



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:04 PM UTC

PDB ID : 5EMW / pdb_00005emw
Title : Crystal structure of the palmitoylated human TEAD3 transcription factor
Authors : Noland, C.L.; Gierke, S.; Schnier, P.D.; Murray, J.; Sandoval, W.N.; Sagolla, M.; Dey, A.; Hannoush, R.N.; Fairbrother, W.J.; Cunningham, C.N.
Deposited on : 2015-11-06
Resolution : 2.55 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

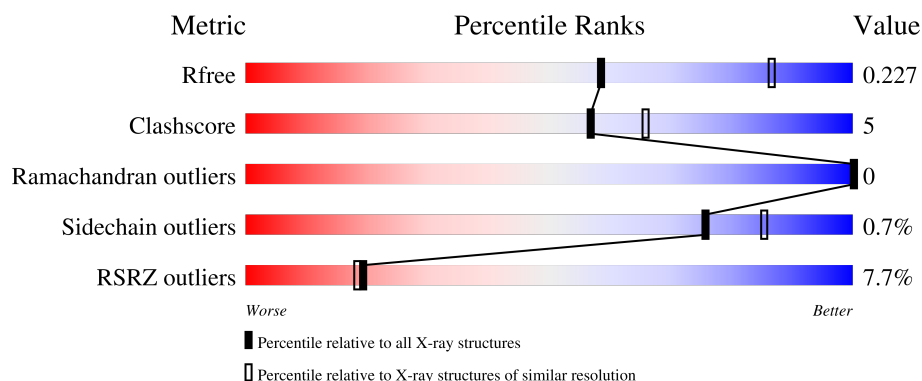
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	217	7% 82% 12% ••
1	B	217	5% 87% 8% 5%
1	C	217	9% 82% 13% •
1	D	217	9% 82% 13% 5%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6834 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 Transcriptional enhancer factor TEF-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	208	Total	C	N	O	S	0	0	0
			1677	1088	275	306	8			
1	B	207	Total	C	N	O	S	0	0	0
			1660	1076	272	304	8			
1	C	208	Total	C	N	O	S	0	0	0
			1686	1091	277	310	8			
1	D	207	Total	C	N	O	S	0	0	0
			1642	1065	266	303	8			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Ca	0	0
			1	1		
2	D	1	Total	Ca	0	0
			1	1		

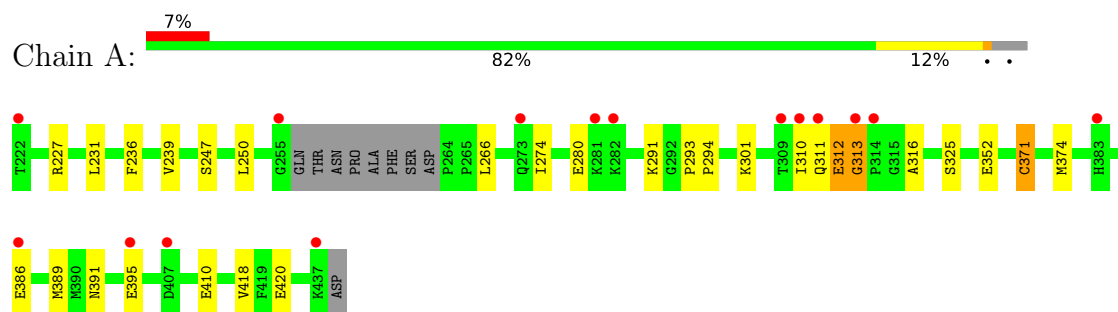
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	48	Total	O	0	0
			48	48		
3	B	53	Total	O	0	1
			54	54		
3	C	39	Total	O	0	0
			39	39		
3	D	26	Total	O	0	0
			26	26		

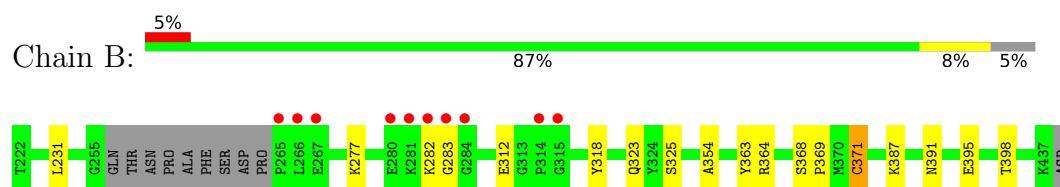
3 Residue-property plots [i](#)

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.

