



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:41 PM UTC

PDB ID : 5W6H / pdb_00005w6h
Title : Crystal structure of Bacteriophage CBA120 tailspike protein 4 enzymatically active domain (TSP4dN, orf213)
Authors : Plattner, M.; Shneider, M.M.; Leiman, P.G.
Deposited on : 2017-06-16
Resolution : 2.29 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

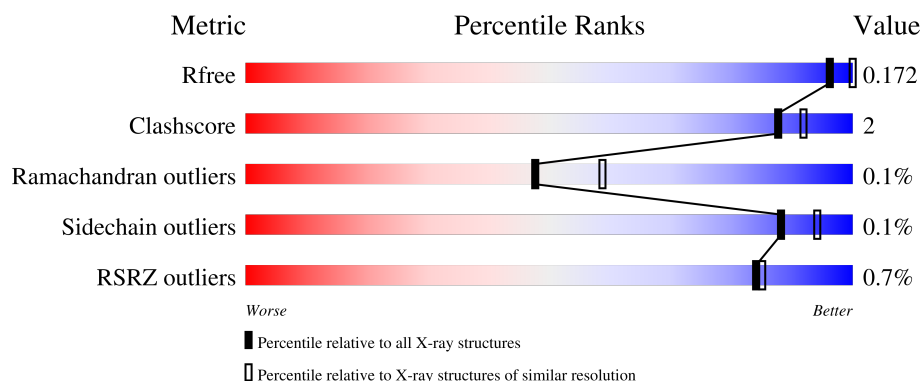
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	697	% 96% .
1	B	697	% 95% .
1	C	697	95% 5%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 17854 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 tailspike protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	697	Total	C	N	O	S	0	5	0
			5212	3296	857	1043	16			
1	B	697	Total	C	N	O	S	0	5	0
			5213	3297	860	1040	16			
1	C	697	Total	C	N	O	S	0	3	0
			5195	3288	854	1037	16			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	340	GLY	-	expression tag	UNP G3M192
A	341	SER	-	expression tag	UNP G3M192
A	342	GLY	-	expression tag	UNP G3M192
A	343	SER	-	expression tag	UNP G3M192
A	1012	ARG	LYS	engineered mutation	UNP G3M192
B	340	GLY	-	expression tag	UNP G3M192
B	341	SER	-	expression tag	UNP G3M192
B	342	GLY	-	expression tag	UNP G3M192
B	343	SER	-	expression tag	UNP G3M192
B	1012	ARG	LYS	engineered mutation	UNP G3M192
C	340	GLY	-	expression tag	UNP G3M192
C	341	SER	-	expression tag	UNP G3M192
C	342	GLY	-	expression tag	UNP G3M192
C	343	SER	-	expression tag	UNP G3M192
C	1012	ARG	LYS	engineered mutation	UNP G3M192

- Molecule 2 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



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

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

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total K 1 1	0	0

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Na 1 1	0	0

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Zn 1 1	0	0

- Molecule 6 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	1	Total	Cl	0	0
			1	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	727	Total	O	0	0
			727	727		
8	B	688	Total	O	0	0
			688	688		
8	C	706	Total	O	0	0
			706	706		

- Molecule 1: tailspike protein 4



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	170.08Å 170.08Å 246.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.29 – 2.29 49.29 – 2.29	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.29-2.29) 99.7 (49.29-2.29)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.92 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.140 , 0.170 0.143 , 0.172	Depositor DCC
R_{free} test set	8080 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	34.7	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	17854	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.14% 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: SO4, CL, K, NA, ZN, ACT

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	0.10	0/5313	0.32	0/7242
1	B	0.10	0/5314	0.33	0/7242
1	C	0.10	0/5299	0.32	0/7223
All	All	0.10	0/15926	0.32	0/21707

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	5212	0	5105	17	0
1	B	5213	0	5115	21	0
1	C	5195	0	5099	20	0
2	A	40	0	30	2	0
2	B	32	0	24	2	0
2	C	32	0	24	4	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	1	0	0	0	0
6	C	5	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	1	0	0	1	0
8	A	727	0	0	4	2
8	B	688	0	0	3	2
8	C	706	0	0	12	1
All	All	17854	0	15397	63	3

