



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 10:09 PM UTC

PDB ID : 7L6G / pdb_00007l6g
Title : MbnP from Methylosinus trichosporium
Authors : Manesis, A.C.; Rosenzweig, A.C.
Deposited on : 2020-12-23
Resolution : 2.04 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

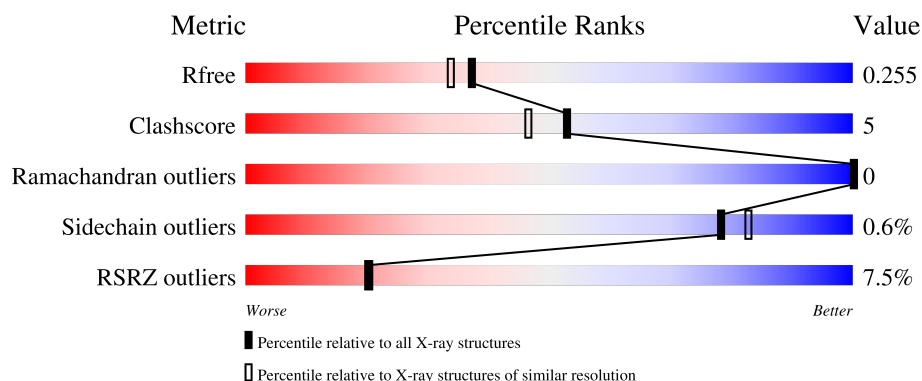
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	299	6% 93% 5% •
1	B	299	5% 85% 12% •
1	C	299	7% 82% 13% • •
1	D	299	6% 86% 9% •
1	E	299	11% 89% 10% •

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Mol	Chain	Length	Quality of chain
1	F	299	10% 83% 14%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13544 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 Metallo-mystery pair system four-Cys motif protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	293	Total	C	N	O	S	0	0	0
			2133	1344	376	404	9			
1	B	289	Total	C	N	O	S	0	0	0
			2109	1330	371	399	9			
1	C	288	Total	C	N	O	S	0	0	0
			2102	1325	370	398	9			
1	D	287	Total	C	N	O	S	0	0	0
			2097	1322	369	397	9			
1	E	295	Total	C	N	O	S	0	0	0
			2146	1352	379	406	9			
1	F	291	Total	C	N	O	S	0	0	0
			2124	1339	374	402	9			

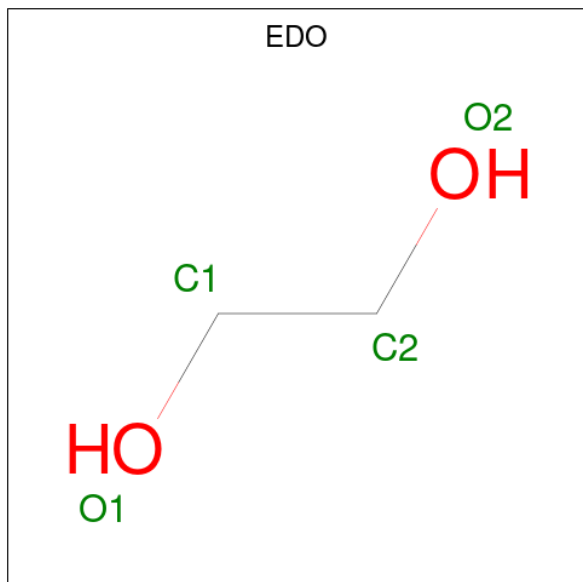
- Molecule 2 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cu	0	0
			1	1		
2	B	1	Total	Cu	0	0
			1	1		
2	C	1	Total	Cu	0	0
			1	1		
2	D	1	Total	Cu	0	0
			1	1		
2	E	1	Total	Cu	0	0
			1	1		
2	F	1	Total	Cu	0	0
			1	1		

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Ca 1 1	0	0
3	B	1	Total Ca 1 1	0	0
3	C	1	Total Ca 1 1	0	0
3	D	1	Total Ca 1 1	0	0
3	E	1	Total Ca 1 1	0	0
3	F	1	Total Ca 1 1	0	0

- 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 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	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

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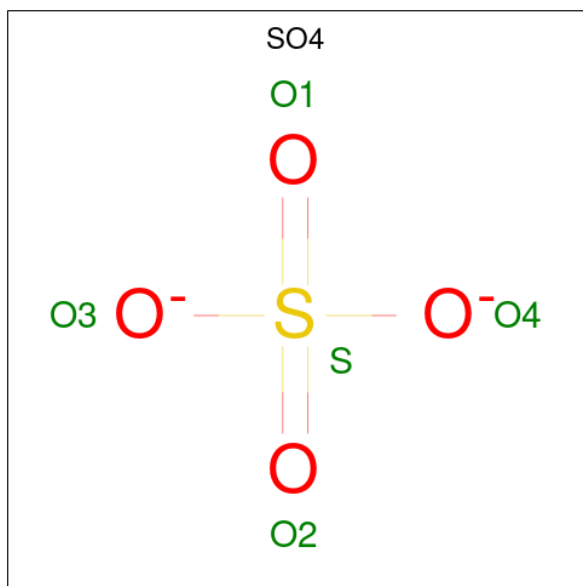
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total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

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

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	F	1	Total	O	S	0	0
			5	4	1		
5	F	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	125	Total	O	0	0
			125	125		
6	B	107	Total	O	0	0
			107	107		

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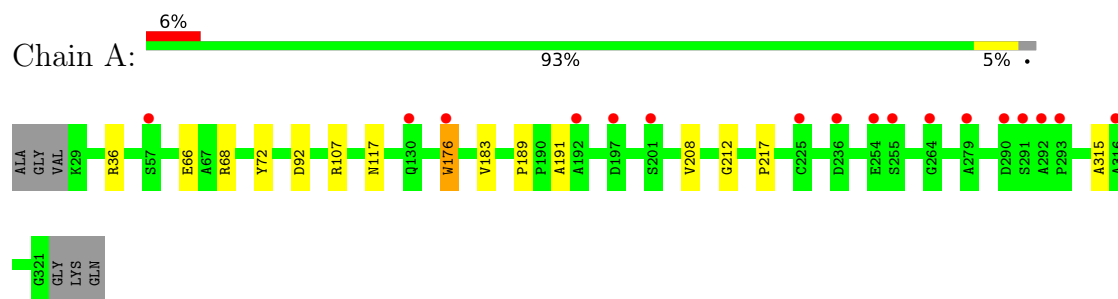
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	104	Total 104	O 104	0	0
6	D	83	Total 83	O 83	0	0
6	E	88	Total 88	O 88	0	0
6	F	75	Total 75	O 75	0	0

