



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:38 AM UTC

PDB ID : 8V5Q / pdb_00008v5q
Title : Varicella Zoster Virus (VZV) glycoprotein E (gE) gI binding domain in complex with human Fab 1E3
Authors : Holzapfel, G.; Seraj, N.; Harshbarger, W.
Deposited on : 2023-11-30
Resolution : 1.90 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

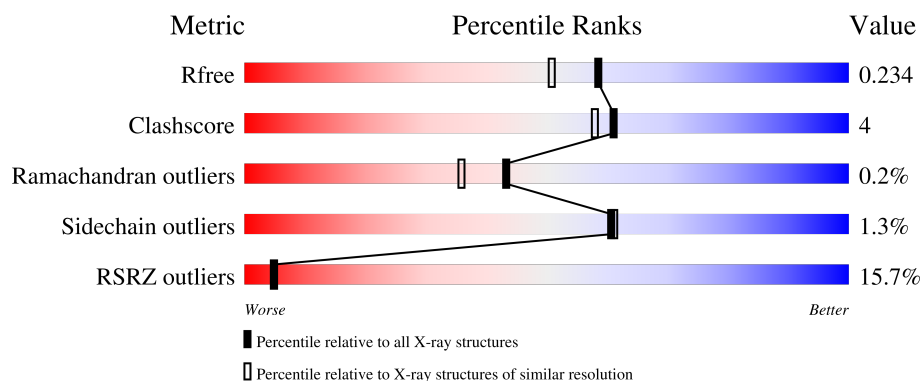
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	H	245	15% 83% 7% 10%
2	L	213	15% 93% 5% ..
3	G	203	9% 47% 9% 43%

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	PEG	H	301	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4451 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 Fab 1E3 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	220	Total	C	N	O	S	0	0	0
			1666	1056	276	330	4			

- Molecule 2 is a protein called Fab 1E3 Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	211	Total	C	N	O	S	0	0	0
			1622	1013	276	327	6			

- Molecule 3 is a protein called Envelope glycoprotein E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	116	Total	C	N	O	S	0	0	0
			948	612	154	181	1			

There are 13 discrepancies between the modelled and reference sequences:

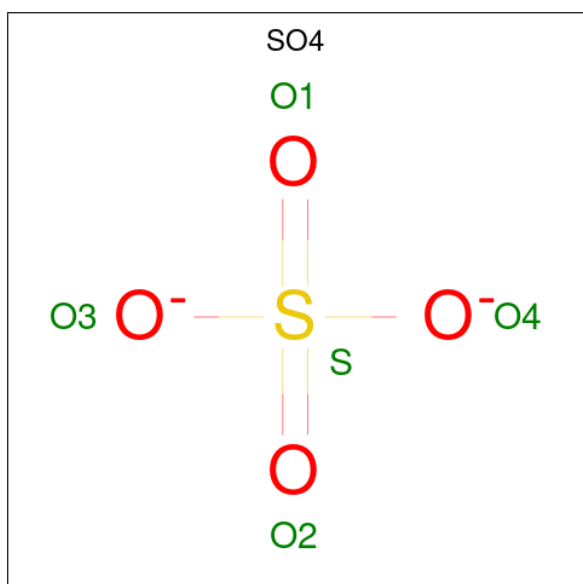
Chain	Residue	Modelled	Actual	Comment	Reference
G	306	GLU	-	expression tag	UNP A6XEF7
G	307	ASN	-	expression tag	UNP A6XEF7
G	308	LEU	-	expression tag	UNP A6XEF7
G	309	TYR	-	expression tag	UNP A6XEF7
G	310	PHE	-	expression tag	UNP A6XEF7
G	311	GLN	-	expression tag	UNP A6XEF7
G	312	GLY	-	expression tag	UNP A6XEF7
G	313	HIS	-	expression tag	UNP A6XEF7
G	314	HIS	-	expression tag	UNP A6XEF7
G	315	HIS	-	expression tag	UNP A6XEF7
G	316	HIS	-	expression tag	UNP A6XEF7
G	317	HIS	-	expression tag	UNP A6XEF7
G	318	HIS	-	expression tag	UNP A6XEF7

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



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

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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

