



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2020 – 06:11 PM BST

PDB ID : 5YZM
Title : Crystal structure of S9 peptidase (inactive form) from *Deinococcus radiodurans* R1
Authors : Yadav, P.; Jamdar, S.N.; Kumar, A.; Ghosh, B.; Makde, R.D.
Deposited on : 2017-12-15
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

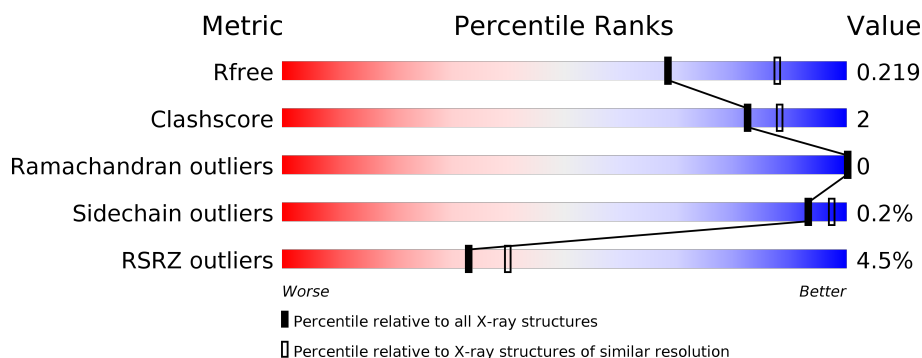
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on 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	656	<div> <div>0%</div> <div> <div></div> <div>87%</div> <div>9%</div> </div> <div>•</div> </div>
1	B	656	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>8%</div> </div> <div>•</div> </div>
1	C	656	<div> <div>7%</div> <div> <div></div> <div>85%</div> <div>6%</div> <div>10%</div> </div> </div>
1	D	656	<div> <div>7%</div> <div> <div></div> <div>82%</div> <div>8%</div> <div>10%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 19434 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 Acyl-peptide hydrolase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	598	Total	C	N	O	S	0	0	0
			4633	2941	831	852	9			
1	B	601	Total	C	N	O	S	0	1	0
			4627	2935	829	854	9			
1	C	593	Total	C	N	O	S	0	0	0
			4560	2897	820	834	9			
1	D	590	Total	C	N	O	S	0	0	0
			4546	2891	815	831	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q9RXY9
A	1	SER	-	expression tag	UNP Q9RXY9
B	0	GLY	-	expression tag	UNP Q9RXY9
B	1	SER	-	expression tag	UNP Q9RXY9
C	0	GLY	-	expression tag	UNP Q9RXY9
C	1	SER	-	expression tag	UNP Q9RXY9
D	0	GLY	-	expression tag	UNP Q9RXY9
D	1	SER	-	expression tag	UNP Q9RXY9

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



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

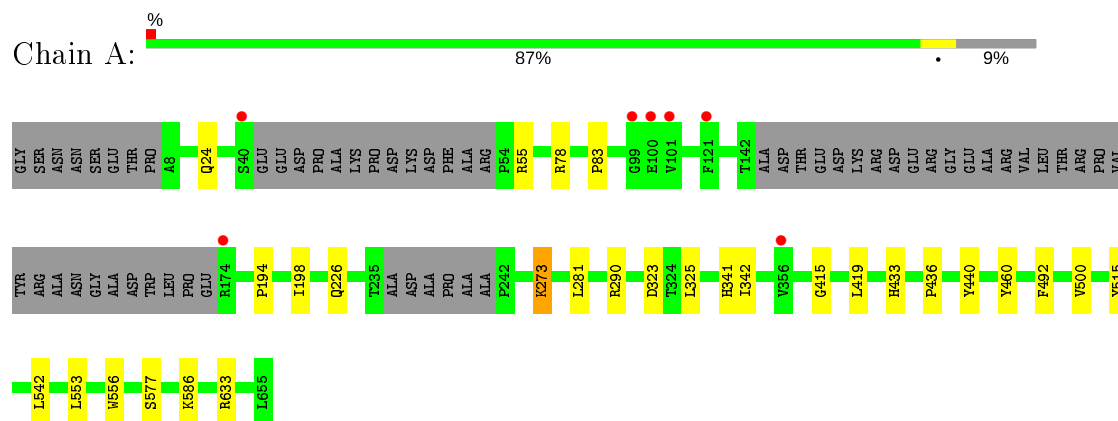
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	305	Total	O	0	0
			305	305		
3	B	327	Total	O	0	0
			327	327		
3	C	221	Total	O	0	0
			221	221		
3	D	199	Total	O	0	0
			199	199		