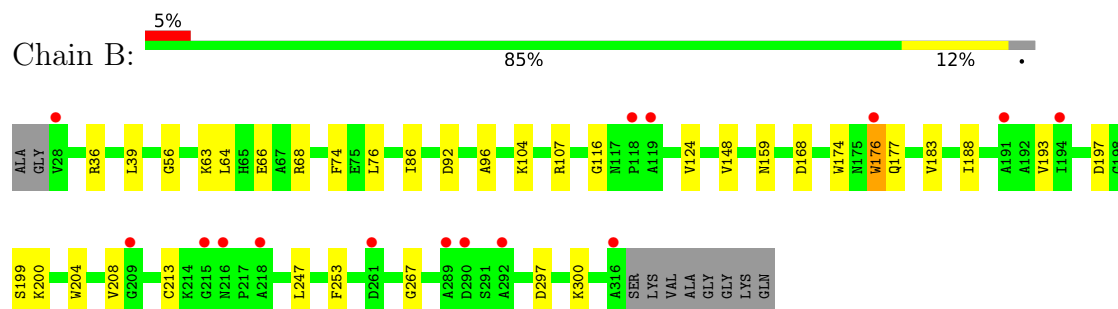
3 Residue-property plots [i](#)

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.

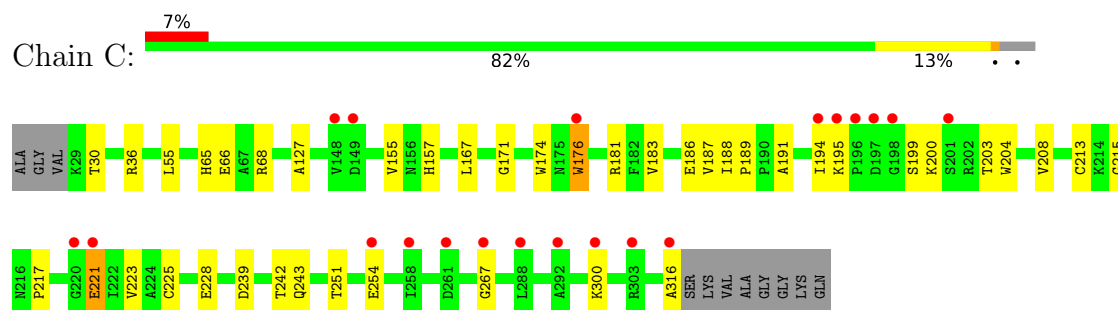
- Molecule 1: Metallo-mystery pair system four-Cys motif protein



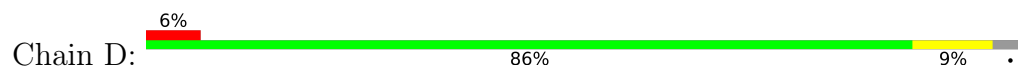
- Molecule 1: Metallo-mystery pair system four-Cys motif protein

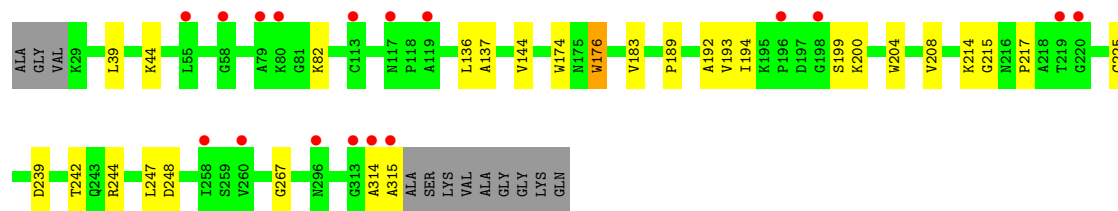


- Molecule 1: Metallo-mystery pair system four-Cys motif protein

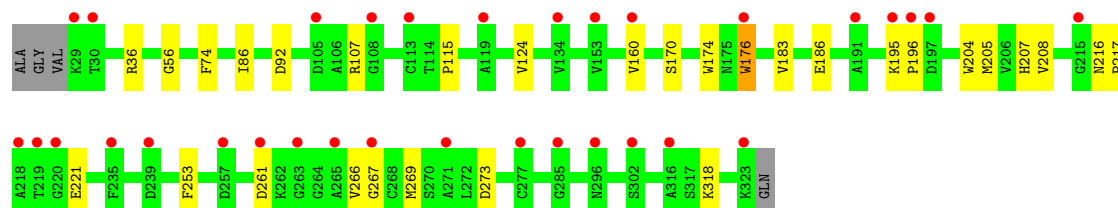
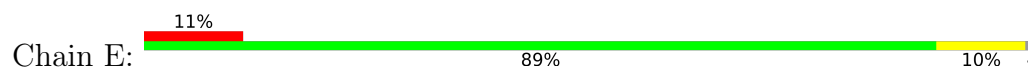


