



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:47 AM UTC

PDB ID : 4KRY / pdb_00004kry
Title : Structure of Aes from E. coli in covalent complex with PMS
Authors : Schiefner, A.; Gerber, K.; Brosig, A.; Boos, W.
Deposited on : 2013-05-17
Resolution : 2.30 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

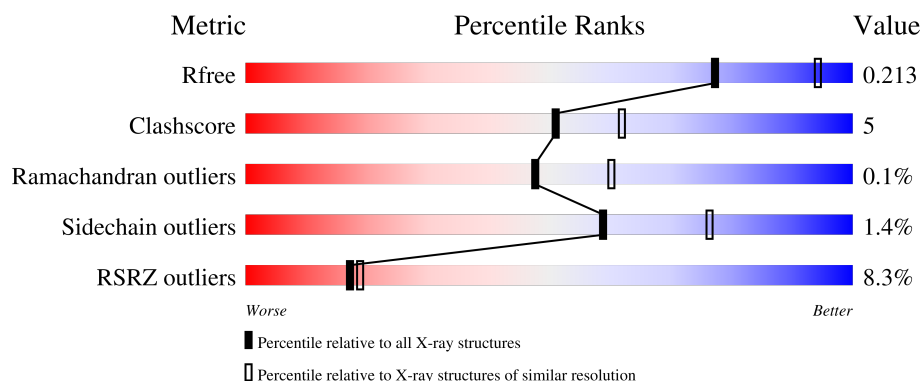
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	333	9% 86% 10% 5%
1	B	333	6% 85% 10% 5%
1	C	333	10% 83% 13% 5%
1	D	333	6% 84% 11% 5%
1	E	333	2% 89% 10% .

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Mol	Chain	Length	Quality of chain
1	F	333	14% 87% 9% 5%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 15961 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 Acetyl esterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	318	Total	C	N	O	S	0	0	0
			2537	1621	424	474	18			
1	B	318	Total	C	N	O	S	0	1	0
			2545	1626	427	474	18			
1	C	318	Total	C	N	O	S	0	2	0
			2554	1631	428	477	18			
1	D	318	Total	C	N	O	S	0	1	0
			2545	1626	427	474	18			
1	E	329	Total	C	N	O	S	0	3	0
			2660	1695	455	490	20			
1	F	318	Total	C	N	O	S	0	0	0
			2537	1621	424	474	18			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	expression tag	UNP P23872
A	-12	ARG	-	expression tag	UNP P23872
A	-11	GLY	-	expression tag	UNP P23872
A	-10	SER	-	expression tag	UNP P23872
A	-9	HIS	-	expression tag	UNP P23872
A	-8	HIS	-	expression tag	UNP P23872
A	-7	HIS	-	expression tag	UNP P23872
A	-6	HIS	-	expression tag	UNP P23872
A	-5	HIS	-	expression tag	UNP P23872
A	-4	HIS	-	expression tag	UNP P23872
A	-3	THR	-	expression tag	UNP P23872
A	-2	ASP	-	expression tag	UNP P23872
A	-1	PRO	-	expression tag	UNP P23872
A	0	ILE	-	expression tag	UNP P23872
B	-13	MET	-	expression tag	UNP P23872
B	-12	ARG	-	expression tag	UNP P23872
B	-11	GLY	-	expression tag	UNP P23872

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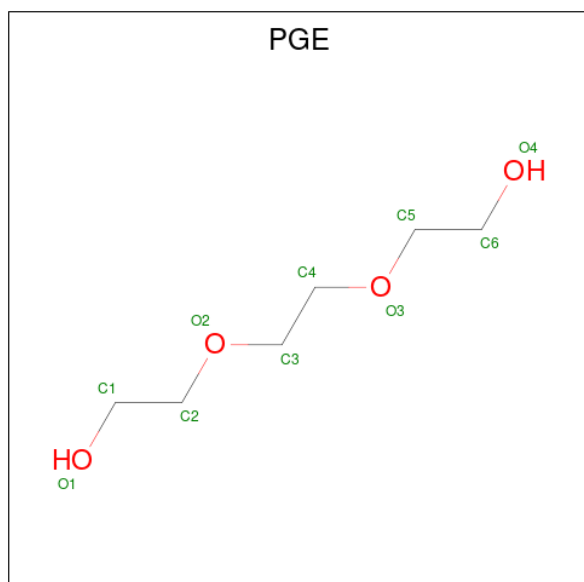
Chain	Residue	Modelled	Actual	Comment	Reference
B	-10	SER	-	expression tag	UNP P23872
B	-9	HIS	-	expression tag	UNP P23872
B	-8	HIS	-	expression tag	UNP P23872
B	-7	HIS	-	expression tag	UNP P23872
B	-6	HIS	-	expression tag	UNP P23872
B	-5	HIS	-	expression tag	UNP P23872
B	-4	HIS	-	expression tag	UNP P23872
B	-3	THR	-	expression tag	UNP P23872
B	-2	ASP	-	expression tag	UNP P23872
B	-1	PRO	-	expression tag	UNP P23872
B	0	ILE	-	expression tag	UNP P23872
C	-13	MET	-	expression tag	UNP P23872
C	-12	ARG	-	expression tag	UNP P23872
C	-11	GLY	-	expression tag	UNP P23872
C	-10	SER	-	expression tag	UNP P23872
C	-9	HIS	-	expression tag	UNP P23872
C	-8	HIS	-	expression tag	UNP P23872
C	-7	HIS	-	expression tag	UNP P23872
C	-6	HIS	-	expression tag	UNP P23872
C	-5	HIS	-	expression tag	UNP P23872
C	-4	HIS	-	expression tag	UNP P23872
C	-3	THR	-	expression tag	UNP P23872
C	-2	ASP	-	expression tag	UNP P23872
C	-1	PRO	-	expression tag	UNP P23872
C	0	ILE	-	expression tag	UNP P23872
D	-13	MET	-	expression tag	UNP P23872
D	-12	ARG	-	expression tag	UNP P23872
D	-11	GLY	-	expression tag	UNP P23872
D	-10	SER	-	expression tag	UNP P23872
D	-9	HIS	-	expression tag	UNP P23872
D	-8	HIS	-	expression tag	UNP P23872
D	-7	HIS	-	expression tag	UNP P23872
D	-6	HIS	-	expression tag	UNP P23872
D	-5	HIS	-	expression tag	UNP P23872
D	-4	HIS	-	expression tag	UNP P23872
D	-3	THR	-	expression tag	UNP P23872
D	-2	ASP	-	expression tag	UNP P23872
D	-1	PRO	-	expression tag	UNP P23872
D	0	ILE	-	expression tag	UNP P23872
E	-13	MET	-	expression tag	UNP P23872
E	-12	ARG	-	expression tag	UNP P23872
E	-11	GLY	-	expression tag	UNP P23872

