



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:29 AM GMT

PDB ID : 3IMF
Title : 1.99 Angstrom resolution crystal structure of a short chain dehydrogenase from Bacillus anthracis str. 'Ames Ancestor'
Authors : Halavaty, A.S.; Minasov, G.; Skarina, T.; Onopriyenko, O.; Gordon, E.; Peterson, S.; Savchenko, A.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2009-08-10
Resolution : 1.99 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

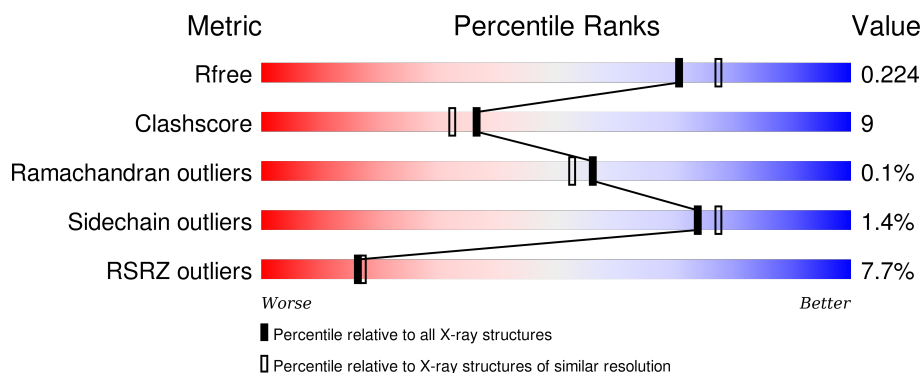
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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}	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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. 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	257	<div> <div>7%</div> <div>80% 16% . .</div> </div>
1	B	257	<div> <div>7%</div> <div>83% 14% .</div> </div>
1	C	257	<div> <div>7%</div> <div>82% 11% 6%</div> </div>
1	D	257	<div> <div>7%</div> <div>81% 14% . .</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8338 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 Short chain dehydrogenase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	248	Total	C	N	O	S	Se	0	9	0
			1957	1229	342	370	4	12			
1	B	249	Total	C	N	O	S	Se	0	8	0
			1950	1225	339	370	4	12			
1	C	241	Total	C	N	O	S	Se	0	8	0
			1898	1198	331	354	4	11			
1	D	248	Total	C	N	O	S	Se	0	6	0
			1927	1212	337	362	4	12			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	EXPRESSION TAG	UNP Q81MP2
A	-1	ASN	-	EXPRESSION TAG	UNP Q81MP2
A	0	ALA	-	EXPRESSION TAG	UNP Q81MP2
B	-2	SER	-	EXPRESSION TAG	UNP Q81MP2
B	-1	ASN	-	EXPRESSION TAG	UNP Q81MP2
B	0	ALA	-	EXPRESSION TAG	UNP Q81MP2
C	-2	SER	-	EXPRESSION TAG	UNP Q81MP2
C	-1	ASN	-	EXPRESSION TAG	UNP Q81MP2
C	0	ALA	-	EXPRESSION TAG	UNP Q81MP2
D	-2	SER	-	EXPRESSION TAG	UNP Q81MP2
D	-1	ASN	-	EXPRESSION TAG	UNP Q81MP2
D	0	ALA	-	EXPRESSION TAG	UNP Q81MP2

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



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

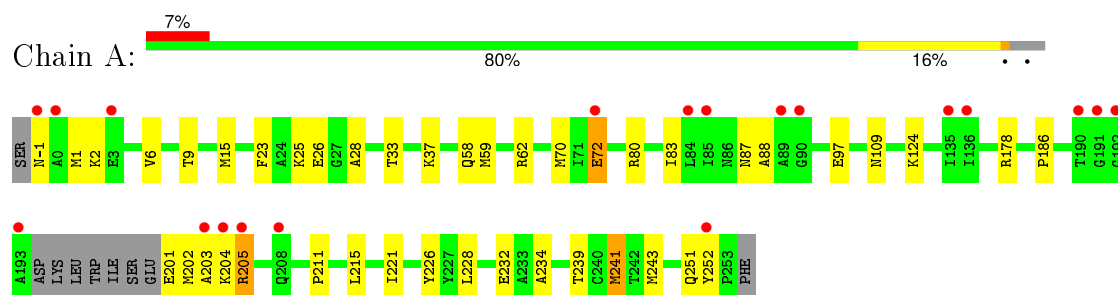
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	146	Total	O	0	5
			148	148		
3	B	152	Total	O	0	6
			153	153		
3	C	155	Total	O	0	8
			157	157		
3	D	139	Total	O	0	4
			140	140		