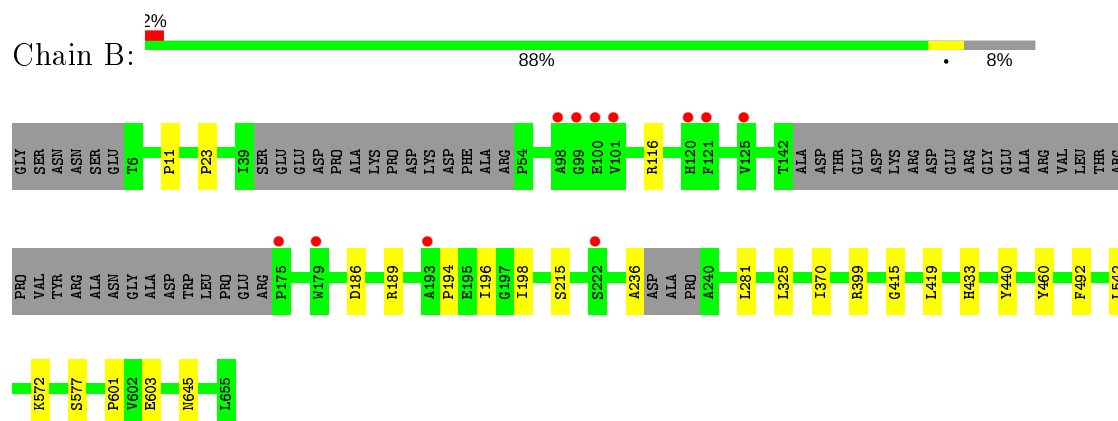
3 Residue-property plots [i](#)

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.

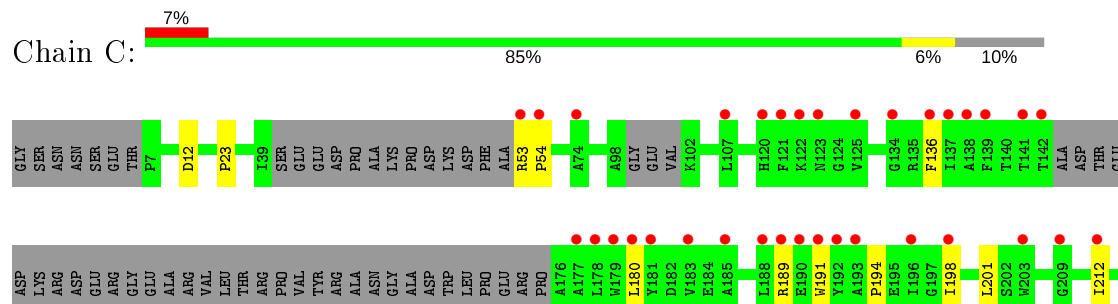
- Molecule 1: Acyl-peptide hydrolase, putative