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (63) 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)
7:C:1110:CL:CL	8:C:1216:HOH:O	2.35	0.81
2:C:1103:ACT:O	8:C:1201:HOH:O	2.12	0.68
2:B:1101:ACT:O	8:B:1201:HOH:O	2.12	0.67
2:C:1102:ACT:O	8:C:1202:HOH:O	2.13	0.65
1:C:487:ASN:HA	1:C:490:LYS:HD3	1.82	0.61
1:A:487:ASN:HA	1:A:490:LYS:HD3	1.82	0.61
1:B:556:LYS:NZ	8:B:1208:HOH:O	2.33	0.61
1:C:481[A]:ASP:OD2	8:C:1203:HOH:O	2.17	0.60
1:C:556:LYS:NZ	8:C:1213:HOH:O	2.32	0.60
1:A:556:LYS:NZ	8:A:1210:HOH:O	2.33	0.57
1:A:962:TRP:HB2	1:A:1029:HIS:HB3	1.87	0.57
1:B:454:THR:OG1	8:B:1202:HOH:O	2.18	0.56
1:C:458:THR:OG1	8:C:1204:HOH:O	2.18	0.56
1:B:962:TRP:HB2	1:B:1029:HIS:HB3	1.88	0.56
1:A:651:ALA:O	8:A:1201:HOH:O	2.18	0.55
1:B:478:SER:HB2	1:B:483[B]:SER:HB3	1.87	0.55
1:B:487:ASN:HA	1:B:490:LYS:HD3	1.89	0.55
2:C:1101:ACT:O	8:C:1205:HOH:O	2.18	0.54
1:C:962:TRP:HB2	1:C:1029:HIS:HB3	1.93	0.51
1:B:742:PHE:HB2	1:B:769:VAL:HA	1.92	0.50
1:C:919:ASN:ND2	8:C:1228:HOH:O	2.45	0.50
1:B:700:ARG:HA	1:B:727:VAL:O	2.12	0.49
1:B:785:GLU:HG3	1:B:811:LEU:HB2	1.94	0.48
2:C:1106:ACT:OXT	8:C:1206:HOH:O	2.20	0.48
1:A:638:ASP:OD2	1:A:643:ASN:ND2	2.44	0.48
1:C:721:PRO:HG2	1:C:724:SER:HB2	1.95	0.48
1:C:700:ARG:HA	1:C:727:VAL:O	2.13	0.48
2:A:1101:ACT:O	8:A:1202:HOH:O	2.20	0.47
1:B:721:PRO:HG2	1:B:724:SER:HB2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:721:PRO:HG2	1:A:724:SER:HB2	1.97	0.47
1:B:478:SER:HB2	1:B:483[A]:SER:HB2	1.97	0.46
1:A:700:ARG:HA	1:A:727:VAL:O	2.15	0.46
1:C:742:PHE:HB2	1:C:769:VAL:HA	1.97	0.46
1:B:837:PRO:HD2	1:B:853:LEU:HD11	1.97	0.45
1:C:346:ARG:NH1	8:C:1219:HOH:O	2.39	0.45
1:A:742:PHE:HB2	1:A:769:VAL:HA	1.99	0.45
1:C:651:ALA:O	8:C:1207:HOH:O	2.21	0.45
1:A:778:VAL:HG21	1:B:807:ASP:HB3	1.98	0.44
1:B:778:VAL:HG21	1:C:807:ASP:HB3	2.00	0.44
1:C:368:LEU:HD13	1:C:403:LEU:HD21	1.99	0.44
1:A:345:LEU:HD22	1:A:359:VAL:HG12	1.99	0.44
1:C:801:SER:C	1:C:802:ARG:HD2	2.43	0.44
1:B:801:SER:C	1:B:802:ARG:HD2	2.43	0.44
1:B:654:THR:HA	1:B:682:SER:O	2.18	0.43
1:A:753:SER:HA	1:A:781:ASN:O	2.18	0.43
1:A:807:ASP:HB3	1:C:778:VAL:HG21	2.00	0.43
1:B:753:SER:HA	1:B:781:ASN:O	2.19	0.43
1:A:654:THR:HA	1:A:682:SER:O	2.19	0.43
1:B:964:LYS:HE3	2:B:1105:ACT:H2	2.01	0.43
6:C:1109:SO4:O3	8:C:1208:HOH:O	2.22	0.43
2:A:1106:ACT:O	8:A:1203:HOH:O	2.21	0.42
1:A:785:GLU:HG3	1:A:811:LEU:HB2	2.01	0.42
1:B:699:TYR:HD2	1:B:700:ARG:HG3	1.85	0.42
1:A:347:GLU:HG2	1:B:347:GLU:HG2	2.02	0.41
1:A:801:SER:C	1:A:802:ARG:HD2	2.44	0.41
1:A:809:THR:HG22	1:A:835:SER:HB3	2.01	0.41
1:B:647:ILE:HD13	1:B:647:ILE:HA	1.95	0.41
1:B:953:PRO:HB3	1:B:1008:PRO:HA	2.02	0.41
1:C:753:SER:HA	1:C:781:ASN:O	2.20	0.41
1:C:809:THR:HG22	1:C:835:SER:HB3	2.03	0.41
1:C:818:THR:OG1	1:C:819:VAL:N	2.53	0.41
1:C:478:SER:HB2	1:C:483:SER:OG	2.20	0.41
1:C:953:PRO:HB3	1:C:1008:PRO:HA	2.02	0.41

