



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 03:04 PM UTC

PDB ID : 4UNM / pdb_00004unm
Title : Structure of Galactose Oxidase homologue from Streptomyces lividans
Authors : Chaplin, A.K.; Hough, M.A.; Worrall, J.A.R.
Deposited on : 2014-05-29
Resolution : 1.77 Å(reported)

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<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

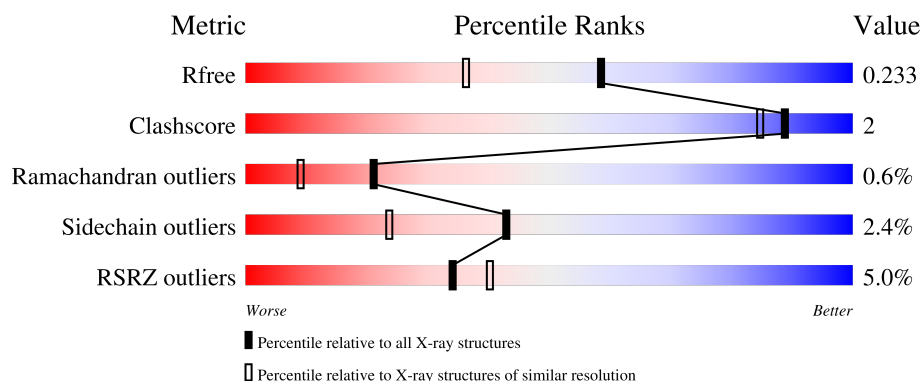
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.77 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	1365 (1.78-1.78)
Clashscore	190562	1395 (1.78-1.78)
Ramachandran outliers	187476	1382 (1.78-1.78)
Sidechain outliers	187428	1382 (1.78-1.78)
RSRZ outliers	180081	1365 (1.78-1.78)

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	615	2% 91% 6% ..
1	B	615	8% 90% 8% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10084 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 SECRETED PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	599	Total	C	N	O	S	50	3	0
			4663	2938	811	903	11			
1	B	609	Total	C	N	O	S	79	1	0
			4725	2979	820	915	11			

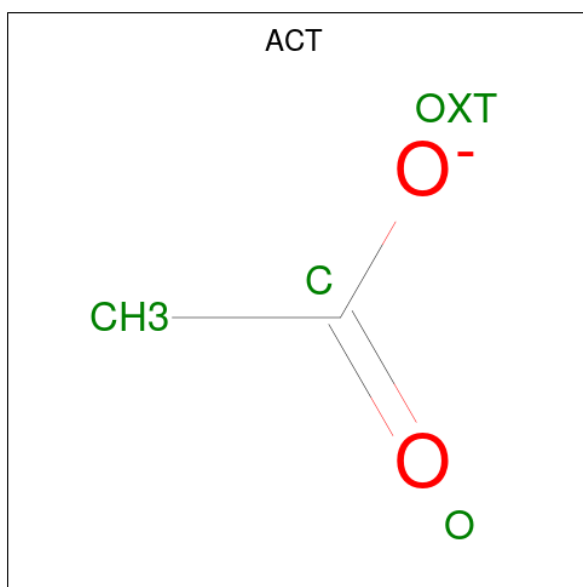
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	31	GLY	-	expression tag	UNP D6EWM0
A	32	SER	-	expression tag	UNP D6EWM0
A	33	HIS	-	expression tag	UNP D6EWM0
A	34	MET	-	expression tag	UNP D6EWM0
B	31	GLY	-	expression tag	UNP D6EWM0
B	32	SER	-	expression tag	UNP D6EWM0
B	33	HIS	-	expression tag	UNP D6EWM0
B	34	MET	-	expression tag	UNP D6EWM0

- 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		

- Molecule 3 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



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

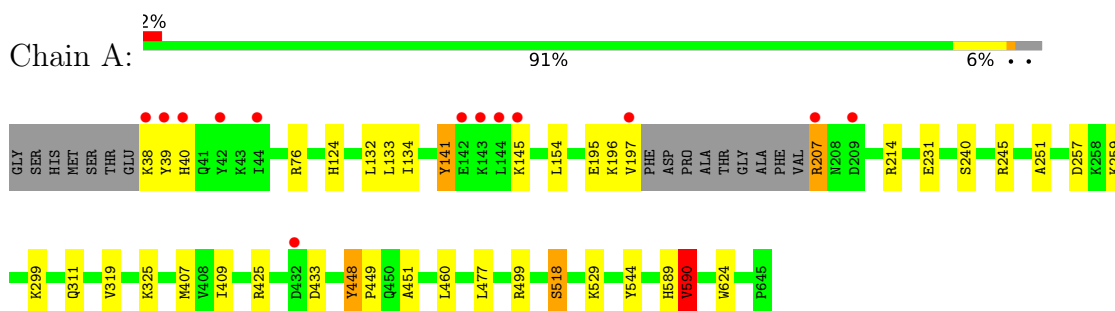
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	417	Total O 417 417	0	0
4	B	261	Total O 261 261	0	0