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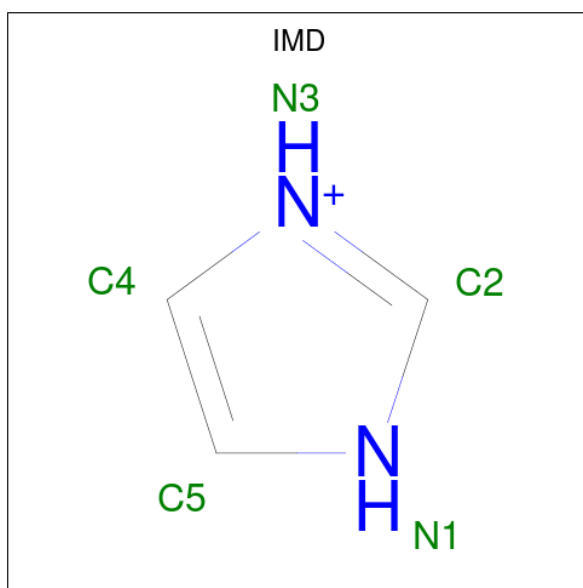
Chain	Residue	Modelled	Actual	Comment	Reference
E	-10	SER	-	expression tag	UNP P23872
E	-9	HIS	-	expression tag	UNP P23872
E	-8	HIS	-	expression tag	UNP P23872
E	-7	HIS	-	expression tag	UNP P23872
E	-6	HIS	-	expression tag	UNP P23872
E	-5	HIS	-	expression tag	UNP P23872
E	-4	HIS	-	expression tag	UNP P23872
E	-3	THR	-	expression tag	UNP P23872
E	-2	ASP	-	expression tag	UNP P23872
E	-1	PRO	-	expression tag	UNP P23872
E	0	ILE	-	expression tag	UNP P23872
F	-13	MET	-	expression tag	UNP P23872
F	-12	ARG	-	expression tag	UNP P23872
F	-11	GLY	-	expression tag	UNP P23872
F	-10	SER	-	expression tag	UNP P23872
F	-9	HIS	-	expression tag	UNP P23872
F	-8	HIS	-	expression tag	UNP P23872
F	-7	HIS	-	expression tag	UNP P23872
F	-6	HIS	-	expression tag	UNP P23872
F	-5	HIS	-	expression tag	UNP P23872
F	-4	HIS	-	expression tag	UNP P23872
F	-3	THR	-	expression tag	UNP P23872
F	-2	ASP	-	expression tag	UNP P23872
F	-1	PRO	-	expression tag	UNP P23872
F	0	ILE	-	expression tag	UNP P23872

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



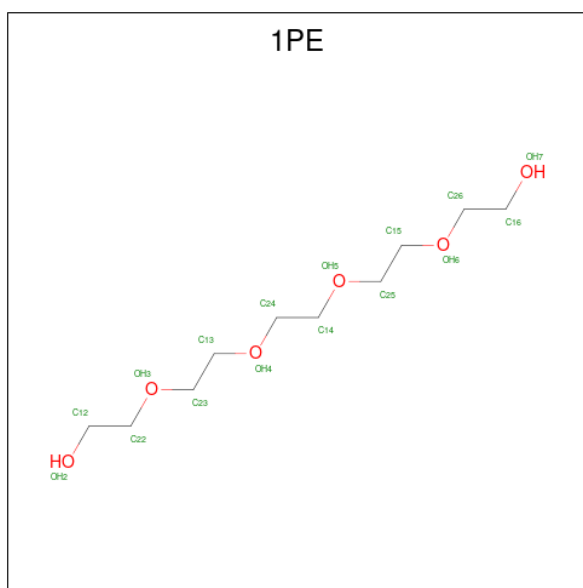
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 10 6 4	0	0
2	A	1	Total C O 10 6 4	0	0
2	B	1	Total C O 10 6 4	0	0
2	C	1	Total C O 10 6 4	0	0
2	D	1	Total C O 10 6 4	0	0
2	D	1	Total C O 10 6 4	0	0
2	E	1	Total C O 10 6 4	0	0
2	F	1	Total C O 10 6 4	0	0

- Molecule 3 is IMIDAZOLE (CCD ID: IMD) (formula: $C_3H_5N_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N 5 3 2	0	0
3	B	1	Total C N 5 3 2	0	0
3	D	1	Total C N 5 3 2	0	0
3	D	1	Total C N 5 3 2	0	0

- Molecule 4 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	C	O	0	0
			16	10	6		
4	E	1	Total	C	O	0	0
			16	10	6		

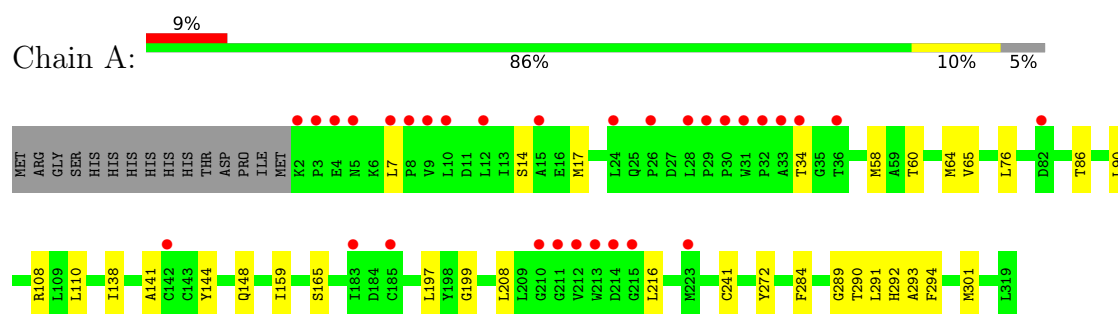
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	72	Total	O	0	0
			72	72		
5	B	82	Total	O	0	1
			83	83		
5	C	45	Total	O	0	0
			45	45		
5	D	98	Total	O	0	0
			98	98		
5	E	116	Total	O	0	1
			117	117		
5	F	36	Total	O	0	0
			36	36		