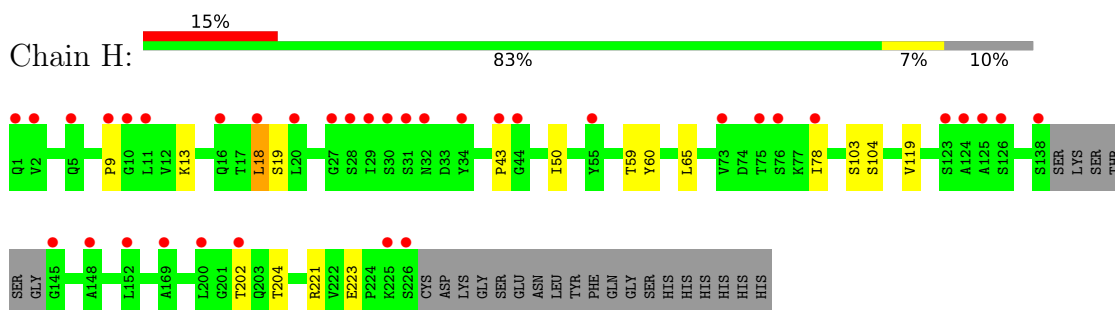
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	56	Total	O	0	0
			56	56		
6	L	89	Total	O	0	0
			89	89		
6	G	32	Total	O	0	0
			32	32		

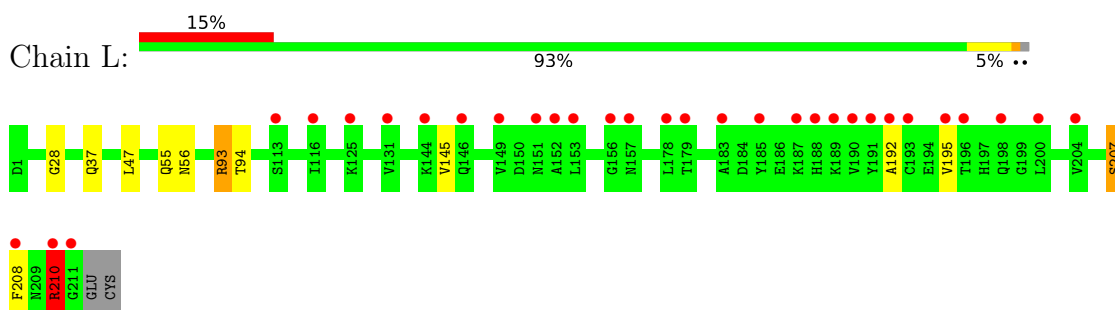
3 Residue-property plots

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.

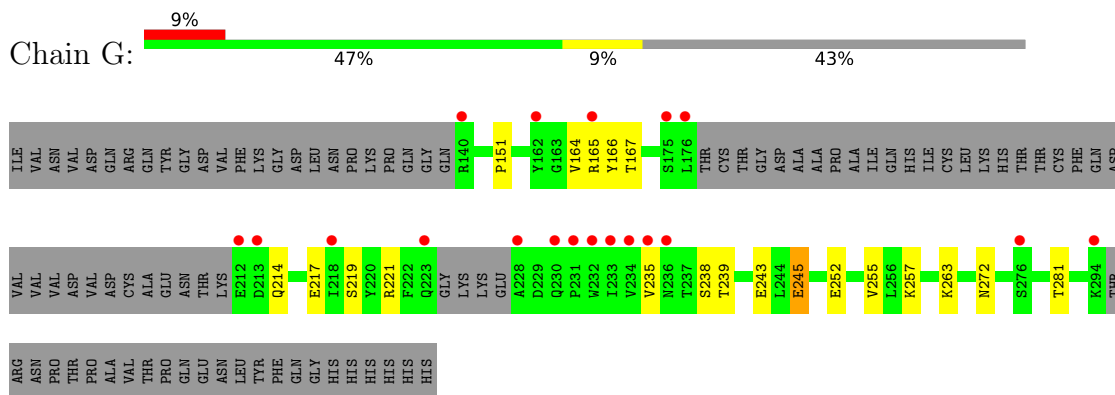
• Molecule 1: Fab 1E3 Heavy Chain



• Molecule 2: Fab 1E3 Light Chain



• Molecule 3: Envelope glycoprotein E



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	44.62Å 193.75Å 179.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.72 – 1.90 33.72 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.4 (33.72-1.90) 89.2 (33.72-1.90)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.63 (at 1.91Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.226 , 0.233 0.227 , 0.234	Depositor DCC
R_{free} test set	1995 reflections (3.23%)	wwPDB-VP
Wilson B-factor (Å ²)	25.6	Xtriage
Anisotropy	0.737	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 43.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4451	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 4.81% 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, PEG

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	H	0.48	0/1708	0.75	1/2334 (0.0%)
2	L	0.52	0/1656	0.78	2/2247 (0.1%)
3	G	0.46	0/972	0.75	1/1325 (0.1%)
All	All	0.49	0/4336	0.76	4/5906 (0.1%)

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	L	0	2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	208	PHE	CA-CB-CG	5.65	119.45	113.80
3	G	245	GLU	CB-CA-C	5.54	119.59	111.73
2	L	210	ARG	N-CA-CB	5.32	119.47	110.49
1	H	43	PRO	CA-N-CD	-5.13	104.82	112.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	L	210	ARG	Sidechain
2	L	93	ARG	Sidechain

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	H	1666	0	1633	13	0
2	L	1622	0	1583	7	0
3	G	948	0	907	13	0
4	G	14	0	20	4	0
4	H	14	0	20	9	0
5	G	10	0	0	0	0
6	G	32	0	0	2	0
6	H	56	0	0	0	0
6	L	89	0	0	0	0
All	All	4451	0	4163	35	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 4.