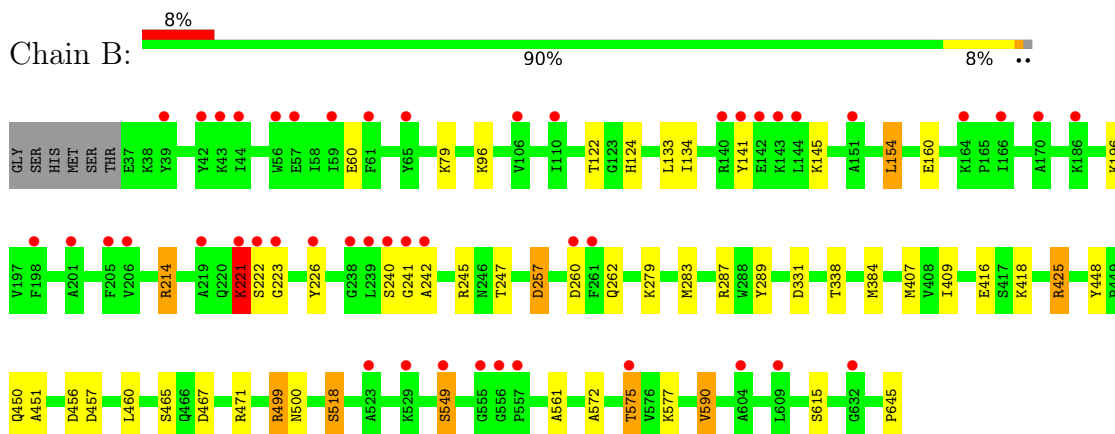
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: SECRETED PROTEIN



• Molecule 1: SECRETED PROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.36Å 126.63Å 107.55Å 90.00° 91.10° 90.00°	Depositor
Resolution (Å)	53.50 – 1.77 53.50 – 1.77	Depositor EDS
% Data completeness (in resolution range)	99.7 (53.50-1.77) 99.7 (53.50-1.77)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 1.77Å)	Xtriage
Refinement program	REFMAC 5.8.0069	Depositor
R, R_{free}	0.188 , 0.228 0.195 , 0.233	Depositor DCC
R_{free} test set	6563 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	23.1	Xtriage
Anisotropy	0.604	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 32.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.032 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10084	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% 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: ACT, CU

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	0.85	3/4777 (0.1%)	0.90	4/6468 (0.1%)
1	B	0.86	10/4837 (0.2%)	0.94	12/6555 (0.2%)
All	All	0.85	13/9614 (0.1%)	0.92	16/13023 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	4
All	All	0	8

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	221	LYS	CD-CE	20.90	2.15	1.52
1	B	245	ARG	CZ-NH1	-10.42	1.18	1.32
1	B	214	ARG	CZ-NH1	9.31	1.45	1.32
1	B	79	LYS	CE-NZ	-8.62	1.23	1.49
1	A	259	LYS	CE-NZ	8.06	1.73	1.49
1	A	245	ARG	CZ-NH1	-7.36	1.22	1.32
1	B	154	LEU	CG-CD1	-6.55	1.30	1.52
1	B	575	THR	CB-OG1	-6.42	1.33	1.43
1	B	242	ALA	CA-CB	-6.21	1.44	1.53
1	B	549	SER	CB-OG	5.82	1.53	1.42
1	A	433	ASP	CG-OD2	-5.46	1.15	1.25
1	B	331	ASP	CG-OD2	-5.45	1.15	1.25
1	B	577	LYS	CG-CD	-5.29	1.36	1.52