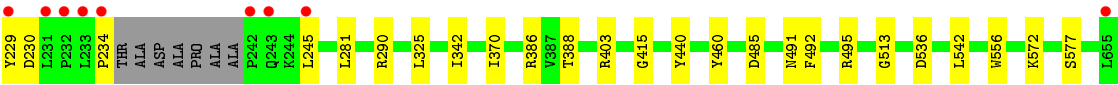


- Molecule 1: Acyl-peptide hydrolase, putative

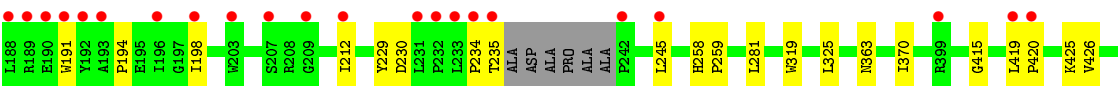
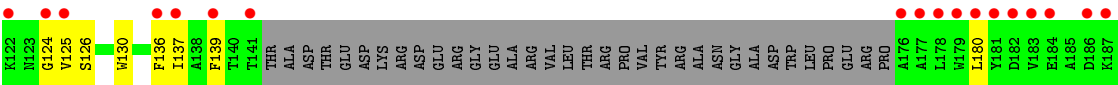
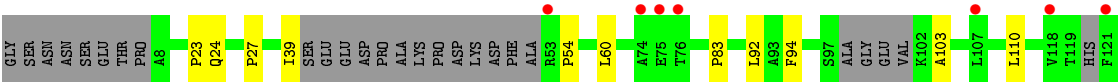
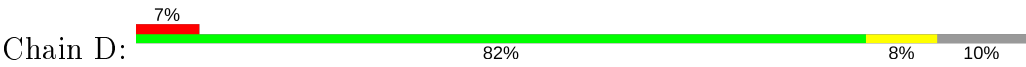


- Molecule 1: Acyl-peptide hydrolase, putative





● Molecule 1: Acyl-peptide hydrolase, putative



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.70Å 195.09Å 107.72Å 90.00° 99.97° 90.00°	Depositor
Resolution (Å)	46.87 – 2.30 48.77 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (46.87-2.30) 99.8 (48.77-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???), REFMAC	Depositor
R, R_{free}	0.189 , 0.219 0.189 , 0.219	Depositor DCC
R_{free} test set	6538 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	34.8	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	19434	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.89% 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: 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	0.25	0/4772	0.47	0/6507
1	B	0.26	0/4765	0.47	0/6504
1	C	0.25	0/4696	0.46	0/6406
1	D	0.25	0/4682	0.46	0/6387
All	All	0.25	0/18915	0.46	0/25804