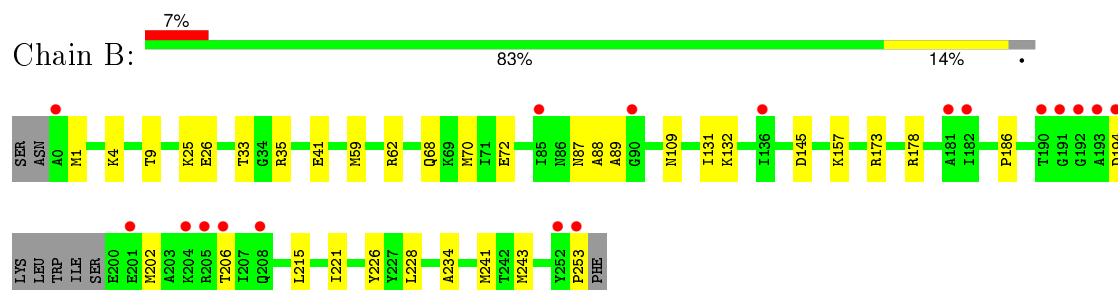
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

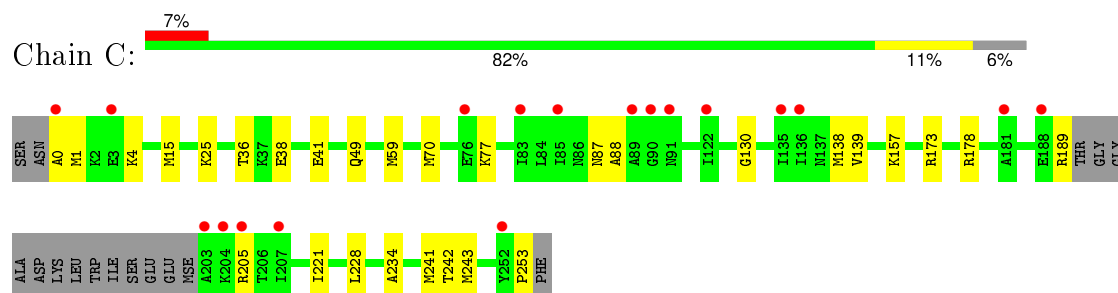
- Molecule 1: Short chain dehydrogenase



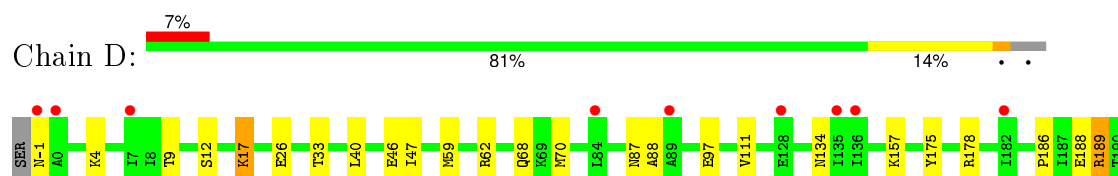
- Molecule 1: Short chain dehydrogenase



- Molecule 1: Short chain dehydrogenase



- Molecule 1: Short chain dehydrogenase





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	174.24Å 89.56Å 71.78Å 90.00° 111.60° 90.00°	Depositor
Resolution (Å)	30.00 – 1.99 29.36 – 1.99	Depositor EDS
% Data completeness (in resolution range)	98.8 (30.00-1.99) 98.9 (29.36-1.99)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.21 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.166 , 0.206 0.189 , 0.224	Depositor DCC
R_{free} test set	3494 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	26.4	Xtriage
Anisotropy	0.313	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 53.6	EDS
Estimated twinning fraction	0.088 for -h-2*l,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	3 of 69189 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8338	wwPDB-VP
Average B, all atoms (Å ²)	22.0	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 67.44 % 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 5.1468e-06. 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.52	0/1977	0.66	0/2647
1	B	0.58	0/1970	0.70	1/2639 (0.0%)
1	C	0.55	0/1919	0.70	0/2572
1	D	0.53	0/1947	0.68	0/2608
All	All	0.55	0/7813	0.68	1/10466 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	145	ASP	CB-CG-OD2	-5.10	113.71	118.30

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	1957	0	1963	51	0
1	B	1950	0	1955	48	0
1	C	1898	0	1921	35	0
1	D	1927	0	1941	48	0
2	B	4	0	3	0	0
2	D	4	0	3	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	148	0	0	4	0
3	B	153	0	0	13	0
3	C	157	0	0	9	0
3	D	140	0	0	4	0
All	All	8338	0	7786	148	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 9.