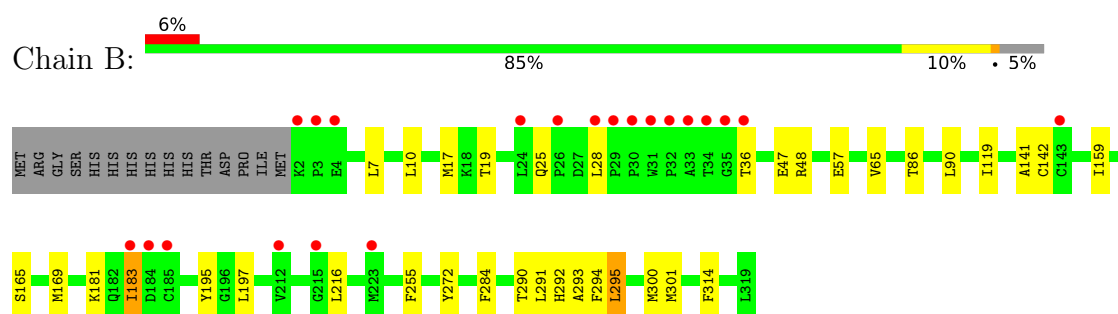
3 Residue-property plots [i](#)

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.

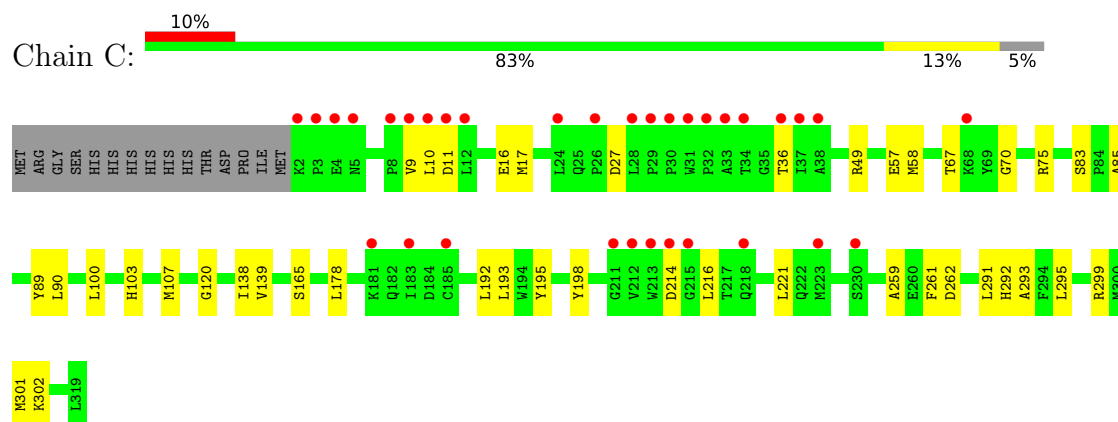
- Molecule 1: Acetyl esterase



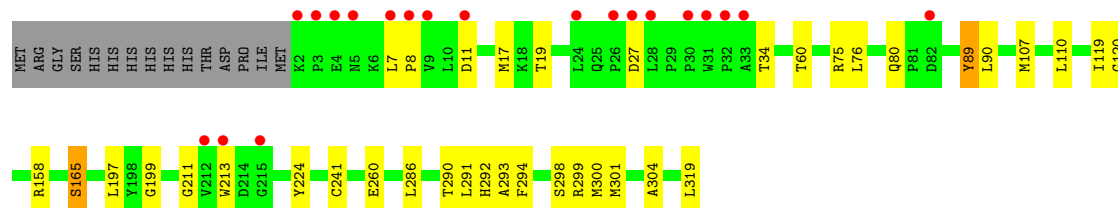
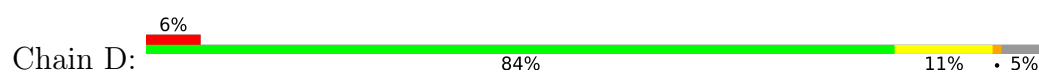
- Molecule 1: Acetyl esterase



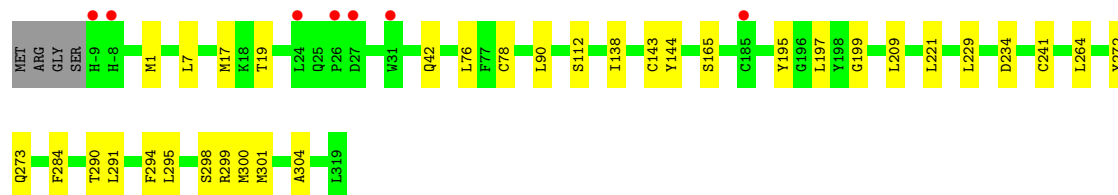
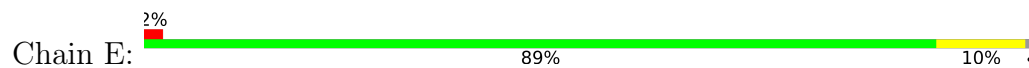
- Molecule 1: Acetyl esterase



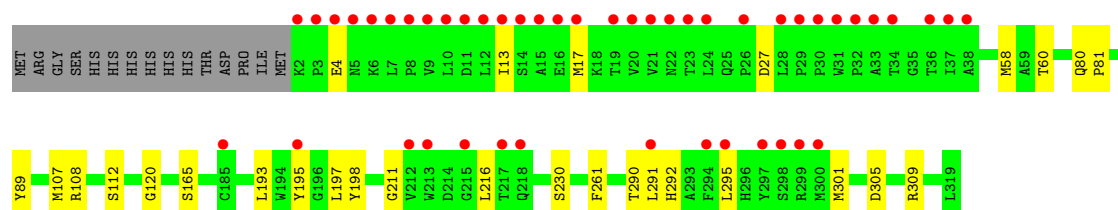
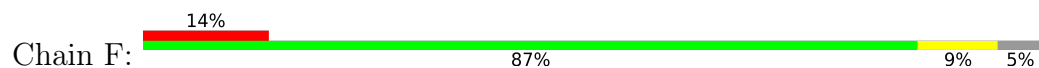
- Molecule 1: Acetyl esterase



• Molecule 1: Acetyl esterase



• Molecule 1: Acetyl esterase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	111.40Å 111.40Å 282.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.37 – 2.30 29.37 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (29.37-2.30) 99.8 (29.37-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.40 (at 2.31Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.179 , 0.209 0.184 , 0.213	Depositor DCC
R_{free} test set	7572 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	34.8	Xtriage
Anisotropy	0.138	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 50.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.068 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	15961	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.61% 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: IMD, PGE, 1PE, SEB