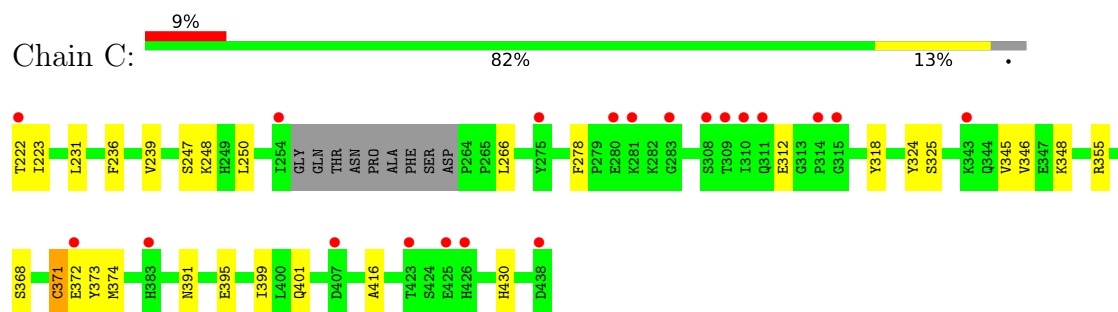
- Molecule 1: Transcriptional enhancer factor TEF-5



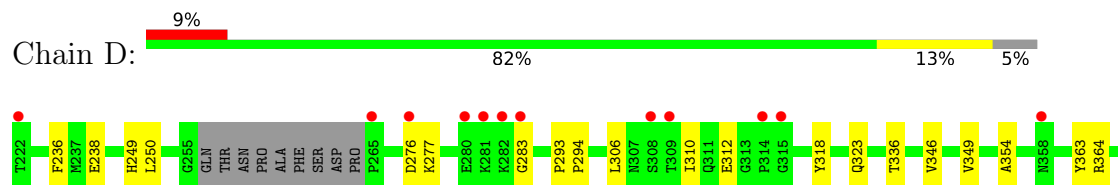
- Molecule 1: Transcriptional enhancer factor TEF-5

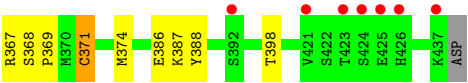


- Molecule 1: Transcriptional enhancer factor TEF-5



- Molecule 1: Transcriptional enhancer factor TEF-5





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.31Å 123.53Å 150.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	95.54 – 2.55 95.54 – 2.55	Depositor EDS
% Data completeness (in resolution range)	93.9 (95.54-2.55) 90.4 (95.54-2.55)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.29 (at 2.55Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.184 , 0.223 0.192 , 0.227	Depositor DCC
R_{free} test set	1922 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å ²)	35.4	Xtriage
Anisotropy	0.306	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6834	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 3.99% 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: CA, P1L

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	0.36	0/1694	0.75	5/2289 (0.2%)
1	B	0.33	0/1675	0.78	3/2264 (0.1%)
1	C	0.39	1/1703 (0.1%)	0.70	0/2302
1	D	0.44	0/1657	0.77	1/2244 (0.0%)
All	All	0.38	1/6729 (0.0%)	0.75	9/9099 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	247	SER	C-O	-5.76	1.17	1.24

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	283	GLY	N-CA-C	-10.95	87.23	113.18
1	B	282	LYS	N-CA-C	9.05	130.08	110.80
1	D	387	LYS	N-CA-C	6.52	118.38	111.28
1	A	312	GLU	N-CA-C	5.22	116.90	108.08
1	B	282	LYS	CB-CA-C	-5.06	100.35	110.42
1	A	316	ALA	N-CA-C	-5.03	103.89	110.53
1	A	311	GLN	N-CA-C	5.02	118.50	112.38
1	A	313	GLY	CA-C-N	-5.00	115.08	120.03
1	A	313	GLY	C-N-CA	-5.00	115.08	120.03

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1677	0	1657	17	1
1	B	1660	0	1634	11	0
1	C	1686	0	1660	19	0
1	D	1642	0	1595	17	1
2	B	1	0	0	0	0
2	D	1	0	0	0	0
3	A	48	0	0	1	0
3	B	54	0	0	1	0
3	C	39	0	0	1	0
3	D	26	0	0	0	0
All	All	6834	0	6546	61	1