All (148) 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:241[B]:MSE:HE3	1:B:241[B]:MSE:CE	1.76	1.15
1:A:241[B]:MSE:CE	1:B:241[B]:MSE:HE2	1.82	1.08
1:A:241[A]:MSE:CE	1:B:241[A]:MSE:HE3	1.91	1.00
1:C:241[A]:MSE:HE1	1:D:241[A]:MSE:HB3	1.44	0.96
1:A:241[A]:MSE:SE	1:B:241[A]:MSE:HE1	2.20	0.92
1:A:241[B]:MSE:CE	1:B:241[B]:MSE:CE	2.46	0.90
1:D:207:ILE:HD12	1:D:207:ILE:C	1.94	0.88
1:A:241[A]:MSE:HE2	1:B:241[A]:MSE:HE3	1.56	0.87
1:A:241[B]:MSE:SE	1:B:241[B]:MSE:HE2	2.26	0.86
1:A:241[B]:MSE:HE3	1:B:241[B]:MSE:HE2	1.44	0.86
1:D:202:MSE:HE3	1:D:204:LYS:H	1.42	0.84
1:C:77[B]:LYS:HG3	3:C:548:HOH:O	1.77	0.84
1:B:157:LYS:HE2	3:B:535:HOH:O	1.78	0.83
1:A:241[A]:MSE:HE2	1:B:241[A]:MSE:CE	2.08	0.83
1:D:207:ILE:HD12	1:D:208:GLN:N	1.95	0.82
1:A:72:GLU:HG2	3:A:443:HOH:O	1.79	0.81
1:A:241[A]:MSE:SE	1:B:241[A]:MSE:CE	2.79	0.81
1:A:241[A]:MSE:CE	1:B:241[A]:MSE:CE	2.60	0.79
1:A:228:LEU:HD21	1:A:241[A]:MSE:SE	2.34	0.78
1:B:186:PRO:HB2	1:B:215:LEU:HD22	1.65	0.78
1:C:241[B]:MSE:SE	1:D:241[B]:MSE:CE	2.82	0.77
1:A:241[B]:MSE:HE1	1:B:241[B]:MSE:HB3	1.68	0.76
1:D:253:PRO:C	3:D:540:HOH:O	2.23	0.76
1:B:35:ARG:HH11	1:B:35:ARG:HG3	1.49	0.75
1:D:228:LEU:HD21	1:D:241[A]:MSE:SE	2.37	0.75
1:A:241[A]:MSE:HB3	1:B:241[A]:MSE:HE1	1.68	0.74
1:C:241[B]:MSE:SE	1:D:241[B]:MSE:HE3	2.37	0.73
1:A:25:LYS:HD2	3:A:471:HOH:O	1.87	0.73
1:D:68[A]:GLN:HG2	3:D:507[A]:HOH:O	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:15:MSE:HE3	1:C:138:MSE:HE2	1.72	0.72
1:C:241[A]:MSE:HE3	1:D:241[A]:MSE:HE2	1.74	0.70
1:B:62:ARG:HD2	1:B:109[B]:ASN:HD22	1.57	0.69
1:B:228:LEU:HD21	1:B:241[B]:MSE:SE	2.42	0.69
1:C:241[A]:MSE:CE	1:D:241[A]:MSE:HE2	2.22	0.69
1:A:241[B]:MSE:HE3	1:B:241[B]:MSE:HE1	1.72	0.69
1:C:241[B]:MSE:SE	1:D:241[B]:MSE:HE1	2.43	0.68
1:A:80[B]:ARG:NH1	3:A:544:HOH:O	2.26	0.67
1:A:59[A]:MSE:SE	1:A:70:MSE:SE	3.12	0.67
1:C:241[A]:MSE:HE3	1:D:241[A]:MSE:CE	2.26	0.66
1:D:202:MSE:CE	1:D:204:LYS:HG3	2.26	0.65
1:A:37:LYS:HG2	1:A:58:GLN:OE1	1.96	0.65
1:A:203:ALA:O	1:A:205:ARG:N	2.30	0.65
1:A:203:ALA:C	1:A:205:ARG:H	2.01	0.65
1:D:188:GLU:OE1	1:D:189:ARG:NH1	2.31	0.64
1:D:59[B]:MSE:SE	1:D:70:MSE:SE	3.15	0.64
1:A:201:GLU:O	1:A:202:MSE:HB2	1.98	0.63
1:D:252:TYR:HB2	1:D:253:PRO:HD2	1.81	0.62
1:C:59[B]:MSE:SE	1:C:70:MSE:SE	3.18	0.62
1:C:241[A]:MSE:SE	1:D:241[A]:MSE:HE2	2.49	0.62