All (35) 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:H:103:SER:HA	4:H:301:PEG:H31	1.55	0.85
1:H:104:SER:H	4:H:301:PEG:C3	1.99	0.76
1:H:103:SER:CA	4:H:301:PEG:H31	2.19	0.73
1:H:221:ARG:NH1	1:H:223:GLU:OE2	2.23	0.70
3:G:217:GLU:HG2	3:G:235:VAL:HB	1.74	0.69
1:H:204:THR:HG23	1:H:221:ARG:HE	1.59	0.67
1:H:104:SER:H	4:H:301:PEG:H31	1.63	0.61
3:G:165:ARG:HD3	3:G:221:ARG:HH21	1.65	0.60
1:H:104:SER:N	4:H:301:PEG:C3	2.69	0.56
1:H:104:SER:N	4:H:301:PEG:H31	2.21	0.55
2:L:37:GLN:HB2	2:L:47:LEU:HD11	1.91	0.53
3:G:165:ARG:CD	3:G:221:ARG:HH21	2.20	0.53
3:G:257:LYS:HE2	6:G:505:HOH:O	2.10	0.52
2:L:145:VAL:HG22	2:L:195:VAL:HG22	1.92	0.52
2:L:192:ALA:HB2	2:L:207:SER:HB3	1.90	0.51
2:L:28:GLY:H	4:G:404:PEG:C3	2.25	0.49
3:G:252:GLU:HB2	3:G:255:VAL:CG1	2.43	0.48
1:H:50:ILE:HG23	1:H:65:LEU:HD13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:301:PEG:H32	6:G:504:HOH:O	2.15	0.47
3:G:245:GLU:OE1	4:G:404:PEG:H22	2.15	0.47
2:L:93:ARG:O	2:L:94:THR:C	2.57	0.46
3:G:167:THR:HG22	3:G:219:SER:HB3	1.98	0.45
3:G:239:THR:O	3:G:243:GLU:HG2	2.16	0.45
4:H:301:PEG:H41	4:H:301:PEG:H21	1.69	0.43
3:G:164:VAL:HB	3:G:166:TYR:CE2	2.54	0.43
1:H:18:LEU:HD12	1:H:119:VAL:HG11	2.01	0.42
2:L:55:GLN:HG3	2:L:56:ASN:N	2.33	0.42
1:H:60:TYR:CZ	3:G:151:PRO:HB2	2.55	0.42
3:G:272:ASN:HA	3:G:281:THR:O	2.20	0.42
4:H:302:PEG:H41	4:H:302:PEG:H22	1.79	0.41
2:L:28:GLY:HA3	4:G:404:PEG:H11	2.03	0.41
3:G:214:GLN:O	3:G:238:SER:HB2	2.21	0.41
3:G:263:LYS:HE3	3:G:263:LYS:HB2	1.90	0.41
1:H:9:PRO:HD2	1:H:19:SER:O	2.21	0.41
1:H:59:THR:OG1	4:G:403:PEG:H42	2.20	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	H	216/245 (88%)	205 (95%)	11 (5%)	0	100	100
2	L	209/213 (98%)	200 (96%)	8 (4%)	1 (0%)	24	16
3	G	110/203 (54%)	108 (98%)	2 (2%)	0	100	100
All	All	535/661 (81%)	513 (96%)	21 (4%)	1 (0%)	43	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	210	ARG

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	H	191/213 (90%)	187 (98%)	4 (2%)	47	44
2	L	185/187 (99%)	183 (99%)	2 (1%)	65	67
3	G	103/182 (57%)	103 (100%)	0	100	100
All	All	479/582 (82%)	473 (99%)	6 (1%)	61	61

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	13	LYS
1	H	18	LEU
1	H	78	ILE
1	H	202	THR
2	L	207	SER
2	L	210	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	41	GLN
1	H	203	GLN
2	L	38	GLN
2	L	137	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 [i](#)