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	221	LYS	CG-CD-CE	-24.38	55.22	111.30
1	B	221	LYS	CD-CE-NZ	-16.19	60.08	111.90
1	B	214	ARG	NE-CZ-NH1	-14.00	107.50	121.50
1	B	154	LEU	CD1-CG-CD2	7.40	127.08	110.80
1	A	245	ARG	NH1-CZ-NH2	-6.70	110.59	119.30
1	B	425	ARG	NE-CZ-NH1	6.49	127.99	121.50
1	A	141	TYR	CA-CB-CG	5.71	124.17	113.90
1	B	425	ARG	NE-CZ-NH2	-5.63	114.13	119.20
1	A	529	LYS	CG-CD-CE	-5.60	98.41	111.30
1	A	477	LEU	CD1-CG-CD2	-5.52	98.66	110.80
1	B	425	ARG	CD-NE-CZ	5.30	131.82	124.40
1	B	425	ARG	CB-CG-CD	5.14	123.11	111.30
1	B	196	LYS	CG-CD-CE	5.08	122.98	111.30
1	B	499[A]	ARG	NE-CZ-NH2	5.05	123.74	119.20
1	B	499[B]	ARG	NE-CZ-NH2	5.05	123.74	119.20
1	B	214	ARG	NH1-CZ-NH2	-5.00	112.79	119.30

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	195	GLU	Peptide
1	A	207	ARG	Peptide
1	A	257	ASP	Peptide
1	A	39	TYR	Peptide
1	B	214	ARG	Sidechain
1	B	223	GLY	Peptide
1	B	241	GLY	Peptide
1	B	257	ASP	Peptide

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	4663	0	4608	16	0
1	B	4725	0	4656	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	12	0	9	0	0
3	B	4	0	3	0	0
4	A	417	0	0	2	0
4	B	261	0	0	1	0
All	All	10084	0	9276	34	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 2.

All (34) 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:B:384:MET:SD	1:B:425:ARG:HD2	2.29	0.73
1:A:325:LYS:NZ	4:A:2166:HOH:O	2.28	0.66
1:A:407:MET:HE3	1:A:409:ILE:HD11	1.78	0.66
1:B:407:MET:HE3	1:B:409:ILE:HD11	1.81	0.63
1:B:467:ASP:OD2	1:B:471:ARG:HD2	2.02	0.58
1:B:124:HIS:HA	1:B:133:LEU:O	2.08	0.54
1:B:572:ALA:O	1:B:575:THR:HG22	2.09	0.53
1:A:132:LEU:HD23	1:A:134:ILE:HD11	1.90	0.52
1:A:299:LYS:HB3	1:A:319:VAL:CG1	2.41	0.50
1:A:196:LYS:O	1:A:207:ARG:O	2.32	0.48
1:B:221:LYS:HB3	1:B:226:TYR:CE2	2.50	0.47
1:B:450:GLN:OE1	1:B:499[A]:ARG:NH1	2.48	0.46
1:B:499[B]:ARG:HA	1:B:518:SER:HB2	1.98	0.46
1:A:124:HIS:HA	1:A:133:LEU:O	2.16	0.46
1:B:499[A]:ARG:HA	1:B:518:SER:HB2	1.98	0.46
1:A:499[B]:ARG:HA	1:A:518:SER:HB2	1.99	0.45
1:A:311:GLN:NE2	4:A:2188:HOH:O	2.40	0.45
1:B:456:ASP:O	1:B:457:ASP:HB2	2.16	0.44
1:B:279:LYS:HE2	4:B:2080:HOH:O	2.17	0.44
1:B:122:THR:HG21	1:B:134:ILE:HD11	1.98	0.44
1:A:451:ALA:HA	1:A:460:LEU:O	2.18	0.43
1:B:289:TYR:HB3	1:B:338:THR:HB	2.00	0.43
1:B:257:ASP:HB3	1:B:416:GLU:OE2	2.19	0.43
1:A:499[A]:ARG:HA	1:A:518:SER:HB2	2.00	0.42
1:A:448:TYR:N	1:A:449:PRO:CD	2.83	0.42
1:A:154:LEU:HD11	1:A:214:ARG:HB3	2.01	0.42
1:A:154:LEU:CD1	1:A:214:ARG:HB3	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:ARG:HD2	1:A:624:TRP:CD1	2.55	0.41
1:B:561:ALA:HA	1:B:645:PRO:HD2	2.01	0.41
1:B:465:SER:HB3	1:B:500:ASN:HB3	2.01	0.41
1:A:231:GLU:HA	1:A:251:ALA:O	2.20	0.41
1:A:589:HIS:C	1:A:590:VAL:HG23	2.45	0.41
1:B:283:MET:HE1	1:B:287:ARG:HB2	2.02	0.41
1:B:451:ALA:HA	1:B:460:LEU:O	2.20	0.41

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	598/615 (97%)	578 (97%)	16 (3%)	4 (1%)	18	8
1	B	608/615 (99%)	581 (96%)	24 (4%)	3 (0%)	24	11
All	All	1206/1230 (98%)	1159 (96%)	40 (3%)	7 (1%)	21	9