- Molecule 1: Metallo-mystery pair system four-Cys motif protein

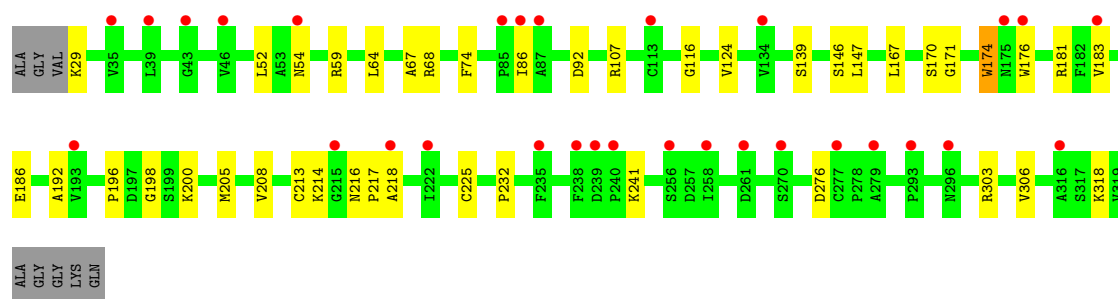
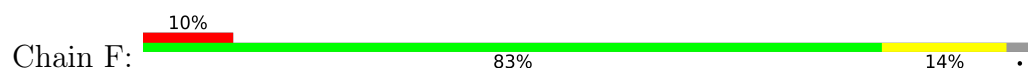




● Molecule 1: Metallo-mystery pair system four-Cys motif protein



● Molecule 1: Metallo-mystery pair system four-Cys motif protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	91.28Å 91.28Å 383.57Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	21.89 – 2.04 21.89 – 2.04	Depositor EDS
% Data completeness (in resolution range)	97.0 (21.89-2.04) 95.9 (21.89-2.04)	Depositor EDS
R_{merge}	0.35	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.98 (at 1.94Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.204 , 0.251 0.208 , 0.255	Depositor DCC
R_{free} test set	5733 reflections (4.58%)	wwPDB-VP
Wilson B-factor (Å ²)	40.4	Xtriage
Anisotropy	0.230	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.058 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13544	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.41 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 8.7483e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: SO4, CU, EDO, KYN, CA

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	0.17	0/2167	0.37	0/2953
1	B	0.16	0/2143	0.38	0/2922
1	C	0.20	0/2136	0.37	0/2912
1	D	0.19	0/2131	0.40	0/2905
1	E	0.16	0/2180	0.35	0/2969
1	F	0.15	0/2158	0.37	0/2941
All	All	0.17	0/12915	0.37	0/17602