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	0.78	0/2586	0.85	0/3516
1	B	0.82	0/2597	0.90	0/3530
1	C	0.67	0/2606	0.81	0/3542
1	D	0.90	1/2597 (0.0%)	0.93	2/3530 (0.1%)
1	E	0.87	0/2719	0.92	0/3697
1	F	0.68	0/2586	0.82	1/3516 (0.0%)
All	All	0.79	1/15691 (0.0%)	0.87	3/21331 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	89	TYR	C-O	6.08	1.31	1.24

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	80	GLN	CA-C-N	-5.32	114.29	120.04
1	D	80	GLN	C-N-CA	-5.32	114.29	120.04
1	F	211	GLY	N-CA-C	5.24	118.94	110.87

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	2537	0	2450	25	0
1	B	2545	0	2463	30	0
1	C	2554	0	2468	27	0
1	D	2545	0	2463	28	0
1	E	2660	0	2563	30	0
1	F	2537	0	2450	19	0
2	A	20	0	28	3	0
2	B	10	0	14	1	0
2	C	10	0	14	2	0
2	D	20	0	28	3	0
2	E	10	0	14	1	0
2	F	10	0	14	2	0
3	A	5	0	5	0	0
3	B	5	0	5	0	0
3	D	10	0	10	0	0
4	D	16	0	22	0	0
4	E	16	0	22	2	0
5	A	72	0	0	0	0
5	B	83	0	0	0	0
5	C	45	0	0	0	0
5	D	98	0	0	3	0
5	E	117	0	0	2	0
5	F	36	0	0	0	0
All	All	15961	0	15033	158	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 (158) 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:F:107:MET:HE1	1:F:120:GLY:HA3	1.33	1.10
1:E:17:MET:HE2	1:E:301:MET:HE1	1.34	1.09
1:D:17:MET:HE2	1:D:301:MET:HE1	1.38	1.04
1:F:107:MET:HE1	1:F:120:GLY:CA	1.96	0.94
1:B:17:MET:HE2	1:B:301:MET:HE1	1.52	0.91
1:F:89:TYR:HB3	1:F:107:MET:HE3	1.53	0.91
1:C:89:TYR:HB3	1:C:107:MET:HE3	1.53	0.90
1:D:107:MET:HE1	1:D:120:GLY:CA	2.00	0.90
1:A:17:MET:HE2	1:A:301:MET:HE1	1.55	0.89
1:C:107:MET:HE1	1:C:120:GLY:HA3	1.55	0.88
1:C:107:MET:HE1	1:C:120:GLY:CA	2.06	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:107:MET:HE1	1:D:120:GLY:HA3	1.58	0.85
1:C:17:MET:HE3	1:C:291:LEU:H	1.42	0.84
1:F:17:MET:HE2	1:F:301:MET:HE1	1.57	0.84
1:C:17:MET:HE2	1:C:301:MET:HE1	1.61	0.82
1:E:76:LEU:CD2	1:E:78[A]:CYS:SG	2.68	0.81
1:D:17:MET:HE3	1:D:290:THR:HA	1.69	0.73
1:B:19:THR:HG22	1:B:300:MET:HE1	1.73	0.71
1:E:17:MET:HE3	1:E:290:THR:HA	1.72	0.70
1:B:181:LYS:HE3	1:B:183:ILE:HD11	1.73	0.70
1:D:107:MET:HE1	1:D:120:GLY:N	2.06	0.69
1:A:64:MET:HE2	2:A:402:PGE:C4	2.22	0.69
1:A:64:MET:HE2	2:A:402:PGE:H42	1.76	0.68
1:E:299[A]:ARG:HH11	1:E:299[A]:ARG:HG2	1.57	0.68
1:F:197:LEU:HD12	2:F:401:PGE:H12	1.76	0.67
1:E:299[A]:ARG:HG2	1:E:299[A]:ARG:NH1	2.09	0.67
1:E:17:MET:HE2	1:E:301:MET:CE	2.20	0.67
1:D:17:MET:HE2	1:D:301:MET:CE	2.20	0.66
1:B:181:LYS:CE	1:B:183:ILE:HD11	2.26	0.65
1:B:17:MET:HE3	1:B:291:LEU:H	1.62	0.65
1:A:197:LEU:H	1:A:197:LEU:HD23	1.62	0.64
1:B:197:LEU:HD12	2:B:401:PGE:H22	1.79	0.64
1:E:17:MET:CE	1:E:301:MET:HE1	2.22	0.64
1:B:47:GLU:OE1	1:B:48:ARG:HD3	1.98	0.63
1:D:89:TYR:HB3	1:D:107:MET:HE3	1.80	0.63
1:B:197:LEU:HD23	1:B:197:LEU:H	1.66	0.60
1:F:305:ASP:OD2	1:F:309:ARG:NH1	2.34	0.60
1:E:221:LEU:HB3	2:E:401:PGE:H32	1.83	0.59
1:C:17:MET:HE2	1:C:301:MET:CE	2.30	0.59
1:B:65:VAL:HG11	1:B:141:ALA:HA	1.85	0.59
1:B:195:TYR:OH	1:B:295:LEU:HB2	2.03	0.58
1:D:107:MET:CE	1:D:120:GLY:CA	2.80	0.58
1:E:299[A]:ARG:HH11	1:E:299[A]:ARG:CG	2.16	0.58
1:E:17:MET:HE3	1:E:290:THR:CA	2.34	0.57
1:D:17:MET:HE3	1:D:290:THR:CA	2.35	0.57
1:A:17:MET:HE3	1:A:291:LEU:H	1.70	0.56
1:D:197:LEU:HD12	2:D:401:PGE:H12	1.87	0.56
1:D:76:LEU:HG	1:D:119:ILE:HG12	1.87	0.56
1:A:197:LEU:HD12	2:A:401:PGE:H22	1.88	0.55
1:E:76:LEU:HD23	1:E:78[A]:CYS:SG	2.47	0.55
1:A:90:LEU:HD22	1:A:138:ILE:CD1	2.37	0.55
1:C:221:LEU:HB3	2:C:401:PGE:C4	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:139:VAL:HG13	1:C:178:LEU:HD21	1.89	0.55
2:D:402:PGE:H12	5:D:566:HOH:O	2.07	0.54
1:F:197:LEU:HD12	2:F:401:PGE:C1	2.36	0.54
1:A:144:TYR:O	1:A:148:GLN:HG2	2.08	0.54
1:B:17:MET:HE3	1:B:290:THR:HA	1.90	0.53
1:B:17:MET:CE	1:B:301:MET:HE1	2.33	0.53
1:C:259:ALA:HB3	1:C:262:ASP:HB2	1.91	0.53
1:D:17:MET:HE1	1:D:294:PHE:HB2	1.91	0.53
1:F:60:THR:HG21	1:F:108:ARG:NH2	2.24	0.53
1:C:57:GLU:O	1:C:58:MET:HB3	2.09	0.52
1:E:229:LEU:HD22	1:E:234:ASP:HB3	1.92	0.52
1:F:107:MET:CE	1:F:120:GLY:CA	2.81	0.52
1:A:58:MET:O	1:A:60:THR:HG23	2.10	0.52