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:247:SER:HB3	1:A:310:ILE:HD12	1.67	0.77
1:C:348:LYS:NZ	1:C:368:SER:OG	2.23	0.71
1:A:312:GLU:HG2	1:A:313:GLY:H	1.58	0.69
1:D:386:GLU:OE2	1:D:388:TYR:HB3	1.94	0.68
1:A:227:ARG:NH1	1:A:410:GLU:OE2	2.27	0.67
1:A:301:LYS:HG2	1:A:418:VAL:HG23	1.76	0.66
1:C:312:GLU:OE2	1:C:318:TYR:OH	2.09	0.64
1:A:352:GLU:OE2	1:C:355:ARG:NH2	2.31	0.63
1:D:371:P1L:H131	1:D:374:MET:HG3	1.82	0.62
1:C:236:PHE:HB3	1:C:250:LEU:HD23	1.81	0.61
1:D:249:HIS:HB2	1:D:310:ILE:HD12	1.82	0.60
1:C:345:VAL:HG12	1:C:346:VAL:HG23	1.81	0.60
1:A:291:LYS:NZ	3:A:501:HOH:O	2.36	0.58
1:C:324:TYR:OH	1:C:401:GLN:OE1	2.22	0.57
1:D:336:THR:HG21	1:D:371:P1L:H111	1.89	0.55
1:D:238:GLU:OE1	1:D:367:ARG:NH1	2.25	0.54
1:C:371:P1L:H141	1:C:374:MET:HE2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:VAL:HG21	1:A:312:GLU:HA	1.92	0.52
1:A:312:GLU:HG2	1:A:313:GLY:N	2.22	0.51
1:B:387:LYS:NZ	3:B:602:HOH:O	2.44	0.51
1:D:323:GLN:HG2	1:D:364:ARG:HG2	1.92	0.51
1:B:277:LYS:HB3	1:B:398:THR:HG21	1.94	0.50
1:A:312:GLU:CG	1:A:313:GLY:N	2.73	0.50
1:C:372:GLU:OE1	1:D:283:GLY:HA3	2.13	0.49
1:A:312:GLU:CG	1:A:313:GLY:H	2.23	0.49
1:B:312:GLU:OE1	1:B:318:TYR:OH	2.32	0.48
1:C:371:P1L:H202	1:C:371:P1L:H171	1.64	0.48
1:C:278:PHE:CZ	1:C:416:ALA:HB1	2.50	0.47
1:A:301:LYS:HE2	1:A:420:GLU:HB2	1.97	0.47
1:A:386:GLU:HB2	1:A:389:MET:HG3	1.97	0.46
1:A:391:ASN:O	1:A:395:GLU:HG3	2.16	0.46
1:B:323:GLN:HG2	1:B:364:ARG:HG2	1.97	0.45
1:C:391:ASN:O	1:C:395:GLU:HG3	2.16	0.45
1:C:348:LYS:HG3	1:D:349:VAL:HB	1.99	0.45
1:C:371:P1L:H122	1:C:399:ILE:HD13	1.99	0.45
1:C:231:LEU:HD11	1:C:325:SER:HB3	1.99	0.44
1:D:236:PHE:HB3	1:D:250:LEU:HD23	2.00	0.44
1:D:312:GLU:OE2	1:D:318:TYR:OH	2.23	0.44
1:B:391:ASN:O	1:B:395:GLU:HG3	2.18	0.44
1:B:371:P1L:H202	1:B:371:P1L:H171	1.69	0.44
1:D:293:PRO:HA	1:D:294:PRO:HD3	1.91	0.44
1:C:239:VAL:HG21	1:C:312:GLU:H	1.82	0.43
1:D:354:ALA:HB2	1:D:363:TYR:CE1	2.54	0.43
1:A:236:PHE:HB3	1:A:250:LEU:HD23	1.99	0.43
1:B:368:SER:HA	1:B:369:PRO:HD3	1.85	0.43
1:B:231:LEU:HD11	1:B:325:SER:HB3	2.01	0.43
1:B:371:P1L:H8C1	1:B:371:P1L:H112	1.86	0.43
1:C:222:THR:OG1	1:C:266:LEU:HD11	2.20	0.42
1:B:354:ALA:HB2	1:B:363:TYR:CE1	2.54	0.42
1:D:371:P1L:H122	1:D:371:P1L:H151	1.72	0.42
1:D:277:LYS:HB3	1:D:398:THR:HG21	2.01	0.42
1:B:371:P1L:H191	1:B:371:P1L:H223	1.80	0.42
1:D:306:LEU:HD21	1:D:371:P1L:H212	2.02	0.42
1:D:276:ASP:OD2	1:D:276:ASP:N	2.53	0.41
1:A:371:P1L:H172	1:A:374:MET:HE2	2.03	0.41
1:D:368:SER:HA	1:D:369:PRO:HD3	1.87	0.41
1:A:293:PRO:HA	1:A:294:PRO:HD3	1.90	0.41
1:C:222:THR:HG23	1:C:223:ILE:HG13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:430:HIS:ND1	3:C:502:HOH:O	2.37	0.41
1:A:231:LEU:HD11	1:A:325:SER:HB3	2.02	0.40
1:C:345:VAL:HG11	1:C:373:TYR:CE1	2.56	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:301:LYS:NZ	1:D:386:GLU:OE1[2_555]	2.13	0.07