All (3) 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)
8:A:1582:HOH:O	8:B:1790:HOH:O[4_474]	2.14	0.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:1650:HOH:O	8:C:1774:HOH:O[2_585]	2.16	0.04
8:A:1718:HOH:O	8:B:1513:HOH:O[3_765]	2.18	0.02

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	700/697 (100%)	674 (96%)	25 (4%)	1 (0%)	48	59
1	B	700/697 (100%)	673 (96%)	26 (4%)	1 (0%)	48	59
1	C	698/697 (100%)	668 (96%)	29 (4%)	1 (0%)	48	59
All	All	2098/2091 (100%)	2015 (96%)	80 (4%)	3 (0%)	48	59

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	727	VAL
1	C	727	VAL
1	B	727	VAL

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	578/573 (101%)	578 (100%)	0	100	100
1	B	578/573 (101%)	578 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	576/573 (100%)	575 (100%)	1 (0%)	87	93
All	All	1732/1719 (101%)	1731 (100%)	1 (0%)	88	94

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	598	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	436	ASN
1	A	774	ASN
1	A	1018	ASN
1	B	436	ASN
1	B	774	ASN
1	B	876	ASN
1	B	902	ASN
1	B	1018	ASN
1	C	444	HIS
1	C	774	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 31 ligands modelled in this entry, 4 are monoatomic - leaving 27 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
2	ACT	B	1102	-	3,3,3	1.30	0	3,3,3	1.38	0
2	ACT	B	1108	-	3,3,3	1.35	0	3,3,3	1.52	0
2	ACT	C	1102	-	3,3,3	1.40	1 (33%)	3,3,3	1.36	0
2	ACT	B	1106	-	3,3,3	1.39	0	3,3,3	1.50	0
2	ACT	A	1101	-	3,3,3	1.35	0	3,3,3	1.37	0
2	ACT	C	1101	-	3,3,3	1.36	0	3,3,3	1.51	0
2	ACT	C	1106	-	3,3,3	1.39	0	3,3,3	1.50	0
6	SO4	C	1109	-	4,4,4	0.23	0	6,6,6	0.06	0
2	ACT	C	1105	-	3,3,3	1.39	1 (33%)	3,3,3	1.39	0
2	ACT	A	1110	-	3,3,3	1.39	0	3,3,3	1.55	0
2	ACT	B	1101	-	3,3,3	1.35	0	3,3,3	1.39	0
2	ACT	A	1105	-	3,3,3	1.41	0	3,3,3	1.49	0
2	ACT	A	1103	-	3,3,3	1.41	1 (33%)	3,3,3	1.35	0
2	ACT	C	1104	-	3,3,3	1.36	0	3,3,3	1.36	0
2	ACT	A	1109	-	3,3,3	1.38	0	3,3,3	1.52	0
2	ACT	B	1105	-	3,3,3	1.36	0	3,3,3	1.38	0
2	ACT	A	1104	-	3,3,3	1.37	0	3,3,3	1.36	0
2	ACT	B	1107	-	3,3,3	1.40	0	3,3,3	1.49	0
2	ACT	B	1103	-	3,3,3	1.36	0	3,3,3	1.35	0
2	ACT	C	1103	-	3,3,3	1.26	0	3,3,3	1.45	0
2	ACT	C	1108	-	3,3,3	1.38	0	3,3,3	1.52	0
2	ACT	C	1107	-	3,3,3	1.37	0	3,3,3	1.35	0
2	ACT	A	1107	-	3,3,3	1.37	0	3,3,3	1.39	0
2	ACT	A	1108	-	3,3,3	1.37	0	3,3,3	1.49	0
2	ACT	A	1106	-	3,3,3	1.33	0	3,3,3	1.50	0
2	ACT	A	1102	-	3,3,3	1.38	0	3,3,3	1.51	0
2	ACT	B	1104	-	3,3,3	1.39	1 (33%)	3,3,3	1.41	0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1102	ACT	CH3-C	2.04	1.57	1.49
2	A	1103	ACT	CH3-C	2.03	1.57	1.49
2	C	1105	ACT	CH3-C	2.02	1.57	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1104	ACT	CH3-C	2.02	1.57	1.49