1:D:211:GLY:HA3	1:D:213:TRP:CZ3	2.45	0.52
1:D:17:MET:HE3	1:D:291:LEU:H	1.75	0.51
1:A:65:VAL:HG11	1:A:141:ALA:HA	1.93	0.51
1:E:90:LEU:HD22	1:E:138:ILE:CD1	2.41	0.50
1:D:19:THR:HG22	1:D:300:MET:HE1	1.93	0.50
1:A:17:MET:HE2	1:A:301:MET:CE	2.33	0.50
1:F:17:MET:HE3	1:F:291:LEU:H	1.77	0.50
1:B:17:MET:HE1	1:B:294:PHE:CB	2.42	0.49
1:C:83:SER:OG	1:C:85:ALA:O	2.30	0.49
1:D:165:SEB:HI2	1:D:224:TYR:CZ	2.48	0.49
1:E:195:TYR:OH	1:E:295:LEU:HB2	2.13	0.49
1:C:221:LEU:HB3	2:C:401:PGE:H42	1.94	0.49
1:E:199:GLY:HA3	1:E:241:CYS:HA	1.95	0.48
1:C:90:LEU:HD22	1:C:138:ILE:CD1	2.44	0.48
1:A:216:LEU:HD11	1:A:292:HIS:CD2	2.48	0.48
1:B:19:THR:CG2	1:B:300:MET:HE1	2.42	0.47
1:A:292:HIS:O	1:A:293:ALA:HB3	2.14	0.47
1:B:57:GLU:HG3	1:C:57:GLU:HG3	1.96	0.47
1:E:17:MET:HE3	1:E:291:LEU:H	1.78	0.47
1:B:17:MET:HE1	1:B:294:PHE:HB3	1.95	0.47
1:B:216:LEU:HD11	1:B:292:HIS:CG	2.49	0.47
1:D:298:SER:HA	1:D:304:ALA:HB3	1.96	0.47
2:D:402:PGE:C1	5:D:566:HOH:O	2.62	0.47
1:D:60:THR:HA	1:D:76:LEU:O	2.15	0.47
1:E:7:LEU:HD12	1:E:209:LEU:HD21	1.97	0.47
1:D:17:MET:HE1	1:D:294:PHE:CB	2.45	0.46
1:E:76:LEU:HD22	1:E:78[A]:CYS:SG	2.53	0.46
1:F:17:MET:HE2	1:F:301:MET:CE	2.38	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:197:LEU:H	1:D:197:LEU:HD23	1.80	0.46
1:E:197:LEU:H	1:E:197:LEU:HD23	1.80	0.46
1:E:273:GLN:NE2	5:E:596:HOH:O	2.49	0.46
1:E:298:SER:HA	1:E:304:ALA:HB3	1.98	0.46
1:E:143:CYS:HB3	4:E:402:1PE:H221	1.98	0.46
1:A:17:MET:HE3	1:A:290:THR:HA	1.98	0.46
1:A:34:THR:O	1:A:34:THR:HG22	2.16	0.46
1:A:110:LEU:HD12	1:A:110:LEU:HA	1.85	0.45
1:E:144:TYR:HB2	4:E:402:1PE:H131	1.98	0.45
1:B:25:GLN:HB2	1:B:28:LEU:HD12	1.97	0.45
1:C:67:THR:OG1	1:C:70:GLY:O	2.30	0.45
1:D:260:GLU:HA	1:D:286:LEU:HD11	1.98	0.45
1:F:13:ILE:HG22	1:F:261:PHE:CD2	2.51	0.45
1:B:255:PHE:HB2	1:B:314:PHE:CD1	2.51	0.45
1:B:216:LEU:HD11	1:B:292:HIS:CD2	2.52	0.45
1:C:9:VAL:HG21	1:C:261:PHE:HB3	1.99	0.45
1:F:58:MET:O	1:F:60:THR:HG23	2.16	0.45
1:F:197:LEU:HD23	1:F:197:LEU:H	1.81	0.45
1:F:195:TYR:OH	1:F:295:LEU:HB2	2.16	0.45
1:E:17:MET:HE1	1:E:294:PHE:HB2	1.99	0.44
1:C:103:HIS:O	1:C:107:MET:HG3	2.18	0.44
1:D:199:GLY:HA3	1:D:241:CYS:HA	1.99	0.44
1:C:17:MET:HE2	1:C:301:MET:SD	2.58	0.44
1:C:299[B]:ARG:HH11	1:C:299[B]:ARG:HG2	1.83	0.44
1:E:17:MET:HE1	1:E:294:PHE:CB	2.47	0.44
1:A:272:TYR:CD1	1:A:284:PHE:HB2	2.52	0.44
1:F:80:GLN:HB2	1:F:81:PRO:HD2	2.00	0.44
1:C:299[B]:ARG:HG2	1:C:299[B]:ARG:NH1	2.33	0.43
1:D:75:ARG:NH1	5:D:536:HOH:O	2.47	0.43
1:D:299[B]:ARG:HD3	1:E:112:SER:O	2.18	0.43
1:E:272:TYR:CD1	1:E:284:PHE:HB2	2.54	0.43
1:A:86:THR:O	1:A:159:ILE:HA	2.18	0.43
1:A:199:GLY:HA3	1:A:241:CYS:HA	1.99	0.43
1:B:169:MET:HE3	1:B:197:LEU:O	2.19	0.43
1:A:60:THR:HG21	1:A:108:ARG:NH2	2.33	0.43
1:F:290:THR:HG22	1:F:301:MET:HE1	2.00	0.43
1:B:17:MET:HE2	1:B:301:MET:CE	2.36	0.43
1:A:17:MET:HE1	1:A:294:PHE:CB	2.48	0.43
1:A:216:LEU:HD11	1:A:292:HIS:CG	2.54	0.42
1:B:17:MET:HE3	1:B:291:LEU:N	2.31	0.42
1:B:86:THR:O	1:B:159:ILE:HA	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:195:TYR:OH	1:C:295:LEU:HB2	2.19	0.42
1:A:60:THR:HA	1:A:76:LEU:O	2.20	0.42
1:E:42:GLN:NE2	5:E:578:HOH:O	2.53	0.42
1:C:216:LEU:HD11	1:C:292:HIS:CD2	2.54	0.42
1:D:158:ARG:NH1	1:D:319:LEU:O	2.53	0.42
1:C:292:HIS:O	1:C:293:ALA:HB3	2.20	0.42
1:B:90:LEU:N	1:B:90:LEU:HD22	2.35	0.41
1:D:7:LEU:HD12	1:D:8:PRO:HD2	2.01	0.41
1:F:216:LEU:HD11	1:F:292:HIS:CG	2.56	0.41
1:C:75:ARG:HB2	1:C:100:LEU:HD13	2.03	0.41
1:B:272:TYR:CD1	1:B:284:PHE:HB2	2.56	0.41
1:B:292:HIS:O	1:B:293:ALA:HB3	2.21	0.41
1:D:292:HIS:O	1:D:293:ALA:HB3	2.21	0.41
1:B:86:THR:HG21	1:B:119:ILE:HD12	2.02	0.41
1:C:16[B]:GLU:HG3	1:C:301:MET:HE3	2.03	0.41
1:A:14:SER:HB3	1:A:289:GLY:HA3	2.03	0.41
1:E:19:THR:HG22	1:E:300:MET:CE	2.52	0.40
1:B:181:LYS:HE2	1:B:183:ILE:HD11	2.02	0.40
1:D:107:MET:CE	1:D:120:GLY:HA3	2.40	0.40
1:A:7:LEU:HD22	1:A:208:LEU:HG	2.02	0.40
1:E:197:LEU:HB3	1:E:264:LEU:HD13	2.03	0.40
1:F:193:LEU:HB3	1:F:198:TYR:OH	2.22	0.40
1:B:57:GLU:HG3	1:C:57:GLU:CG	2.52	0.40
1:C:193:LEU:HB3	1:C:198:TYR:OH	2.21	0.40