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	4633	0	4372	18	0
1	B	4627	0	4351	15	0
1	C	4560	0	4289	23	0
1	D	4546	0	4273	33	0
2	A	4	0	3	0	0
2	B	4	0	3	0	0
2	C	4	0	3	0	0
2	D	4	0	3	0	0
3	A	305	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	327	0	0	1	0
3	C	221	0	0	2	0
3	D	199	0	0	1	0
All	All	19434	0	17297	88	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 (88) 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:403:ARG:NH2	3:C:801:HOH:O	2.23	0.71
1:A:226:GLN:NE2	3:A:801:HOH:O	2.21	0.71
1:C:290:ARG:NH2	1:C:342:ILE:O	2.28	0.67
1:C:491:ASN:OD1	1:C:495:ARG:NH1	2.30	0.65
1:B:194:PRO:HG3	1:B:198:ILE:HG13	1.82	0.61
1:C:194:PRO:HG3	1:C:198:ILE:HG13	1.84	0.60
1:D:194:PRO:HG3	1:D:198:ILE:HG13	1.84	0.58
1:C:53:ARG:HD2	1:C:54:PRO:HD2	1.85	0.58
1:B:572:LYS:NZ	3:B:806:HOH:O	2.36	0.57
1:D:27:PRO:O	1:D:363:ASN:ND2	2.38	0.57
1:C:189:ARG:HH21	1:C:234:PRO:HB2	1.70	0.55
1:D:451:MET:HE1	1:D:458:VAL:HG13	1.89	0.55
1:D:103:ALA:HB3	1:D:125:VAL:H	1.71	0.55
1:B:189:ARG:HH22	1:B:236:ALA:HB3	1.71	0.54
1:C:191:TRP:CD1	1:C:234:PRO:HG3	2.43	0.54
1:A:194:PRO:HG3	1:A:198:ILE:HG13	1.89	0.54
1:A:290:ARG:NH2	1:A:342:ILE:O	2.42	0.53
1:A:55:ARG:NH2	3:A:809:HOH:O	2.42	0.53
1:A:586:LYS:NZ	3:A:803:HOH:O	2.35	0.52
1:C:281:LEU:HD13	1:C:325:LEU:HD23	1.91	0.52
1:A:553:LEU:HD22	1:D:614:LYS:HD3	1.90	0.52
1:D:136:PHE:HB3	1:D:180:LEU:HD11	1.91	0.52
1:B:542:LEU:HD13	1:B:577:SER:HA	1.92	0.52
1:D:542:LEU:HG	1:D:556:TRP:CZ2	2.45	0.52
1:B:433:HIS:HB3	1:B:440:TYR:CZ	2.45	0.51
1:C:572:LYS:NZ	3:C:805:HOH:O	2.42	0.51
1:D:425:LYS:NZ	3:D:802:HOH:O	2.37	0.51
1:D:420:PRO:HG2	1:D:426:VAL:HG11	1.91	0.51
1:A:281:LEU:HD13	1:A:325:LEU:HD23	1.92	0.50
1:C:386:ARG:NH1	1:C:388:THR:O	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:433:HIS:HB3	1:A:440:TYR:CZ	2.46	0.49
1:D:92:LEU:HG	1:D:110:LEU:HD11	1.95	0.49
1:B:281:LEU:HD13	1:B:325:LEU:HD23	1.93	0.49
1:C:230:ASP:HB2	1:C:245:LEU:HD12	1.94	0.49
1:D:440:TYR:CD2	1:D:460:TYR:HB2	2.48	0.48
1:D:39:ILE:HD12	1:D:54:PRO:HB2	1.94	0.48
1:C:542:LEU:HG	1:C:556:TRP:CZ2	2.48	0.48
1:A:542:LEU:HD13	1:A:577:SER:HA	1.96	0.47
1:C:201:LEU:HD23	1:C:212:ILE:HG22	1.96	0.47
1:C:415:GLY:HA3	1:C:492:PHE:CE1	2.50	0.47
1:D:103:ALA:O	1:D:124:GLY:HA2	2.15	0.47
1:B:440:TYR:CD2	1:B:460:TYR:HB2	2.49	0.47
1:D:230:ASP:HB2	1:D:245:LEU:HG	1.97	0.46
1:D:281:LEU:HD13	1:D:325:LEU:HD23	1.98	0.46
1:C:491:ASN:O	1:C:495:ARG:HG2	2.16	0.46