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 [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	2133	0	2100	16	0
1	B	2109	0	2074	22	0
1	C	2102	0	2065	29	0
1	D	2097	0	2060	18	0
1	E	2146	0	2116	22	0
1	F	2124	0	2092	31	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	20	0	30	3	0
4	B	12	0	18	2	0
4	C	12	0	18	2	0
4	D	24	0	36	4	0
4	E	48	0	72	1	0
4	F	28	0	42	2	0
5	A	30	0	0	1	0
5	B	10	0	0	0	0
5	C	15	0	0	0	0
5	D	15	0	0	0	0
5	E	15	0	0	0	0
5	F	10	0	0	0	0
6	A	125	0	0	2	0
6	B	107	0	0	0	0
6	C	104	0	0	0	0
6	D	83	0	0	1	0
6	E	88	0	0	1	0
6	F	75	0	0	2	0
All	All	13544	0	12723	129	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 (129) 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:C:215:GLY:CA	1:C:221:GLU:OE2	2.29	0.80
1:D:225:CYS:H	4:D:407:EDO:H22	1.46	0.79
1:C:228:GLU:H	1:C:300:LYS:HZ1	1.33	0.77
1:C:215:GLY:HA2	1:C:221:GLU:OE2	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:214:LYS:HD3	1:D:215:GLY:H	1.58	0.68
1:B:183:VAL:HB	1:B:208:VAL:HB	1.76	0.67
1:D:194:ILE:HD12	1:D:199:SER:O	1.93	0.67
1:C:155:VAL:HG13	1:C:167:LEU:HD21	1.76	0.66
1:D:248:ASP:HB2	4:D:406:EDO:H11	1.77	0.65
1:A:176:TRP:H	1:A:176:TRP:CD1	2.12	0.65
1:B:297:ASP:HA	1:B:300:LYS:HE2	1.79	0.65
1:A:176:TRP:H	1:A:176:TRP:HD1	1.45	0.64
1:D:214:LYS:HD3	1:D:215:GLY:N	2.13	0.63
1:A:117:ASN:ND2	1:E:92:ASP:OD2	2.26	0.62
1:D:183:VAL:HB	1:D:208:VAL:HB	1.80	0.62
1:F:303:ARG:HD3	1:F:306:VAL:HG11	1.80	0.62
1:F:183:VAL:HB	1:F:208:VAL:HB	1.82	0.60
1:B:168:ASP:OD1	1:F:107:ARG:NH2	2.35	0.60
1:E:186:GLU:HG2	1:E:205:MET:HG2	1.82	0.60
1:D:82:LYS:NZ	6:D:502:HOH:O	2.34	0.59
1:F:116:GLY:H	4:F:406:EDO:H12	1.67	0.59
1:B:107:ARG:HD3	1:F:92:ASP:HB3	1.83	0.59
1:C:183:VAL:HB	1:C:208:VAL:HB	1.84	0.58
1:F:216:ASN:ND2	1:F:218:ALA:H	2.01	0.57
1:C:228:GLU:H	1:C:300:LYS:NZ	2.00	0.57
1:C:228:GLU:HG3	1:C:300:LYS:HZ1	1.69	0.57
1:B:63:LYS:NZ	1:F:170:SER:OG	2.37	0.57
1:A:66:GLU:OE1	1:A:68:ARG:NH2	2.39	0.56
1:E:183:VAL:HB	1:E:208:VAL:HB	1.87	0.56
1:F:303:ARG:O	1:F:306:VAL:HG12	2.05	0.56
1:A:183:VAL:HB	1:A:208:VAL:HB	1.88	0.55
1:C:242:THR:HG23	1:C:243:GLN:HG3	1.88	0.55
1:E:207:HIS:HB2	1:E:269:MET:HG2	1.89	0.55
1:F:241:LYS:HG2	1:F:318:LYS:HB2	1.87	0.55
1:E:36:ARG:HD3	4:E:409:EDO:H11	1.89	0.55
1:F:192:ALA:HB3	1:F:200:LYS:HD3	1.89	0.55
1:A:176:TRP:CD1	1:A:176:TRP:N	2.75	0.54
1:B:56:GLY:HA2	1:B:253:PHE:O	2.07	0.54
1:A:68:ARG:HH12	4:A:407:EDO:H12	1.71	0.53
1:F:74:PHE:HB3	1:F:86:ILE:HD12	1.90	0.53
1:D:314:ALA:HB1	1:F:214:LYS:HG2	1.90	0.53
1:C:36:ARG:HD2	4:C:404:EDO:H22	1.91	0.53
1:C:215:GLY:HA3	1:C:221:GLU:OE2	2.08	0.53
1:E:160:VAL:HG21	1:E:170:SER:HA	1.91	0.52
1:C:171:GLY:O	1:C:181:ARG:NH1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:TRP:HB2	1:A:217:PRO:HG2	1.91	0.51
1:A:36:ARG:HE	1:A:315:ALA:HB1	1.76	0.50
1:A:212:GLY:N	5:A:411:SO4:O4	2.30	0.50
1:B:36:ARG:HH12	4:B:403:EDO:H22	1.75	0.50
1:D:39:LEU:HD12	1:D:247:LEU:HB3	1.94	0.50
1:C:66:GLU:OE2	1:C:68:ARG:NE	2.45	0.50
1:C:251:THR:O	1:C:254:GLU:HG2	2.11	0.50
1:B:197:ASP:HB2	1:B:199:SER:H	1.77	0.50
1:F:303:ARG:HB3	1:F:306:VAL:CG1	2.42	0.49
1:C:316:ALA:N	4:C:404:EDO:O1	2.40	0.49
1:E:204:TRP:CE2	1:E:267:GLY:HA2	2.47	0.49
1:C:157:HIS:CE1	1:C:223:VAL:HG11	2.47	0.49
1:B:193:VAL:O	1:B:200:LYS:HA	2.13	0.48
1:C:30:THR:HB	1:C:127:ALA:HB1	1.96	0.48
1:C:195:LYS:HD2	1:C:199:SER:HB2	1.94	0.48
1:E:56:GLY:HA2	1:E:253:PHE:O	2.14	0.48
1:E:318:LYS:NZ	1:F:198:GLY:O	2.46	0.48
1:F:68:ARG:NH1	6:F:504:HOH:O	2.38	0.47
1:B:96:ALA:HB2	1:B:148:VAL:HG13	1.96	0.47
1:E:195:LYS:HB3	1:E:196:PRO:HD2	1.96	0.47
1:F:186:GLU:HG2	1:F:205:MET:HG2	1.95	0.47
1:B:66:GLU:OE2	1:B:68:ARG:NH2	2.46	0.47
1:D:189:PRO:HG3	1:D:193:VAL:HG22	1.97	0.47
1:C:217:PRO:HG3	1:C:223:VAL:CG2	2.45	0.47
1:E:176:TRP:H	1:E:176:TRP:CD1	2.32	0.47
1:A:72:TYR:OH	4:A:405:EDO:H22	2.15	0.47
1:D:192:ALA:HB3	1:D:200:LYS:HE2	1.97	0.47
1:B:76:LEU:HG	1:B:86:ILE:HD11	1.97	0.46
1:F:74:PHE:CZ	1:F:124:VAL:HG21	2.50	0.46
1:C:194:ILE:HD13	1:C:200:LYS:HG2	1.97	0.46
1:D:176:TRP:HB3	1:D:217:PRO:HG2	1.96	0.46
1:F:64:LEU:HD11	1:F:67:ALA:HB2	1.97	0.46
1:E:176:TRP:CB	1:E:217:PRO:HG2	2.45	0.46
1:B:92:ASP:HB3	1:F:107:ARG:HD2	1.97	0.46
1:B:64:LEU:O	1:B:104:LYS:NZ	2.42	0.46
1:C:186:GLU:HB3	1:C:203:THR:HG21	1.97	0.46
1:C:194:ILE:HD11	1:C:200:LYS:HE3	1.98	0.46
1:F:216:ASN:HD22	1:F:217:PRO:HD2	1.80	0.45
1:C:176:TRP:CD1	1:C:176:TRP:H	2.34	0.45
1:D:44:LYS:HA	4:D:404:EDO:H11	1.97	0.45
1:F:303:ARG:HB3	1:F:306:VAL:HG12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:189:PRO:HG2	1:C:191:ALA:O	2.17	0.44
1:C:213:CYS:HA	1:C:225:CYS:HA	1.99	0.44
1:C:217:PRO:HG3	1:C:223:VAL:HG21	1.98	0.44
1:D:204:TRP:CE2	1:D:267:GLY:HA2	2.52	0.44
1:E:273:ASP:OD1	1:E:273:ASP:N	2.45	0.44
1:B:39:LEU:HD12	1:B:247:LEU:HB3	1.99	0.44
1:F:174:KYN:HBA	4:F:408:EDO:H12	2.00	0.44
1:B:74:PHE:CZ	1:B:124:VAL:HG21	2.53	0.44
1:A:189:PRO:HG2	1:A:191:ALA:O	2.18	0.43
1:B:159:ASN:HB2	1:B:176:TRP:CH2	2.53	0.43
1:E:74:PHE:CZ	1:E:124:VAL:HG21	2.54	0.43
1:B:63:LYS:HB2	1:B:188:ILE:HB	1.99	0.43
1:F:29:LYS:HE3	1:F:29:LYS:HB3	1.72	0.43
6:A:518:HOH:O	1:E:107:ARG:HD2	2.18	0.43
1:D:244:ARG:HB3	1:D:315:ALA:HB2	2.01	0.43
1:C:239:ASP:HB3	1:C:242:THR:HG22	2.00	0.43
1:B:204:TRP:CE2	1:B:267:GLY:HA2	2.54	0.43
1:B:116:GLY:H	4:B:405:EDO:H12	1.83	0.42
1:C:204:TRP:CE2	1:C:267:GLY:HA2	2.54	0.42
1:E:176:TRP:H	1:E:176:TRP:HD1	1.68	0.42
1:E:176:TRP:HB3	1:E:217:PRO:HG2	2.00	0.42
1:F:139:SER:HA	1:F:232:PRO:HA	2.02	0.42
1:B:197:ASP:HB2	1:B:199:SER:OG	2.19	0.42
1:E:74:PHE:HB3	1:E:86:ILE:HD12	2.02	0.42
1:E:216:ASN:O	1:E:221:GLU:HG2	2.19	0.42
1:E:115:PRO:HG2	1:F:196:PRO:HB3	2.01	0.42
1:A:107:ARG:HD3	1:E:92:ASP:HB3	2.00	0.42
1:E:261:ASP:CG	1:E:266:VAL:HA	2.45	0.41
1:F:146:SER:OG	1:F:147:LEU:N	2.52	0.41
1:F:213:CYS:HA	1:F:225:CYS:HA	2.00	0.41
1:F:52:LEU:HD11	1:F:64:LEU:HB2	2.01	0.41
1:A:36:ARG:NH1	6:A:516:HOH:O	2.53	0.41
1:B:177:GLN:NE2	1:B:213:CYS:O	2.51	0.41
1:D:144:VAL:HG21	4:D:407:EDO:H11	2.03	0.41
1:F:276:ASP:O	6:F:501:HOH:O	2.22	0.41
1:D:136:LEU:HG	1:D:137:ALA:N	2.36	0.41
1:D:239:ASP:HB3	1:D:242:THR:HB	2.03	0.41
1:C:65:HIS:HB2	1:C:188:ILE:HD11	2.03	0.41
1:F:54:ASN:HB3	1:F:59:ARG:HB3	2.03	0.41
1:F:171:GLY:O	1:F:181:ARG:NH1	2.54	0.40
1:A:92:ASP:OD1	4:A:404:EDO:O1	2.33	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:ARG:HD2	6:E:528:HOH:O	2.22	0.40
1:C:55:LEU:HD21	1:C:187:VAL:HG11	2.03	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	290/299 (97%)	280 (97%)	10 (3%)	0	100	100
1	B	286/299 (96%)	275 (96%)	11 (4%)	0	100	100
1	C	285/299 (95%)	276 (97%)	9 (3%)	0	100	100
1	D	284/299 (95%)	271 (95%)	13 (5%)	0	100	100
1	E	292/299 (98%)	282 (97%)	10 (3%)	0	100	100
1	F	288/299 (96%)	274 (95%)	14 (5%)	0	100	100
All	All	1725/1794 (96%)	1658 (96%)	67 (4%)	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	219/222 (99%)	218 (100%)	1 (0%)	81	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	217/222 (98%)	216 (100%)	1 (0%)	81	85
1	C	216/222 (97%)	214 (99%)	2 (1%)	70	75
1	D	216/222 (97%)	215 (100%)	1 (0%)	81	85
1	E	220/222 (99%)	219 (100%)	1 (0%)	81	85
1	F	219/222 (99%)	217 (99%)	2 (1%)	70	75
All	All	1307/1332 (98%)	1299 (99%)	8 (1%)	78	83