1:A:178:ARG:HD3	1:A:234:ALA:O	2.00	0.61
1:C:228:LEU:HD21	1:C:241[B]:MSE:SE	2.51	0.61
1:B:202:MSE:O	1:B:206:THR:HG23	2.01	0.61
1:C:228:LEU:HD11	1:C:241[B]:MSE:HG3	1.84	0.60
1:D:202:MSE:HE3	1:D:204:LYS:N	2.13	0.59
1:B:9:THR:O	1:B:87:ASN:HB3	2.03	0.59
1:A:241[B]:MSE:CE	1:B:241[B]:MSE:SE	3.01	0.58
1:B:253:PRO:C	3:B:470:HOH:O	2.41	0.58
1:D:178:ARG:HD3	1:D:234:ALA:O	2.04	0.57
1:B:132[A]:LYS:HE2	3:B:478:HOH:O	2.05	0.57
1:A:37:LYS:HE2	1:A:58:GLN:OE1	2.05	0.57
1:D:-1:ASN:O	1:D:4:LYS:HE3	2.05	0.57
1:B:89:ALA:HB3	3:B:273:HOH:O	2.06	0.56
1:B:1:MSE:HE3	3:B:465:HOH:O	2.05	0.56
1:B:35:ARG:HD2	1:B:59[A]:MSE:O	2.06	0.56
1:C:241[B]:MSE:CE	1:D:241[B]:MSE:HE3	2.37	0.55
1:A:239:THR:HG22	3:B:292:HOH:O	2.06	0.55
1:A:232[B]:GLU:HG2	3:B:413[B]:HOH:O	2.06	0.55
1:B:25:LYS:HE2	3:B:428:HOH:O	2.06	0.55
1:C:38:GLU:H	1:C:38:GLU:CD	2.10	0.55
1:A:186:PRO:HB2	1:A:215:LEU:HD22	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203:ALA:C	1:A:205:ARG:N	2.59	0.54
1:A:1:MSE:HB3	1:A:28:ALA:HB2	1.88	0.54
1:D:17:LYS:HD3	1:D:47:ILE:HD11	1.90	0.54
1:A:241[B]:MSE:HE3	1:B:241[B]:MSE:SE	2.57	0.54
1:D:9:THR:HA	1:D:33:THR:OG1	2.08	0.54
1:C:178:ARG:HD3	1:C:234:ALA:O	2.09	0.53
1:A:241[B]:MSE:HE1	1:B:241[B]:MSE:SE	2.59	0.53
1:A:124:LYS:HE2	1:D:97:GLU:O	2.08	0.52
1:B:26:GLU:HG3	1:B:226:TYR:CE1	2.45	0.52
1:B:59[A]:MSE:SE	1:B:70:MSE:SE	3.28	0.52
1:B:178:ARG:HD3	1:B:234:ALA:O	2.09	0.52
1:A:37:LYS:CG	1:A:58:GLN:OE1	2.58	0.52
1:D:111:VAL:HG11	1:D:157:LYS:HD2	1.90	0.52
1:B:25:LYS:NZ	3:B:380[A]:HOH:O	2.42	0.51
1:C:139:VAL:HA	1:C:157[A]:LYS:HD2	1.92	0.51
1:C:253:PRO:C	3:C:469:HOH:O	2.49	0.50
1:D:87:ASN:O	1:D:88:ALA:C	2.49	0.50
1:D:134[B]:ASN:ND2	1:D:178:ARG:NH2	2.59	0.50
1:C:139:VAL:HA	1:C:157[B]:LYS:HD2	1.94	0.50
1:C:130:GLY:HA2	3:C:296:HOH:O	2.12	0.49
1:A:87:ASN:O	1:A:88:ALA:C	2.50	0.49
1:A:186:PRO:HB2	1:A:215:LEU:CD2	2.41	0.49
1:C:221:ILE:HD13	1:C:243:MSE:SE	2.62	0.49
1:D:207:ILE:CD1	1:D:207:ILE:C	2.67	0.49
1:D:62:ARG:NH1	3:D:334:HOH:O	2.46	0.48
1:A:241[A]:MSE:HE1	1:B:241[A]:MSE:HE3	1.91	0.48
1:D:134[B]:ASN:HD21	1:D:178:ARG:NH2	2.10	0.48
1:D:9:THR:O	1:D:87:ASN:HB3	2.13	0.48
1:C:189:ARG:O	3:C:343:HOH:O	2.20	0.48
1:B:87:ASN:O	1:B:88:ALA:C	2.52	0.48
1:C:15:MSE:HE1	3:C:499:HOH:O	2.14	0.47
1:B:35:ARG:NH1	1:B:35:ARG:HG3	2.22	0.47
1:A:26:GLU:HG3	1:A:226:TYR:CE1	2.50	0.47