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	203/217 (94%)	199 (98%)	4 (2%)	0	100	100
1	B	202/217 (93%)	197 (98%)	5 (2%)	0	100	100
1	C	203/217 (94%)	202 (100%)	1 (0%)	0	100	100
1	D	202/217 (93%)	199 (98%)	3 (2%)	0	100	100
All	All	810/868 (93%)	797 (98%)	13 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	181/195 (93%)	178 (98%)	3 (2%)	53	72
1	B	178/195 (91%)	178 (100%)	0	100	100
1	C	183/195 (94%)	182 (100%)	1 (0%)	81	88
1	D	174/195 (89%)	173 (99%)	1 (1%)	78	87
All	All	716/780 (92%)	711 (99%)	5 (1%)	76	85

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

Mol	Chain	Res	Type
1	A	266	LEU
1	A	274	ILE
1	A	280	GLU
1	C	248	LYS
1	D	346	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	383	HIS
1	B	366	HIS
1	C	253	HIS
1	D	344	GLN
1	D	396	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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	P1L	C	371	1	21,22,23	0.70	0	19,23,25	1.27	3 (15%)
1	P1L	D	371	1	21,22,23	0.71	0	19,23,25	1.38	2 (10%)
1	P1L	B	371	1	21,22,23	0.69	0	19,23,25	1.37	3 (15%)
1	P1L	A	371	1	21,22,23	0.64	0	19,23,25	1.27	2 (10%)

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	P1L	C	371	1	-	7/20/22/24	-
1	P1L	D	371	1	-	10/20/22/24	-
1	P1L	B	371	1	-	8/20/22/24	-
1	P1L	A	371	1	-	8/20/22/24	-

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	371	P1L	C8-C7-SG	-4.11	108.50	113.40
1	A	371	P1L	CB-SG-C7	3.64	105.76	100.76
1	B	371	P1L	CB-SG-C7	3.60	105.71	100.76
1	C	371	P1L	CB-SG-C7	3.54	105.62	100.76
1	D	371	P1L	CB-SG-C7	3.28	105.27	100.76
1	A	371	P1L	C8-C7-SG	-3.24	109.54	113.40
1	B	371	P1L	C8-C7-SG	-3.24	109.54	113.40
1	C	371	P1L	C8-C7-SG	-2.90	109.94	113.40
1	B	371	P1L	O7-C7-SG	2.78	126.22	122.68
1	C	371	P1L	O7-C7-SG	2.08	125.33	122.68

There are no chirality outliers.

All (33) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	371	P1L	O7-C7-SG-CB
1	A	371	P1L	C8-C7-SG-CB
1	B	371	P1L	O7-C7-SG-CB
1	B	371	P1L	C8-C7-SG-CB