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	176	TRP
1	B	176	TRP
1	C	176	TRP
1	C	221	GLU
1	D	176	TRP
1	E	176	TRP
1	F	167	LEU
1	F	176	TRP

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

Mol	Chain	Res	Type
1	A	31	GLN
1	A	287	ASN
1	C	159	ASN
1	C	287	ASN
1	D	117	ASN
1	D	287	ASN
1	F	216	ASN

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	KYN	C	174	1	13,14,15	0.77	0	13,18,20	0.84	1 (7%)
1	KYN	F	174	1	13,14,15	0.81	0	13,18,20	0.98	2 (15%)
1	KYN	D	174	1	13,14,15	0.80	0	13,18,20	0.90	1 (7%)
1	KYN	B	174	1	13,14,15	0.79	0	13,18,20	0.82	1 (7%)
1	KYN	E	174	1	13,14,15	0.78	0	13,18,20	0.88	1 (7%)
1	KYN	A	174	1	13,14,15	0.80	0	13,18,20	0.86	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
1	KYN	C	174	1	-	1/9/10/12	0/1/1/1
1	KYN	F	174	1	-	1/9/10/12	0/1/1/1
1	KYN	D	174	1	-	0/9/10/12	0/1/1/1
1	KYN	B	174	1	-	0/9/10/12	0/1/1/1
1	KYN	E	174	1	-	0/9/10/12	0/1/1/1
1	KYN	A	174	1	-	0/9/10/12	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	174	KYN	CA-CB-C1	-2.67	109.94	113.10
1	F	174	KYN	CA-CB-C1	-2.23	110.46	113.10
1	B	174	KYN	CA-CB-C1	-2.21	110.48	113.10
1	F	174	KYN	CB-C1-CD2	-2.19	117.28	119.82
1	C	174	KYN	CA-CB-C1	-2.04	110.68	113.10
1	E	174	KYN	CA-CB-C1	-2.04	110.68	113.10