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	518	SER
1	B	518	SER
1	A	40	HIS
1	A	448	TYR
1	B	448	TYR
1	A	590	VAL
1	B	590	VAL

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	501/510 (98%)	493 (98%)	8 (2%)	55	38
1	B	506/510 (99%)	490 (97%)	16 (3%)	34	13
All	All	1007/1020 (99%)	983 (98%)	24 (2%)	43	24

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	LYS
1	A	141	TYR
1	A	145	LYS
1	A	197	VAL
1	A	240	SER
1	A	425	ARG
1	A	544	TYR
1	A	590	VAL
1	B	60	GLU
1	B	96	LYS
1	B	141	TYR
1	B	145	LYS
1	B	154	LEU
1	B	160	GLU
1	B	221	LYS
1	B	222	SER
1	B	240	SER
1	B	247	THR
1	B	260	ASP
1	B	262	GLN
1	B	418	LYS
1	B	549	SER
1	B	590	VAL
1	B	615	SER

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	262	GLN
1	B	68	ASN
1	B	208	ASN
1	B	535	GLN
1	B	621	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	$\# Z > 2$
3	ACT	A	701	-	3,3,3	1.58	1 (33%)	3,3,3	0.94	0
3	ACT	A	703	-	3,3,3	0.62	0	3,3,3	0.97	0
3	ACT	A	702	-	3,3,3	0.81	0	3,3,3	0.78	0
3	ACT	B	701	-	3,3,3	0.86	0	3,3,3	0.92	0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	701	ACT	O-C	2.58	1.33	1.22

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	599/615 (97%)	0.01	13 (2%) 62 70	11, 24, 39, 55	45 (7%)
1	B	609/615 (99%)	0.56	47 (7%) 19 23	16, 32, 49, 72	59 (9%)
All	All	1208/1230 (98%)	0.29	60 (4%) 34 40	11, 27, 47, 72	104 (8%)

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	65	TYR	5.3
1	A	144	LEU	5.0
1	B	143	LYS	4.6
1	B	144	LEU	4.4
1	A	38	LYS	4.1
1	B	239	LEU	4.1
1	A	197	VAL	4.0
1	B	39	TYR	3.9
1	A	142	GLU	3.8
1	B	261	PHE	3.4
1	B	241	GLY	3.3
1	B	242	ALA	3.2
1	A	207	ARG	3.1
1	A	39	TYR	3.1
1	B	549	SER	3.0
1	B	222	SER	3.0
1	A	209	ASP	2.9
1	B	142	GLU	2.9
1	B	44	ILE	2.9
1	B	223	GLY	2.8
1	B	170	ALA	2.8
1	B	201	ALA	2.8
1	B	42	TYR	2.8
1	B	226	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	164	LYS	2.7
1	B	206	VAL	2.7
1	B	61	PHE	2.7
1	B	140	ARG	2.7
1	B	575	THR	2.6
1	A	44	ILE	2.6
1	B	529	LYS	2.6
1	B	557	PRO	2.6
1	B	260	ASP	2.5
1	B	555	GLY	2.5
1	B	186	LYS	2.5
1	B	56	TRP	2.4
1	A	145	LYS	2.4
1	B	110	ILE	2.4
1	B	198	PHE	2.4
1	B	240	SER	2.4
1	B	205	PHE	2.4
1	A	42	TYR	2.4
1	A	143	LYS	2.4
1	B	221	LYS	2.3
1	B	59	ILE	2.3
1	B	238	GLY	2.3
1	B	556	GLY	2.3
1	B	57	GLU	2.3
1	B	141	TYR	2.3
1	A	432	ASP	2.2
1	B	219	ALA	2.2
1	B	604	ALA	2.2
1	B	609	LEU	2.2
1	B	43	LYS	2.1
1	B	166	ILE	2.1
1	B	106	VAL	2.1
1	B	151	ALA	2.1
1	B	523	ALA	2.1
1	B	632	GLY	2.1
1	A	40	HIS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ACT	A	701	4/4	0.74	0.20	26,32,35,39	0
3	ACT	B	701	4/4	0.83	0.23	25,27,27,31	4
3	ACT	A	703	4/4	0.92	0.12	37,43,44,48	0
3	ACT	A	702	4/4	0.92	0.15	17,18,18,19	4
2	CU	B	700	1/1	0.98	0.04	30,30,30,30	0
2	CU	A	700	1/1	1.00	0.02	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.