There are no symmetry-related clashes.

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	315/333 (95%)	306 (97%)	9 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	316/333 (95%)	302 (96%)	14 (4%)	0	100	100
1	C	317/333 (95%)	302 (95%)	15 (5%)	0	100	100
1	D	316/333 (95%)	302 (96%)	14 (4%)	0	100	100
1	E	329/333 (99%)	317 (96%)	11 (3%)	1 (0%)	36	46
1	F	315/333 (95%)	303 (96%)	11 (4%)	1 (0%)	36	46
All	All	1908/1998 (96%)	1832 (96%)	74 (4%)	2 (0%)	48	60

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	1	MET
1	F	4	GLU

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	264/278 (95%)	264 (100%)	0	100	100
1	B	265/278 (95%)	259 (98%)	6 (2%)	44	63
1	C	266/278 (96%)	258 (97%)	8 (3%)	36	53
1	D	265/278 (95%)	260 (98%)	5 (2%)	50	69
1	E	278/278 (100%)	278 (100%)	0	100	100
1	F	264/278 (95%)	261 (99%)	3 (1%)	65	81
All	All	1602/1668 (96%)	1580 (99%)	22 (1%)	59	76

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	7	LEU
1	B	10	LEU
1	B	36	THR
1	B	142	CYS

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Mol	Chain	Res	Type
1	B	183	ILE
1	B	295	LEU
1	C	10	LEU
1	C	11	ASP
1	C	27	ASP
1	C	36	THR
1	C	49	ARG
1	C	192	LEU
1	C	214	ASP
1	C	302	LYS
1	D	11	ASP
1	D	27	ASP
1	D	34	THR
1	D	90	LEU
1	D	110	LEU
1	F	27	ASP
1	F	112	SER
1	F	230	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	40	GLN
1	C	71	GLN
1	C	148	GLN
1	C	218	GLN
1	E	71	GLN
1	F	115	GLN
1	F	146	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

6 non-standard protein/DNA/RNA residues 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
1	SEB	F	165	1	15,16,17	2.63	1 (6%)	16,21,23	1.52	2 (12%)
1	SEB	C	165	1	15,16,17	2.58	1 (6%)	16,21,23	1.17	1 (6%)
1	SEB	A	165	1	15,16,17	2.27	1 (6%)	16,21,23	1.53	2 (12%)
1	SEB	B	165	1	15,16,17	2.37	1 (6%)	16,21,23	1.29	1 (6%)
1	SEB	E	165	1	15,16,17	1.84	1 (6%)	16,21,23	1.33	1 (6%)
1	SEB	D	165	1	15,16,17	1.78	1 (6%)	16,21,23	1.11	2 (12%)

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
1	SEB	F	165	1	-	2/10/13/15	0/1/1/1
1	SEB	C	165	1	-	0/10/13/15	0/1/1/1
1	SEB	A	165	1	-	1/10/13/15	0/1/1/1
1	SEB	B	165	1	-	0/10/13/15	0/1/1/1
1	SEB	E	165	1	-	0/10/13/15	0/1/1/1
1	SEB	D	165	1	-	1/10/13/15	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	165	SEB	CE-SD	-9.82	1.68	1.78
1	C	165	SEB	CE-SD	-9.71	1.68	1.78
1	B	165	SEB	CE-SD	-8.90	1.69	1.78
1	A	165	SEB	CE-SD	-8.22	1.70	1.78
1	E	165	SEB	CE-SD	-6.56	1.71	1.78
1	D	165	SEB	CE-SD	-6.34	1.71	1.78

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	165	SEB	OG-CB-CA	4.70	113.39	107.63
1	E	165	SEB	OG-CB-CA	4.52	113.16	107.63
1	B	165	SEB	OG-CB-CA	4.33	112.93	107.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	165	SEB	OG-CB-CA	4.28	112.86	107.63
1	C	165	SEB	OG-CB-CA	3.06	111.37	107.63
1	A	165	SEB	OD1-SD-CE	2.77	114.82	108.71
1	F	165	SEB	OG-SD-CE	2.67	111.54	104.18
1	D	165	SEB	OG-CB-CA	2.49	110.68	107.63
1	D	165	SEB	CB-OG-SD	2.08	123.78	119.30

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	F	165	SEB	SD-CE-CZ-CH2
1	F	165	SEB	SD-CE-CZ-CH1
1	D	165	SEB	CA-CB-OG-SD
1	A	165	SEB	SD-CE-CZ-CH1