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Mol	Chain	Res	Type	Atoms
1	C	371	P1L	O7-C7-SG-CB
1	C	371	P1L	C8-C7-SG-CB
1	D	371	P1L	O7-C7-SG-CB
1	D	371	P1L	C8-C7-SG-CB
1	B	371	P1L	C10-C11-C12-C13
1	C	371	P1L	C11-C12-C13-C14
1	D	371	P1L	C16-C17-C18-C19
1	D	371	P1L	C14-C15-C16-C17
1	B	371	P1L	C11-C12-C13-C14
1	D	371	P1L	C13-C14-C15-C16
1	A	371	P1L	C17-C18-C19-C20
1	A	371	P1L	C11-C12-C13-C14
1	C	371	P1L	C15-C16-C17-C18
1	C	371	P1L	C13-C14-C15-C16
1	B	371	P1L	C15-C16-C17-C18
1	A	371	P1L	C11-C10-C9-C8
1	B	371	P1L	C9-C10-C11-C12
1	A	371	P1L	C9-C10-C11-C12
1	B	371	P1L	C18-C19-C20-C21
1	D	371	P1L	C19-C20-C21-C22
1	A	371	P1L	C18-C19-C20-C21
1	C	371	P1L	C17-C18-C19-C20
1	C	371	P1L	C19-C20-C21-C22
1	D	371	P1L	C12-C13-C14-C15
1	A	371	P1L	C10-C11-C12-C13
1	D	371	P1L	C9-C10-C11-C12
1	D	371	P1L	C15-C16-C17-C18
1	B	371	P1L	C11-C10-C9-C8
1	D	371	P1L	C11-C10-C9-C8

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	371	P1L	3	0
1	D	371	P1L	4	0
1	B	371	P1L	3	0
1	A	371	P1L	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	207/217 (95%)	0.18	15 (7%) 21 20	20, 38, 73, 92	0
1	B	206/217 (94%)	0.07	10 (4%) 35 34	21, 37, 63, 79	0
1	C	207/217 (95%)	0.28	20 (9%) 13 12	23, 40, 76, 85	0
1	D	206/217 (94%)	0.51	19 (9%) 14 14	25, 46, 85, 101	0
All	All	826/868 (95%)	0.26	64 (7%) 19 18	20, 40, 76, 101	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	265	PRO	4.6
1	D	424	SER	4.1
1	D	265	PRO	4.0
1	D	315	GLY	3.9
1	A	407	ASP	3.6
1	D	426	HIS	3.6
1	A	311	GLN	3.6
1	B	283	GLY	3.6
1	B	282	LYS	3.5
1	A	222	THR	3.5
1	D	282	LYS	3.5
1	D	281	LYS	3.5
1	D	309	THR	3.4
1	C	372	GLU	3.3
1	C	310	ILE	3.2
1	D	423	THR	3.2
1	A	255	GLY	3.2
1	D	437	LYS	3.2
1	C	283	GLY	3.1
1	C	309	THR	3.0
1	B	314	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	314	PRO	2.9
1	C	311	GLN	2.8
1	A	386	GLU	2.8
1	D	425	GLU	2.8
1	D	308	SER	2.8
1	A	309	THR	2.8
1	D	314	PRO	2.8
1	C	407	ASP	2.7
1	C	315	GLY	2.7
1	D	421	VAL	2.6
1	C	438	ASP	2.6
1	A	282	LYS	2.6
1	D	358	ASN	2.6
1	C	383	HIS	2.6
1	C	426	HIS	2.6
1	D	222	THR	2.6
1	C	222	THR	2.5
1	C	308	SER	2.5
1	B	280	GLU	2.5
1	B	266	LEU	2.5
1	A	314	PRO	2.5
1	D	283	GLY	2.5
1	B	267	GLU	2.4
1	C	254	ILE	2.4
1	C	423	THR	2.4
1	B	315	GLY	2.4
1	C	281	LYS	2.4
1	C	275	TYR	2.3
1	A	273	GLN	2.3
1	C	280	GLU	2.3
1	C	425	GLU	2.3
1	A	383	HIS	2.3
1	A	310	ILE	2.3
1	A	395	GLU	2.2
1	D	276	ASP	2.2
1	D	280	GLU	2.1
1	D	392	SER	2.1
1	B	284	GLY	2.1
1	A	313	GLY	2.1
1	A	437	LYS	2.1
1	B	281	LYS	2.1
1	A	281	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	343	LYS	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	P1L	C	371	23/24	0.91	0.17	33,47,69,80	0
1	P1L	A	371	23/24	0.92	0.14	27,46,61,71	0
1	P1L	D	371	23/24	0.92	0.16	25,55,72,80	0
1	P1L	B	371	23/24	0.93	0.15	25,43,67,80	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(Å ²)	Q<0.9
2	CA	D	501	1/1	0.93	0.14	44,44,44,44	0
2	CA	B	501	1/1	0.95	0.09	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.