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C	174	KYN	CB-C1-CD2-CE2
1	F	174	KYN	CB-C1-CD2-CE2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	F	174	KYN	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 67 ligands modelled in this entry, 12 are monoatomic - leaving 55 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	404	-	3,3,3	0.43	0	2,2,2	0.38	0
5	SO4	E	416	-	4,4,4	0.23	0	6,6,6	0.08	0
4	EDO	F	408	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	D	405	-	3,3,3	0.42	0	2,2,2	0.38	0
4	EDO	F	407	-	3,3,3	0.43	0	2,2,2	0.38	0
5	SO4	F	411	-	4,4,4	0.24	0	6,6,6	0.08	0
5	SO4	E	417	-	4,4,4	0.23	0	6,6,6	0.08	0
4	EDO	E	413	-	3,3,3	0.43	0	2,2,2	0.35	0
5	SO4	C	408	-	4,4,4	0.23	0	6,6,6	0.09	0
4	EDO	F	406	-	3,3,3	0.43	0	2,2,2	0.34	0
5	SO4	D	409	-	4,4,4	0.23	0	6,6,6	0.07	0
4	EDO	E	401	-	3,3,3	0.42	0	2,2,2	0.42	0
4	EDO	E	405	-	3,3,3	0.44	0	2,2,2	0.33	0
4	EDO	C	403	-	3,3,3	0.42	0	2,2,2	0.36	0
4	EDO	E	409	-	3,3,3	0.43	0	2,2,2	0.33	0
4	EDO	F	404	-	3,3,3	0.44	0	2,2,2	0.33	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	A	403	-	3,3,3	0.42	0	2,2,2	0.37	0
4	EDO	B	403	-	3,3,3	0.42	0	2,2,2	0.38	0
4	EDO	B	405	-	3,3,3	0.42	0	2,2,2	0.38	0
4	EDO	D	408	-	3,3,3	0.39	0	2,2,2	0.41	0
5	SO4	A	408	-	4,4,4	0.23	0	6,6,6	0.10	0
5	SO4	D	410	-	4,4,4	0.23	0	6,6,6	0.07	0
4	EDO	D	407	-	3,3,3	0.43	0	2,2,2	0.36	0
4	EDO	F	409	-	3,3,3	0.42	0	2,2,2	0.39	0
5	SO4	C	406	-	4,4,4	0.23	0	6,6,6	0.07	0
4	EDO	D	403	-	3,3,3	0.42	0	2,2,2	0.38	0
4	EDO	A	405	-	3,3,3	0.41	0	2,2,2	0.38	0
4	EDO	E	408	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	E	412	-	3,3,3	0.43	0	2,2,2	0.37	0
4	EDO	D	406	-	3,3,3	0.44	0	2,2,2	0.24	0
5	SO4	A	412	-	4,4,4	0.24	0	6,6,6	0.08	0
4	EDO	C	405	-	3,3,3	0.41	0	2,2,2	0.29	0
4	EDO	D	404	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	E	407	-	3,3,3	0.42	0	2,2,2	0.39	0
4	EDO	F	403	-	3,3,3	0.44	0	2,2,2	0.37	0
5	SO4	A	410	-	4,4,4	0.23	0	6,6,6	0.07	0
5	SO4	B	406	-	4,4,4	0.24	0	6,6,6	0.19	0
5	SO4	D	411	-	4,4,4	0.24	0	6,6,6	0.08	0
5	SO4	A	409	-	4,4,4	0.24	0	6,6,6	0.07	0
5	SO4	B	407	-	4,4,4	0.24	0	6,6,6	0.07	0
4	EDO	E	406	-	3,3,3	0.43	0	2,2,2	0.39	0
4	EDO	E	404	-	3,3,3	0.42	0	2,2,2	0.37	0
4	EDO	A	407	-	3,3,3	0.43	0	2,2,2	0.35	0
4	EDO	B	404	-	3,3,3	0.42	0	2,2,2	0.41	0
4	EDO	E	411	-	3,3,3	0.42	0	2,2,2	0.36	0
4	EDO	F	405	-	3,3,3	0.42	0	2,2,2	0.39	0
4	EDO	C	404	-	3,3,3	0.41	0	2,2,2	0.46	0
4	EDO	E	410	-	3,3,3	0.43	0	2,2,2	0.38	0
5	SO4	E	415	-	4,4,4	0.24	0	6,6,6	0.07	0
4	EDO	A	406	-	3,3,3	0.41	0	2,2,2	0.39	0
5	SO4	F	410	-	4,4,4	0.23	0	6,6,6	0.07	0
5	SO4	A	411	-	4,4,4	0.24	0	6,6,6	0.10	0
5	SO4	A	413	-	4,4,4	0.24	0	6,6,6	0.07	0
5	SO4	C	407	-	4,4,4	0.23	0	6,6,6	0.07	0
4	EDO	E	414	-	3,3,3	0.44	0	2,2,2	0.36	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	404	-	-	0/1/1/1	-
4	EDO	F	408	-	-	0/1/1/1	-
4	EDO	D	405	-	-	0/1/1/1	-
4	EDO	F	407	-	-	0/1/1/1	-
4	EDO	E	413	-	-	0/1/1/1	-
4	EDO	F	406	-	-	0/1/1/1	-
4	EDO	E	401	-	-	1/1/1/1	-
4	EDO	E	405	-	-	1/1/1/1	-
4	EDO	C	403	-	-	0/1/1/1	-
4	EDO	E	409	-	-	0/1/1/1	-
4	EDO	F	404	-	-	1/1/1/1	-
4	EDO	A	403	-	-	0/1/1/1	-
4	EDO	B	403	-	-	0/1/1/1	-
4	EDO	B	405	-	-	0/1/1/1	-
4	EDO	D	408	-	-	1/1/1/1	-
4	EDO	D	407	-	-	0/1/1/1	-
4	EDO	F	409	-	-	1/1/1/1	-
4	EDO	D	403	-	-	0/1/1/1	-
4	EDO	A	405	-	-	1/1/1/1	-
4	EDO	E	408	-	-	0/1/1/1	-
4	EDO	E	412	-	-	1/1/1/1	-
4	EDO	D	406	-	-	1/1/1/1	-
4	EDO	C	405	-	-	1/1/1/1	-
4	EDO	D	404	-	-	0/1/1/1	-
4	EDO	E	407	-	-	0/1/1/1	-
4	EDO	F	403	-	-	1/1/1/1	-
4	EDO	E	406	-	-	0/1/1/1	-
4	EDO	E	404	-	-	1/1/1/1	-
4	EDO	A	407	-	-	0/1/1/1	-
4	EDO	B	404	-	-	0/1/1/1	-
4	EDO	E	411	-	-	0/1/1/1	-
4	EDO	F	405	-	-	0/1/1/1	-
4	EDO	C	404	-	-	0/1/1/1	-
4	EDO	E	410	-	-	0/1/1/1	-
4	EDO	A	406	-	-	1/1/1/1	-
4	EDO	E	414	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	406	EDO	O1-C1-C2-O2
4	E	404	EDO	O1-C1-C2-O2
4	C	405	EDO	O1-C1-C2-O2
4	F	409	EDO	O1-C1-C2-O2
4	E	405	EDO	O1-C1-C2-O2
4	E	412	EDO	O1-C1-C2-O2
4	F	403	EDO	O1-C1-C2-O2
4	A	406	EDO	O1-C1-C2-O2
4	E	401	EDO	O1-C1-C2-O2
4	A	405	EDO	O1-C1-C2-O2
4	F	404	EDO	O1-C1-C2-O2
4	D	408	EDO	O1-C1-C2-O2

There are no ring outliers.