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1102	ACT	1	0
2	A	1101	ACT	1	0
2	C	1101	ACT	1	0
2	C	1106	ACT	1	0
6	C	1109	SO4	1	0
2	B	1101	ACT	1	0
2	B	1105	ACT	1	0
2	C	1103	ACT	1	0
2	A	1106	ACT	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	697/697 (100%)	-0.59	5 (0%) 84 85	14, 33, 62, 121	5 (0%)
1	B	697/697 (100%)	-0.56	7 (1%) 79 81	16, 34, 57, 107	5 (0%)
1	C	697/697 (100%)	-0.62	3 (0%) 88 89	18, 34, 50, 118	3 (0%)
All	All	2091/2091 (100%)	-0.59	15 (0%) 84 85	14, 34, 56, 121	13 (0%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	340	GLY	6.1
1	C	340	GLY	6.0
1	A	340	GLY	5.8
1	A	341	SER	3.4
1	B	341	SER	3.3
1	A	342	GLY	3.0
1	B	342	GLY	2.8
1	C	342	GLY	2.6
1	A	641	TYR	2.5
1	C	341	SER	2.4
1	A	343	SER	2.3
1	B	346[A]	ARG	2.3
1	B	765	PHE	2.1
1	B	475	ALA	2.0
1	B	454	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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
2	ACT	A	1106	4/4	0.69	0.29	63,71,72,81	0
2	ACT	A	1107	4/4	0.70	0.34	67,67,73,82	0
2	ACT	A	1105	4/4	0.71	0.26	67,67,73,82	0
2	ACT	B	1103	4/4	0.75	0.24	55,63,63,69	0
2	ACT	B	1104	4/4	0.75	0.24	48,60,61,65	0
2	ACT	C	1107	4/4	0.78	0.21	60,60,64,72	0
2	ACT	C	1108	4/4	0.78	0.24	73,74,74,75	0
2	ACT	C	1104	4/4	0.79	0.25	53,67,70,74	0
2	ACT	A	1104	4/4	0.79	0.22	54,61,61,71	0
2	ACT	A	1103	4/4	0.79	0.19	50,50,58,63	0
2	ACT	A	1108	4/4	0.80	0.25	71,76,76,81	0
2	ACT	C	1105	4/4	0.80	0.22	63,70,70,71	0
2	ACT	A	1110	4/4	0.81	0.22	53,54,64,65	0
2	ACT	C	1106	4/4	0.81	0.19	53,57,58,60	0
2	ACT	B	1107	4/4	0.82	0.18	55,62,63,70	0
2	ACT	B	1102	4/4	0.83	0.27	59,71,73,79	0
2	ACT	B	1105	4/4	0.83	0.25	61,65,66,67	0
2	ACT	B	1108	4/4	0.87	0.18	57,63,67,71	0
2	ACT	B	1106	4/4	0.87	0.20	59,62,67,69	0
2	ACT	A	1101	4/4	0.87	0.16	47,56,57,57	0
2	ACT	C	1103	4/4	0.89	0.15	40,52,53,55	0
2	ACT	A	1102	4/4	0.89	0.19	71,74,75,79	0
2	ACT	C	1101	4/4	0.89	0.15	49,51,53,54	0
2	ACT	A	1109	4/4	0.90	0.19	59,62,62,68	0
2	ACT	B	1101	4/4	0.90	0.15	46,53,55,58	0
2	ACT	C	1102	4/4	0.90	0.15	41,54,56,59	0
6	SO4	C	1109	5/5	0.91	0.11	76,83,86,89	0
7	CL	C	1110	1/1	0.97	0.09	56,56,56,56	0
3	K	A	1111	1/1	0.98	0.20	70,70,70,70	0
4	NA	A	1112	1/1	0.99	0.09	39,39,39,39	0
5	ZN	A	1113	1/1	1.00	0.14	57,57,57,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.