6 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	$\# Z > 2$
4	PEG	G	404	-	6,6,6	0.10	0	5,5,5	0.12	0
4	PEG	H	302	-	6,6,6	0.13	0	5,5,5	0.10	0
4	PEG	H	301	-	6,6,6	0.10	0	5,5,5	0.10	0
5	SO4	G	402	-	4,4,4	0.40	0	6,6,6	0.07	0
4	PEG	G	403	-	6,6,6	0.14	0	5,5,5	0.06	0
5	SO4	G	401	-	4,4,4	0.47	0	6,6,6	0.09	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	PEG	G	403	-	-	3/4/4/4	-
4	PEG	H	301	-	-	2/4/4/4	-
4	PEG	H	302	-	-	2/4/4/4	-
4	PEG	G	404	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	G	403	PEG	C1-C2-O2-C3
4	H	301	PEG	C4-C3-O2-C2
4	H	302	PEG	C4-C3-O2-C2
4	G	404	PEG	O1-C1-C2-O2
4	G	404	PEG	O2-C3-C4-O4
4	G	403	PEG	O1-C1-C2-O2
4	G	403	PEG	C4-C3-O2-C2
4	G	404	PEG	C1-C2-O2-C3
4	H	301	PEG	C1-C2-O2-C3
4	G	404	PEG	C4-C3-O2-C2
4	H	302	PEG	O2-C3-C4-O4

There are no ring outliers.

4 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	404	PEG	3	0
4	H	302	PEG	1	0
4	H	301	PEG	8	0
4	G	403	PEG	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	H	220/245 (89%)	1.13	36 (16%) 4 4	23, 43, 67, 84	0
2	L	211/213 (99%)	0.91	31 (14%) 6 6	22, 41, 70, 75	0
3	G	116/203 (57%)	1.05	19 (16%) 4 4	23, 39, 68, 95	0
All	All	547/661 (82%)	1.03	86 (15%) 5 5	22, 42, 68, 95	0

All (86) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	G	176	LEU	6.5
1	H	125	ALA	4.9
1	H	28	SER	4.4
1	H	126	SER	4.4
1	H	1	GLN	4.0
1	H	27	GLY	3.9
3	G	228	ALA	3.8
3	G	223	GLN	3.8
1	H	78	ILE	3.7
2	L	144	LYS	3.7
1	H	43	PRO	3.7
1	H	9	PRO	3.6
3	G	162	TYR	3.5
3	G	294	LYS	3.5
1	H	20	LEU	3.4
1	H	225	LYS	3.4
2	L	191	TYR	3.4
2	L	208	PHE	3.4
3	G	236	ASN	3.3
1	H	75	THR	3.3
2	L	210	ARG	3.3
1	H	138	SER	3.3
1	H	2	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	H	226	SER	3.1
2	L	200	LEU	3.1
3	G	175	SER	3.1
2	L	198	GLN	3.0
1	H	124	ALA	3.0
2	L	146	GLN	3.0
2	L	149	VAL	2.9
1	H	30	SER	2.9
3	G	212	GLU	2.9
1	H	202	THR	2.8
3	G	230	GLN	2.8
3	G	231	PRO	2.8
1	H	44	GLY	2.8
2	L	196	THR	2.8
2	L	193	CYS	2.7
3	G	234	VAL	2.7
1	H	29	ILE	2.7
2	L	195	VAL	2.7
3	G	233	ILE	2.6
3	G	213	ASP	2.6
2	L	192	ALA	2.6
3	G	235	VAL	2.6
1	H	32	ASN	2.6
2	L	152	ALA	2.5
2	L	178	LEU	2.5
2	L	153	LEU	2.5
1	H	16	GLN	2.5
1	H	148	ALA	2.4
2	L	187	LYS	2.4
3	G	232	TRP	2.4
2	L	190	VAL	2.4
1	H	169	ALA	2.4
1	H	10	GLY	2.4
2	L	183	ALA	2.3
2	L	131	VAL	2.3
2	L	157	ASN	2.3
2	L	188	HIS	2.3
1	H	145	GLY	2.3
2	L	204	VAL	2.3
2	L	113	SER	2.2
3	G	218	ILE	2.2
3	G	140	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	H	73	VAL	2.2
1	H	31	SER	2.2
2	L	211	GLY	2.2
1	H	76	SER	2.2
3	G	276	SER	2.2
2	L	189	LYS	2.2
2	L	116	ILE	2.1
1	H	123	SER	2.1
1	H	11	LEU	2.1
1	H	152	LEU	2.1
1	H	200	LEU	2.1
2	L	156	GLY	2.1
1	H	18	LEU	2.1
2	L	125	LYS	2.0
1	H	34	TYR	2.0
1	H	55	TYR	2.0
2	L	185	TYR	2.0
2	L	179	THR	2.0
3	G	165	ARG	2.0
1	H	5	GLN	2.0
2	L	151	ASN	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
5	SO4	G	402	5/5	0.69	0.16	48,50,61,67	0
4	PEG	G	404	7/7	0.74	0.18	39,44,49,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	PEG	H	301	7/7	0.76	0.19	35,40,54,55	0
4	PEG	H	302	7/7	0.77	0.18	41,53,57,60	0
4	PEG	G	403	7/7	0.80	0.16	47,49,59,59	0
5	SO4	G	401	5/5	0.98	0.06	29,33,35,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.