2,2,2	0.38	0
5	PE4	A	502	-	15,15,23	0.77	0	14,14,22	0.66	0
4	SO4	A	501	-	4,4,4	0.23	0	6,6,6	0.28	0
6	EDO	A	506	-	3,3,3	0.49	0	2,2,2	0.39	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	EDO	D	202	-	3,3,3	0.61	0	2,2,2	0.20	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
6	EDO	A	504	-	-	0/1/1/1	-
6	EDO	A	503	-	-	1/1/1/1	-
6	EDO	A	505	-	-	1/1/1/1	-
6	EDO	A	507	-	-	0/1/1/1	-
6	EDO	D	201	-	-	0/1/1/1	-
5	PE4	A	502	-	-	5/13/13/21	-
6	EDO	A	508	-	-	0/1/1/1	-
6	EDO	A	506	-	-	0/1/1/1	-
6	EDO	D	202	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	502	PE4	O1-C1-C2-O2
5	A	502	PE4	O2-C3-C4-O3
6	A	503	EDO	O1-C1-C2-O2
5	A	502	PE4	C5-C6-O4-C7
5	A	502	PE4	C8-C7-O4-C6
5	A	502	PE4	C4-C3-O2-C2
6	A	505	EDO	O1-C1-C2-O2

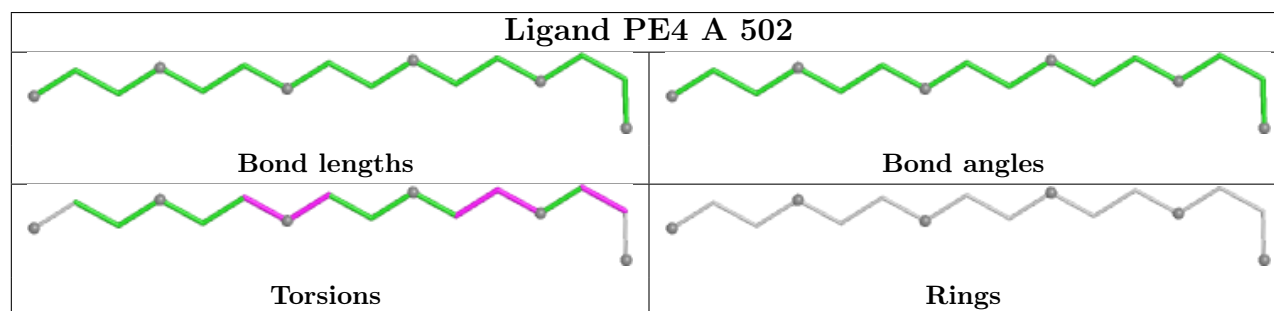
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	505	EDO	2	0
6	A	506	EDO	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	382/443 (86%)	0.44	29 (7%) 20 20	50, 74, 122, 155	0
2	C	0/5	-	-	-	-
3	D	80/138 (57%)	0.35	1 (1%) 75 76	64, 84, 124, 137	0
All	All	462/586 (78%)	0.43	30 (6%) 25 26	50, 77, 122, 155	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	370	GLY	4.8
1	A	192	VAL	4.6
3	D	80	GLY	4.3
1	A	189	ALA	4.3
1	A	139	TYR	4.0
1	A	301	GLY	3.6
1	A	371	PHE	3.3
1	A	13	THR	3.2
1	A	-2	GLY	3.2
1	A	17	GLY	3.1
1	A	18	THR	3.0
1	A	395	LYS	2.9
1	A	379	GLY	2.8
1	A	188	VAL	2.5
1	A	364	ILE	2.5
1	A	149	ASP	2.5
1	A	303	THR	2.5
1	A	273	VAL	2.5
1	A	378	PRO	2.4
1	A	300	LYS	2.4
1	A	305	THR	2.4
1	A	367	ASN	2.4
1	A	1	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	342	VAL	2.3
1	A	159	GLY	2.2
1	A	350	PRO	2.1
1	A	347	HIS	2.1
1	A	170	GLU	2.1
1	A	335	THR	2.1
1	A	334	GLY	2.1

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](#)

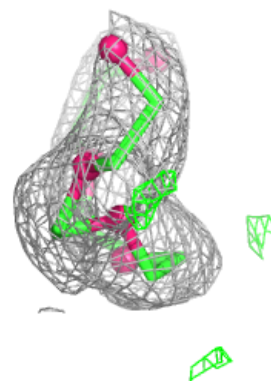
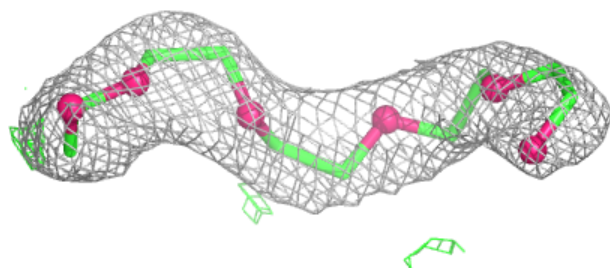
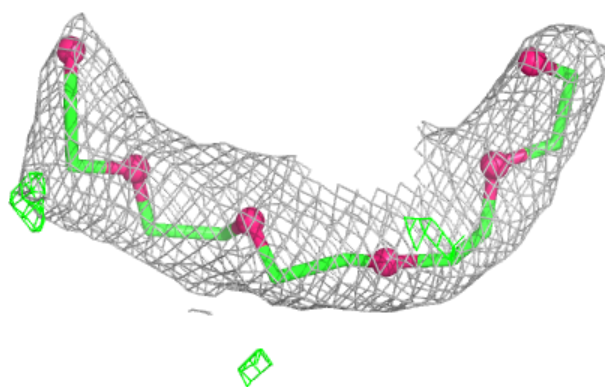
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	EDO	A	508	4/4	0.66	0.15	128,128,129,129	0
6	EDO	D	202	4/4	0.72	0.21	112,114,115,116	0
5	PE4	A	502	16/24	0.85	0.15	86,97,109,109	0
6	EDO	A	506	4/4	0.86	0.13	94,95,97,99	0
6	EDO	A	503	4/4	0.86	0.14	55,60,71,79	0
6	EDO	A	505	4/4	0.86	0.18	73,76,79,83	0
6	EDO	D	201	4/4	0.87	0.19	79,79,82,86	0
6	EDO	A	507	4/4	0.87	0.18	106,107,107,107	0
6	EDO	A	504	4/4	0.89	0.18	82,85,91,94	0
4	SO4	A	501	5/5	0.95	0.06	82,83,85,89	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around PE4 A 502:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.