1:C:23:PRO:HG3	1:C:370:ILE:HG13	1.96	0.46
1:C:440:TYR:CD2	1:C:460:TYR:HB2	2.50	0.46
1:B:601:PRO:HB2	1:B:603:GLU:HG3	1.97	0.46
1:D:103:ALA:HB3	1:D:124:GLY:HA3	1.98	0.45
1:B:116:ARG:NH2	1:B:186:ASP:OD2	2.50	0.45
1:D:258:HIS:CG	1:D:259:PRO:HD2	2.51	0.45
1:A:542:LEU:HG	1:A:556:TRP:CZ2	2.52	0.45
1:B:116:ARG:HH22	1:B:186:ASP:CG	2.20	0.45
1:D:23:PRO:HG3	1:D:370:ILE:HG13	1.98	0.45
1:C:513:GLY:HA2	1:C:536:ASP:O	2.17	0.45
1:D:433:HIS:HB3	1:D:440:TYR:CZ	2.52	0.45
1:C:212:ILE:HG13	1:C:229:TYR:HB2	1.98	0.45
1:A:440:TYR:CD2	1:A:460:TYR:HB2	2.53	0.44
1:B:415:GLY:HA3	1:B:492:PHE:CE1	2.53	0.44
1:D:485:ASP:N	1:D:485:ASP:OD1	2.51	0.44
1:B:23:PRO:HG3	1:B:370:ILE:HG13	2.00	0.44
1:D:125:VAL:HG23	1:D:139:PHE:CD1	2.53	0.44
1:C:542:LEU:HD13	1:C:577:SER:HA	2.00	0.43
1:D:191:TRP:NE1	1:D:234:PRO:HD3	2.33	0.43
1:A:24:GLN:HG3	1:A:83:PRO:O	2.19	0.43
1:D:513:GLY:HA2	1:D:536:ASP:O	2.18	0.43
1:D:419:LEU:HD21	1:D:500:VAL:HG11	2.01	0.43
1:A:273:LYS:HG2	1:A:273:LYS:H	1.65	0.43
1:C:485:ASP:N	1:C:485:ASP:OD1	2.52	0.43
1:D:319:TRP:CE2	1:D:325:LEU:HD13	2.54	0.42
1:C:136:PHE:HB3	1:C:180:LEU:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:ARG:HD3	1:A:633:ARG:O	2.19	0.42
1:A:323:ASP:O	1:A:341:HIS:HA	2.20	0.42
1:D:130:TRP:CH2	1:D:137:ILE:HD11	2.55	0.41
1:D:415:GLY:HA3	1:D:492:PHE:CE1	2.55	0.41
1:B:11:PRO:HG2	1:B:645:ASN:OD1	2.21	0.41
1:C:12:ASP:OD1	1:C:53:ARG:NH2	2.53	0.41
1:D:60:LEU:HD11	1:D:94:PHE:CG	2.56	0.41
1:D:24:GLN:HG3	1:D:83:PRO:O	2.21	0.41
1:A:436:PRO:HB3	1:A:515:TYR:CD2	2.56	0.41
1:D:491:ASN:O	1:D:495:ARG:HG2	2.21	0.41
1:A:419:LEU:HD21	1:A:500:VAL:HG11	2.03	0.41
1:B:196:ILE:HG21	1:B:215:SER:O	2.21	0.40
1:B:399:ARG:HD3	1:B:419:LEU:O	2.21	0.40
1:D:92:LEU:HD23	1:D:92:LEU:HA	1.94	0.40
1:A:415:GLY:HA3	1:A:492:PHE:CE1	2.57	0.40
1:D:125:VAL:HG22	1:D:126:SER:N	2.36	0.40
1:D:212:ILE:HG13	1:D:229:TYR:HB2	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	590/656 (90%)	578 (98%)	12 (2%)	0	100	100
1	B	594/656 (90%)	582 (98%)	12 (2%)	0	100	100
1	C	583/656 (89%)	572 (98%)	11 (2%)	0	100	100
1	D	578/656 (88%)	566 (98%)	12 (2%)	0	100	100
All	All	2345/2624 (89%)	2298 (98%)	47 (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	466/526 (89%)	465 (100%)	1 (0%)	93	97
1	B	463/526 (88%)	463 (100%)	0	100	100
1	C	454/526 (86%)	454 (100%)	0	100	100
1	D	454/526 (86%)	452 (100%)	2 (0%)	91	96
All	All	1837/2104 (87%)	1834 (100%)	3 (0%)	93	97