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	165	SEB	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

14 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	$\# Z > 2$
2	PGE	B	401	-	9,9,9	0.51	0	8,8,8	0.42	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	IMD	A	403	-	5,5,5	0.56	0	5,5,5	0.51	0
3	IMD	D	404	-	5,5,5	0.66	0	5,5,5	0.50	0
2	PGE	E	401	-	9,9,9	0.63	0	8,8,8	0.54	0
3	IMD	D	405	-	5,5,5	0.87	0	5,5,5	0.39	0
4	1PE	E	402	-	15,15,15	0.75	0	14,14,14	0.91	0
2	PGE	C	401	-	9,9,9	0.39	0	8,8,8	0.27	0
4	1PE	D	403	-	15,15,15	0.57	0	14,14,14	0.42	0
3	IMD	B	402	-	5,5,5	0.65	0	5,5,5	0.73	0
2	PGE	A	402	-	9,9,9	0.74	0	8,8,8	0.61	0
2	PGE	D	401	-	9,9,9	0.71	0	8,8,8	0.60	0
2	PGE	D	402	-	9,9,9	0.56	0	8,8,8	0.46	0
2	PGE	F	401	-	9,9,9	0.48	0	8,8,8	0.83	0
2	PGE	A	401	-	9,9,9	0.54	0	8,8,8	0.29	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
2	PGE	B	401	-	-	5/7/7/7	-
3	IMD	A	403	-	-	-	0/1/1/1
3	IMD	D	404	-	-	-	0/1/1/1
2	PGE	E	401	-	-	5/7/7/7	-
4	1PE	E	402	-	-	9/13/13/13	-
3	IMD	D	405	-	-	-	0/1/1/1
2	PGE	C	401	-	-	5/7/7/7	-
4	1PE	D	403	-	-	4/13/13/13	-
3	IMD	B	402	-	-	-	0/1/1/1
2	PGE	A	402	-	-	5/7/7/7	-
2	PGE	D	401	-	-	5/7/7/7	-
2	PGE	D	402	-	-	1/7/7/7	-
2	PGE	F	401	-	-	5/7/7/7	-
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 (47) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	402	1PE	C14-C24-OH4-C13
2	B	401	PGE	O2-C3-C4-O3
2	E	401	PGE	O2-C3-C4-O3
2	B	401	PGE	O1-C1-C2-O2
2	F	401	PGE	O1-C1-C2-O2
4	D	403	1PE	OH2-C12-C22-OH3
2	A	401	PGE	O2-C3-C4-O3
2	A	401	PGE	O3-C5-C6-O4
2	A	402	PGE	O1-C1-C2-O2
4	E	402	1PE	OH7-C16-C26-OH6
2	A	402	PGE	O2-C3-C4-O3
2	E	401	PGE	C4-C3-O2-C2
2	F	401	PGE	O2-C3-C4-O3
2	A	402	PGE	O3-C5-C6-O4
2	E	401	PGE	O3-C5-C6-O4
2	A	401	PGE	O1-C1-C2-O2
4	D	403	1PE	OH7-C16-C26-OH6
4	E	402	1PE	OH6-C15-C25-OH5
2	C	401	PGE	O3-C5-C6-O4
2	D	401	PGE	O1-C1-C2-O2
2	E	401	PGE	O1-C1-C2-O2
2	F	401	PGE	O3-C5-C6-O4
4	E	402	1PE	OH2-C12-C22-OH3
4	D	403	1PE	OH5-C14-C24-OH4
4	E	402	1PE	C15-C25-OH5-C14
4	E	402	1PE	C13-C23-OH3-C22
2	D	402	PGE	C1-C2-O2-C3
2	F	401	PGE	C3-C4-O3-C5
4	D	403	1PE	C13-C23-OH3-C22
2	A	402	PGE	C6-C5-O3-C4
2	C	401	PGE	C4-C3-O2-C2
4	E	402	1PE	OH4-C13-C23-OH3
2	B	401	PGE	C4-C3-O2-C2
2	C	401	PGE	C6-C5-O3-C4
2	B	401	PGE	C6-C5-O3-C4
2	C	401	PGE	C3-C4-O3-C5
2	D	401	PGE	O3-C5-C6-O4
2	C	401	PGE	C1-C2-O2-C3
2	A	402	PGE	C3-C4-O3-C5
2	D	401	PGE	C4-C3-O2-C2
4	E	402	1PE	C24-C14-OH5-C25
2	B	401	PGE	C3-C4-O3-C5
2	E	401	PGE	C3-C4-O3-C5

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Mol	Chain	Res	Type	Atoms
2	F	401	PGE	C1-C2-O2-C3
2	D	401	PGE	O2-C3-C4-O3
4	E	402	1PE	OH5-C14-C24-OH4
2	D	401	PGE	C3-C4-O3-C5

There are no ring outliers.

9 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	PGE	1	0
2	E	401	PGE	1	0
4	E	402	1PE	2	0
2	C	401	PGE	2	0
2	A	402	PGE	2	0
2	D	401	PGE	1	0
2	D	402	PGE	2	0
2	F	401	PGE	2	0
2	A	401	PGE	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	317/333 (95%)	0.28	31 (9%) 13 14	25, 39, 88, 113	0
1	B	317/333 (95%)	0.11	21 (6%) 24 26	21, 37, 74, 115	1 (0%)
1	C	317/333 (95%)	0.44	33 (10%) 11 13	22, 53, 95, 134	2 (0%)
1	D	317/333 (95%)	0.07	20 (6%) 26 28	18, 31, 83, 128	1 (0%)
1	E	328/333 (98%)	-0.12	7 (2%) 63 65	16, 32, 52, 107	3 (0%)
1	F	317/333 (95%)	0.73	47 (14%) 5 6	33, 50, 122, 144	0
All	All	1913/1998 (95%)	0.25	159 (8%) 17 19	16, 39, 91, 144	7 (0%)

All (159) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	212	VAL	8.8
1	F	12	LEU	7.9
1	F	24	LEU	7.8
1	D	3	PRO	7.4
1	F	15	ALA	7.3
1	C	212	VAL	7.1
1	F	26	PRO	7.0
1	D	26	PRO	6.5
1	E	31	TRP	6.3
1	F	8	PRO	6.1
1	F	7	LEU	6.0
1	F	10	LEU	6.0
1	F	3	PRO	6.0
1	E	-9	HIS	5.8
1	D	2	LYS	5.7
1	D	32	PRO	5.7
1	B	33	ALA	5.6
1	F	5	ASN	5.5
1	D	212	VAL	5.3