13 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	404	EDO	1	0
4	F	408	EDO	1	0
4	F	406	EDO	1	0
4	E	409	EDO	1	0
4	B	403	EDO	1	0
4	B	405	EDO	1	0
4	D	407	EDO	2	0
4	A	405	EDO	1	0
4	D	406	EDO	1	0
4	D	404	EDO	1	0
4	A	407	EDO	1	0
4	C	404	EDO	2	0
5	A	411	SO4	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	292/299 (97%)	0.56	17 (5%)	29 29	26, 39, 64, 94	0
1	B	288/299 (96%)	0.59	15 (5%)	33 33	31, 44, 73, 98	0
1	C	287/299 (95%)	0.60	20 (6%)	22 22	30, 42, 70, 96	0
1	D	286/299 (95%)	0.74	17 (5%)	28 28	28, 48, 82, 126	0
1	E	294/299 (98%)	0.85	32 (10%)	10 10	33, 47, 74, 85	0
1	F	290/299 (96%)	0.96	30 (10%)	12 11	32, 52, 79, 90	0
All	All	1737/1794 (96%)	0.72	131 (7%)	20 20	26, 45, 74, 126	0

All (131) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	220	GLY	6.9
1	E	119	ALA	5.3
1	C	196	PRO	4.9
1	D	196	PRO	4.8
1	D	198	GLY	4.4
1	E	257	ASP	4.3
1	E	302	SER	4.3
1	F	261	ASP	4.2
1	B	289	ALA	4.2
1	A	176	TRP	4.0
1	A	255	SER	3.9
1	D	80	LYS	3.9
1	B	261	ASP	3.9
1	E	271	ALA	3.8
1	D	258	ILE	3.8
1	B	316	ALA	3.8
1	B	215	GLY	3.7
1	E	218	ALA	3.6
1	D	315	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
1	F	279	ALA	3.5
1	D	220	GLY	3.5
1	C	195	LYS	3.5
1	E	263	GLY	3.4
1	D	79	ALA	3.4
1	D	113	CYS	3.3
1	E	113	CYS	3.3
1	C	221	GLU	3.3
1	A	57	SER	3.3
1	B	28	VAL	3.3
1	A	236	ASP	3.3
1	C	292	ALA	3.2
1	C	316	ALA	3.2
1	A	264	GLY	3.2
1	B	191	ALA	3.2
1	E	108	GLY	3.2
1	B	119	ALA	3.1
1	C	261	ASP	3.1
1	E	323	LYS	3.1
1	F	238	PHE	3.1
1	E	160	VAL	3.1
1	F	258	ILE	3.1
1	B	194	ILE	3.0
1	C	176	TRP	3.0
1	A	130	GLN	3.0
1	A	316	ALA	2.9
1	F	85	PRO	2.9
1	F	87	ALA	2.9
1	F	239	ASP	2.8
1	C	194	ILE	2.8
1	C	197	ASP	2.8
1	F	240	PRO	2.8
1	F	277	CYS	2.8
1	F	175	ASN	2.7
1	A	197	ASP	2.7
1	F	222	ILE	2.7
1	F	256	SER	2.6
1	C	258	ILE	2.6
1	C	198	GLY	2.6
1	C	254	GLU	2.6
1	A	192	ALA	2.6
1	E	277	CYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	293	PRO	2.6
1	B	290	ASP	2.6
1	D	55	LEU	2.6
1	A	292	ALA	2.6
1	F	316	ALA	2.6
1	E	153	VAL	2.5
1	F	193	VAL	2.5
1	A	291	SER	2.5
1	F	54	ASN	2.5
1	A	201	SER	2.5
1	E	196	PRO	2.5
1	F	218	ALA	2.5
1	F	235	PHE	2.5
1	F	176	TRP	2.5
1	A	279	ALA	2.5
1	B	292	ALA	2.5
1	D	58	GLY	2.5
1	F	86	ILE	2.5
1	F	35	VAL	2.4
1	F	113	CYS	2.4
1	E	219	THR	2.4
1	E	296	ASN	2.4
1	F	293	PRO	2.4
1	D	313	GLY	2.4
1	E	176	TRP	2.4
1	D	117	ASN	2.3
1	D	260	VAL	2.3
1	E	30	THR	2.3
1	C	303	ARG	2.3
1	B	118	PRO	2.3
1	D	219	THR	2.3
1	A	225	CYS	2.3
1	D	314	ALA	2.3
1	E	316	ALA	2.3
1	E	215	GLY	2.3
1	E	239	ASP	2.3
1	E	29	LYS	2.3
1	E	195	LYS	2.3
1	E	197	ASP	2.3
1	F	134	VAL	2.2
1	A	290	ASP	2.2
1	E	105	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	176	TRP	2.2
1	C	148	VAL	2.2
1	E	261	ASP	2.2
1	F	215	GLY	2.2
1	E	134	VAL	2.2
1	F	183	VAL	2.2
1	E	267	GLY	2.2
1	E	285	GLY	2.2
1	E	191	ALA	2.2
1	F	270	SER	2.2
1	F	39	LEU	2.1
1	A	254	GLU	2.1
1	B	209	GLY	2.1
1	C	267	GLY	2.1
1	E	220	GLY	2.1
1	B	218	ALA	2.1
1	E	265	ALA	2.1
1	C	149	ASP	2.1
1	C	300	LYS	2.1
1	D	119	ALA	2.1
1	C	201	SER	2.1
1	B	216	ASN	2.1
1	E	235	PHE	2.1
1	F	46	VAL	2.1
1	F	43	GLY	2.0
1	D	296	ASN	2.0
1	F	296	ASN	2.0
1	C	288	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	KYN	F	174	14/15	0.81	0.13	27,40,48,48	0
1	KYN	C	174	14/15	0.85	0.11	30,40,51,58	0
1	KYN	A	174	14/15	0.85	0.12	28,30,44,47	0
1	KYN	D	174	14/15	0.87	0.12	39,44,59,59	0
1	KYN	E	174	14/15	0.90	0.13	32,45,50,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	KYN	B	174	14/15	0.90	0.10	32,41,52,63	0