1:D:202:MSE:SE	1:D:203:ALA:H	2.48	0.47
1:D:12:SER:HB3	1:D:40:LEU:HD23	1.97	0.47
1:D:46:GLU:HG2	1:D:47:ILE:HD12	1.97	0.46
1:C:157[A]:LYS:NZ	3:C:330:HOH:O	2.48	0.46
1:B:68[B]:GLN:NE2	1:B:72:GLU:OE2	2.47	0.46
1:A:62:ARG:HD2	1:A:109:ASN:HB3	1.97	0.45
1:C:241[B]:MSE:CE	1:D:241[B]:MSE:CE	2.94	0.45
1:D:207:ILE:CD1	1:D:208:GLN:N	2.75	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1:MSE:HE3	3:C:468:HOH:O	2.17	0.45
1:B:41:GLU:HG2	3:B:272:HOH:O	2.16	0.44
1:D:207:ILE:HD12	1:D:208:GLN:CA	2.47	0.44
1:C:59[B]:MSE:HE3	1:C:59[B]:MSE:HB2	1.96	0.44
1:A:97[A]:GLU:OE2	1:D:175:TYR:OH	2.33	0.44
1:D:202:MSE:HE2	1:D:204:LYS:HG3	1.98	0.43
1:A:241[A]:MSE:SE	1:B:241[A]:MSE:HE3	2.59	0.43
1:A:15:MSE:HE2	3:A:565:HOH:O	2.19	0.43
1:D:26:GLU:HG3	1:D:226:TYR:CE1	2.54	0.43
1:D:186:PRO:HB2	1:D:215:LEU:HD22	2.00	0.43
1:C:25:LYS:HG2	1:C:49:GLN:NE2	2.33	0.43
1:A:211:PRO:O	1:B:173:ARG:HA	2.19	0.43
1:D:224:LEU:HB2	1:D:243:MSE:HE1	2.01	0.43
1:B:1:MSE:CE	3:B:465:HOH:O	2.67	0.42
1:B:131:ILE:HD13	3:B:451:HOH:O	2.20	0.42
1:A:9:THR:HA	1:A:33:THR:OG1	2.19	0.42
1:A:201:GLU:N	1:A:205:ARG:NH1	2.68	0.42
1:A:251:GLN:O	1:A:252:TYR:CD1	2.72	0.42
1:C:1:MSE:CE	3:C:468:HOH:O	2.67	0.41
1:C:241[B]:MSE:HB3	1:D:241[B]:MSE:HE1	2.01	0.41
1:A:221:ILE:HD13	1:A:243:MSE:SE	2.70	0.41
1:B:62:ARG:CD	1:B:109[B]:ASN:HD22	2.28	0.41
1:C:0:ALA:HB3	1:C:4:LYS:NZ	2.34	0.41
1:B:9:THR:HA	1:B:33:THR:OG1	2.21	0.41
1:D:241[A]:MSE:HA	3:D:302:HOH:O	2.20	0.41
1:C:41:GLU:HG2	3:C:557:HOH:O	2.21	0.41
1:D:224:LEU:HB2	1:D:243:MSE:CE	2.51	0.41
1:C:173:ARG:HA	1:D:211:PRO:O	2.21	0.41
1:B:4:LYS:HE3	3:B:343:HOH:O	2.21	0.41
1:B:221:ILE:HD13	1:B:243:MSE:SE	2.71	0.41
1:C:15:MSE:CE	1:C:138:MSE:HE2	2.48	0.40
1:A:1:MSE:HE2	1:A:23:PHE:HD1	1.86	0.40
1:D:224:LEU:HD22	1:D:243:MSE:HE3	2.03	0.40
1:A:-1:ASN:N	1:A:2:LYS:HB3	2.37	0.40
1:B:62:ARG:HD2	1:B:109[B]:ASN:ND2	2.31	0.40
1:C:87:ASN:O	1:C:88:ALA:C	2.59	0.40
1:A:6:VAL:HG22	1:A:83:ILE:HD12	2.02	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	253/257 (98%)	246 (97%)	6 (2%)	1 (0%)	39	33
1	B	253/257 (98%)	245 (97%)	8 (3%)	0	100	100
1	C	245/257 (95%)	238 (97%)	7 (3%)	0	100	100
1	D	250/257 (97%)	244 (98%)	6 (2%)	0	100	100
All	All	1001/1028 (97%)	973 (97%)	27 (3%)	1 (0%)	56	53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	204	LYS