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Mol	Chain	Res	Type	RSRZ
1	C	3	PRO	5.2
1	A	2	LYS	5.1
1	C	28	LEU	5.0
1	D	5	ASN	5.0
1	A	29	PRO	5.0
1	C	34	THR	5.0
1	E	-8	HIS	4.8
1	F	2	LYS	4.7
1	C	30	PRO	4.7
1	A	30	PRO	4.7
1	C	213	TRP	4.6
1	C	33	ALA	4.6
1	F	33	ALA	4.6
1	C	29	PRO	4.6
1	F	19	THR	4.5
1	F	21	VAL	4.5
1	F	294	PHE	4.5
1	C	26	PRO	4.5
1	B	30	PRO	4.3
1	D	7	LEU	4.3
1	F	31	TRP	4.3
1	F	298	SER	4.3
1	A	31	TRP	4.2
1	F	37	ILE	4.2
1	A	24	LEU	4.2
1	F	17	MET	4.1
1	F	30	PRO	4.1
1	F	13	ILE	4.0
1	F	6	LYS	4.0
1	A	10	LEU	4.0
1	E	24	LEU	4.0
1	A	26	PRO	4.0
1	F	29	PRO	4.0
1	F	28	LEU	4.0
1	F	4	GLU	4.0
1	A	3	PRO	3.9
1	C	32	PRO	3.9
1	A	9	VAL	3.9
1	C	24	LEU	3.9
1	F	20	VAL	3.8
1	C	31	TRP	3.8
1	F	299	ARG	3.8

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Mol	Chain	Res	Type	RSRZ
1	B	24	LEU	3.8
1	C	214	ASP	3.7
1	E	26	PRO	3.7
1	F	300	MET	3.7
1	B	185	CYS	3.7
1	D	31	TRP	3.7
1	F	16	GLU	3.6
1	D	24	LEU	3.6
1	B	32	PRO	3.6
1	F	38	ALA	3.6
1	F	9	VAL	3.4
1	A	15	ALA	3.4
1	C	38	ALA	3.4
1	F	32	PRO	3.4
1	B	31	TRP	3.4
1	B	215	GLY	3.4
1	A	7	LEU	3.3
1	A	12	LEU	3.3
1	A	215	GLY	3.2
1	E	27	ASP	3.2
1	C	215	GLY	3.1
1	A	183	ILE	3.1
1	A	213	TRP	3.1
1	B	34	THR	3.0
1	D	27	ASP	3.0
1	F	11	ASP	3.0
1	D	8	PRO	3.0
1	A	28	LEU	3.0
1	B	212	VAL	3.0
1	F	34	THR	3.0
1	F	23	THR	3.0
1	F	36	THR	3.0
1	F	213	TRP	3.0
1	C	8	PRO	3.0
1	B	29	PRO	2.9
1	B	183	ILE	2.9
1	C	10	LEU	2.9
1	A	185	CYS	2.9
1	F	295	LEU	2.8
1	D	4	GLU	2.8
1	B	36	THR	2.8
1	C	37	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	212	VAL	2.8
1	C	9	VAL	2.8
1	B	143	CYS	2.8
1	F	14	SER	2.8
1	C	36	THR	2.8
1	C	211	GLY	2.8
1	F	185	CYS	2.8
1	A	4	GLU	2.8
1	B	3	PRO	2.7
1	D	30	PRO	2.7
1	C	2	LYS	2.7
1	C	68	LYS	2.7
1	D	11	ASP	2.7
1	A	34	THR	2.6
1	A	211	GLY	2.6
1	D	215	GLY	2.6
1	F	217	THR	2.6
1	F	291	LEU	2.6
1	D	213	TRP	2.5
1	F	195	TYR	2.5
1	D	28	LEU	2.5
1	A	33	ALA	2.5
1	D	33	ALA	2.5
1	A	8	PRO	2.4
1	C	230	SER	2.4
1	B	28	LEU	2.4
1	F	297	TYR	2.4
1	C	11	ASP	2.4
1	F	215	GLY	2.4
1	C	4	GLU	2.4
1	B	35	GLY	2.4
1	B	223	MET	2.4
1	A	82	ASP	2.3
1	C	183	ILE	2.3
1	A	223	MET	2.3
1	A	142	CYS	2.3
1	A	210	GLY	2.3
1	C	218	GLN	2.3
1	D	9	VAL	2.3
1	B	26	PRO	2.2
1	C	181	LYS	2.2
1	C	223	MET	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	2	LYS	2.2
1	F	218	GLN	2.2
1	C	12	LEU	2.2
1	D	82	ASP	2.2
1	C	185	CYS	2.2
1	A	36	THR	2.2
1	F	22	ASN	2.1
1	B	4	GLU	2.1
1	E	185	CYS	2.1
1	A	214	ASP	2.1
1	A	5	ASN	2.0
1	A	32	PRO	2.0
1	B	184	ASP	2.0
1	C	5	ASN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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
1	SEB	D	165	16/17	0.94	0.13	26,32,35,35	0
1	SEB	C	165	16/17	0.96	0.12	41,59,67,68	0
1	SEB	A	165	16/17	0.96	0.10	33,44,48,48	0
1	SEB	E	165	16/17	0.96	0.11	28,36,38,38	0
1	SEB	F	165	16/17	0.96	0.12	39,54,64,64	0
1	SEB	B	165	16/17	0.97	0.10	33,43,48,49	0

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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	IMD	A	403	5/5	0.79	0.29	85,88,91,93	0
2	PGE	A	402	10/10	0.80	0.22	53,61,64,65	0
3	IMD	D	404	5/5	0.85	0.25	62,63,64,65	0
4	1PE	E	402	16/16	0.86	0.19	48,71,86,87	0
2	PGE	D	402	10/10	0.88	0.14	40,43,55,56	0
2	PGE	A	401	10/10	0.88	0.18	55,61,77,78	0
2	PGE	F	401	10/10	0.89	0.15	47,57,73,75	0
2	PGE	D	401	10/10	0.91	0.14	44,46,64,64	0
4	1PE	D	403	16/16	0.92	0.11	48,61,64,64	0
3	IMD	B	402	5/5	0.92	0.12	47,49,50,52	0
3	IMD	D	405	5/5	0.93	0.11	43,45,48,48	0
2	PGE	B	401	10/10	0.93	0.13	42,53,73,76	0
2	PGE	E	401	10/10	0.93	0.12	34,42,56,58	0
2	PGE	C	401	10/10	0.95	0.10	44,53,66,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.