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	A	409	5/5	0.37	0.13	131,135,137,138	0
4	EDO	E	414	4/4	0.39	0.21	51,51,52,53	0
5	SO4	C	406	5/5	0.39	0.14	123,125,129,130	0
4	EDO	E	404	4/4	0.44	0.25	69,69,70,73	0
5	SO4	A	413	5/5	0.48	0.18	143,146,148,149	0
5	SO4	C	408	5/5	0.49	0.13	133,133,137,140	0
5	SO4	D	409	5/5	0.54	0.15	135,136,137,139	0
4	EDO	F	409	4/4	0.58	0.16	61,64,65,69	0
5	SO4	C	407	5/5	0.58	0.15	130,131,132,134	0
4	EDO	F	404	4/4	0.59	0.20	68,68,71,74	0
4	EDO	D	405	4/4	0.59	0.15	74,77,78,79	0
4	EDO	A	403	4/4	0.61	0.22	79,86,89,90	0
4	EDO	E	412	4/4	0.61	0.22	62,65,69,77	0
4	EDO	E	413	4/4	0.61	0.18	62,65,68,70	0
5	SO4	E	416	5/5	0.62	0.15	124,130,131,135	0
4	EDO	E	407	4/4	0.63	0.21	71,72,77,79	0
5	SO4	A	412	5/5	0.63	0.14	125,128,129,133	0
4	EDO	E	410	4/4	0.64	0.15	66,69,69,70	0
4	EDO	B	403	4/4	0.66	0.17	87,87,90,91	0
4	EDO	E	409	4/4	0.67	0.22	81,84,86,87	0
4	EDO	A	405	4/4	0.68	0.16	62,63,67,73	0
4	EDO	F	408	4/4	0.69	0.20	64,65,68,72	0
4	EDO	E	405	4/4	0.69	0.21	53,54,54,55	0
5	SO4	E	417	5/5	0.70	0.13	111,112,114,119	0
4	EDO	D	406	4/4	0.71	0.22	57,65,68,77	0
5	SO4	A	411	5/5	0.71	0.12	101,105,110,112	0
4	EDO	D	408	4/4	0.72	0.19	49,50,64,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	EDO	D	404	4/4	0.72	0.12	76,77,79,79	0
4	EDO	A	407	4/4	0.73	0.14	58,60,60,62	0
4	EDO	E	411	4/4	0.73	0.33	115,116,118,118	0
5	SO4	F	410	5/5	0.73	0.17	112,113,118,120	0
4	EDO	E	406	4/4	0.74	0.16	56,58,62,71	0
4	EDO	E	401	4/4	0.75	0.15	53,63,64,64	0
5	SO4	D	410	5/5	0.75	0.15	118,122,126,131	0
5	SO4	D	411	5/5	0.75	0.18	132,136,137,141	0
4	EDO	F	406	4/4	0.76	0.11	68,70,74,80	0
4	EDO	F	403	4/4	0.77	0.17	49,53,54,56	0
4	EDO	D	403	4/4	0.77	0.21	85,86,87,87	0
4	EDO	A	404	4/4	0.77	0.19	80,80,81,82	0
5	SO4	F	411	5/5	0.77	0.13	111,113,117,117	0
4	EDO	B	404	4/4	0.78	0.14	55,56,57,57	0
5	SO4	E	415	5/5	0.78	0.09	103,108,112,114	0
4	EDO	D	407	4/4	0.79	0.24	59,63,66,69	0
5	SO4	A	410	5/5	0.79	0.13	129,131,134,135	0
4	EDO	A	406	4/4	0.80	0.13	85,86,86,87	0
4	EDO	B	405	4/4	0.81	0.12	61,66,70,71	0
5	SO4	A	408	5/5	0.81	0.11	80,83,84,86	0
5	SO4	B	407	5/5	0.82	0.12	97,98,102,103	0
4	EDO	C	404	4/4	0.82	0.13	63,70,71,72	0
4	EDO	C	405	4/4	0.82	0.18	58,59,59,59	0
4	EDO	F	407	4/4	0.84	0.13	62,65,69,70	0
5	SO4	B	406	5/5	0.85	0.11	74,75,77,82	0
4	EDO	F	405	4/4	0.86	0.10	54,64,73,80	0
4	EDO	C	403	4/4	0.87	0.13	74,75,75,75	0
4	EDO	E	408	4/4	0.87	0.14	60,66,69,73	0
2	CU	B	401	1/1	0.94	0.07	49,49,49,49	0
2	CU	F	401	1/1	0.94	0.12	54,54,54,54	0
2	CU	A	401	1/1	0.94	0.08	44,44,44,44	0
2	CU	C	401	1/1	0.95	0.07	49,49,49,49	0
3	CA	B	402	1/1	0.95	0.06	54,54,54,54	0
2	CU	E	402	1/1	0.95	0.08	54,54,54,54	0
3	CA	F	402	1/1	0.96	0.10	51,51,51,51	0
3	CA	E	403	1/1	0.96	0.10	58,58,58,58	0
3	CA	D	402	1/1	0.97	0.05	52,52,52,52	0
2	CU	D	401	1/1	0.97	0.06	52,52,52,52	0
3	CA	A	402	1/1	0.98	0.03	37,37,37,37	0
3	CA	C	402	1/1	0.98	0.10	43,43,43,43	0

6.5 Other polymers ⓘ

There are no such residues in this entry.