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	273	LYS
1	D	235	THR
1	D	614	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	442	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ACT	D	701	-	1,3,3	6.74	1 (100%)	0,3,3	0.00	-
2	ACT	C	701	-	1,3,3	6.21	1 (100%)	0,3,3	0.00	-
2	ACT	B	701	-	1,3,3	6.29	1 (100%)	0,3,3	0.00	-
2	ACT	A	701	-	1,3,3	6.61	1 (100%)	0,3,3	0.00	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	701	ACT	CH3-C	6.74	1.57	1.48
2	A	701	ACT	CH3-C	6.61	1.57	1.48
2	B	701	ACT	CH3-C	6.29	1.56	1.48
2	C	701	ACT	CH3-C	6.21	1.56	1.48

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	598/656 (91%)	-0.07	7 (1%) 79 83	23, 34, 59, 88	0
1	B	601/656 (91%)	0.00	11 (1%) 68 74	23, 33, 61, 88	0
1	C	593/656 (90%)	0.26	43 (7%) 15 20	23, 41, 75, 96	0
1	D	590/656 (89%)	0.31	47 (7%) 12 16	23, 44, 77, 95	0
All	All	2382/2624 (90%)	0.13	108 (4%) 33 40	23, 37, 71, 96	0

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	121	PHE	6.4
1	D	179	TRP	6.1
1	C	121	PHE	5.6
1	D	136	PHE	5.5
1	D	181	TYR	5.4
1	C	191	TRP	5.3
1	D	188	LEU	5.2
1	D	232	PRO	5.0
1	D	180	LEU	5.0
1	D	137	ILE	5.0
1	D	233	LEU	4.8
1	C	180	LEU	4.8
1	C	192	TYR	4.7
1	D	196	ILE	4.7
1	C	181	TYR	4.6
1	D	177	ALA	4.5
1	C	188	LEU	4.5
1	D	191	TRP	4.4
1	D	234	PRO	4.3
1	C	137	ILE	4.2
1	D	183	VAL	4.1

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Mol	Chain	Res	Type	RSRZ
1	C	231	LEU	4.1
1	C	198	ILE	4.0
1	D	231	LEU	4.0
1	C	136	PHE	4.0
1	C	234	PRO	3.8
1	A	101	VAL	3.8
1	C	107	LEU	3.7
1	C	189	ARG	3.7
1	D	193	ALA	3.5
1	D	182	ASP	3.5
1	D	139	PHE	3.5
1	D	209	GLY	3.4
1	D	107	LEU	3.4
1	D	192	TYR	3.4
1	C	203	TRP	3.3
1	B	121	PHE	3.3
1	C	229	TYR	3.3
1	D	122	LYS	3.3
1	D	125	VAL	3.3
1	C	193	ALA	3.3
1	C	139	PHE	3.3
1	C	141	THR	3.3
1	C	125	VAL	3.3
1	D	141	THR	3.3
1	A	40	SER	3.2
1	C	232	PRO	3.2
1	A	99	GLY	3.2
1	C	196	ILE	3.2
1	D	178	LEU	3.2
1	D	235	THR	3.1
1	D	74	ALA	3.0
1	B	179	TRP	2.9
1	C	183	VAL	2.9
1	C	54	PRO	2.8
1	C	138	ALA	2.8
1	D	76	THR	2.8
1	D	190	GLU	2.8
1	B	101	VAL	2.8
1	D	118	VAL	2.8
1	C	134	GLY	2.7
1	C	122	LYS	2.7
1	C	53	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	209	GLY	2.6
1	D	124	GLY	2.6
1	C	179	TRP	2.6
1	C	233	LEU	2.6
1	A	100	GLU	2.6
1	D	53	ARG	2.5
1	C	74	ALA	2.5
1	D	212	ILE	2.5
1	C	120	HIS	2.5
1	D	189	ARG	2.5
1	C	212	ILE	2.5
1	C	177	ALA	2.4
1	B	99	GLY	2.4
1	D	203	TRP	2.4
1	C	142	THR	2.3
1	B	125	VAL	2.3
1	B	120	HIS	2.3
1	D	186	ASP	2.3
1	D	245	LEU	2.3
1	B	175	PRO	2.3
1	D	207	SER	2.3
1	C	123	ASN	2.2
1	C	242	PRO	2.2
1	B	100	GLU	2.2
1	C	243	GLN	2.2
1	A	121	PHE	2.2
1	C	178	LEU	2.2
1	C	245	LEU	2.2
1	D	420	PRO	2.2
1	B	98	ALA	2.1
1	D	187	LYS	2.1
1	D	75	GLU	2.1
1	D	399	ARG	2.1
1	C	185	ALA	2.1
1	D	184	GLU	2.1
1	B	193	ALA	2.1
1	D	242	PRO	2.1
1	B	222	SER	2.0
1	C	190	GLU	2.0
1	A	174	ARG	2.0
1	D	198	ILE	2.0
1	D	176	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	356	VAL	2.0
1	C	655	LEU	2.0
1	D	419	LEU	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 [i](#)

There are no monosaccharides 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	ACT	A	701	4/4	0.94	0.19	33,39,42,46	0
2	ACT	B	701	4/4	0.95	0.12	33,35,36,39	0
2	ACT	D	701	4/4	0.95	0.14	27,31,33,38	0
2	ACT	C	701	4/4	0.98	0.16	29,29,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.