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	202/192 (105%)	198 (98%)	4 (2%)	63	65
1	B	202/192 (105%)	201 (100%)	1 (0%)	92	94
1	C	197/192 (103%)	194 (98%)	3 (2%)	72	75
1	D	199/192 (104%)	195 (98%)	4 (2%)	63	65
All	All	800/768 (104%)	788 (98%)	12 (2%)	74	75

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	GLU
1	A	205	ARG
1	A	241[A]	MSE
1	A	241[B]	MSE
1	B	194	ASP
1	C	36	THR
1	C	205	ARG
1	C	242	THR
1	D	17	LYS
1	D	189	ARG
1	D	202	MSE
1	D	207	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 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	B	255	-	1,3,3	1.17	0	0,3,3	0.00	-
2	ACT	D	255	-	1,3,3	1.45	0	0,3,3	0.00	-

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
2	ACT	B	255	-	-	0/0/0/0	0/0/0/0
2	ACT	D	255	-	-	0/0/0/0	0/0/0/0

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	238/257 (92%)	0.45	19 (7%)	15 16	11, 21, 32, 41	0
1	B	239/257 (92%)	0.41	18 (7%)	17 18	2, 20, 30, 45	0
1	C	232/257 (90%)	0.30	18 (7%)	16 17	5, 20, 32, 51	0
1	D	238/257 (92%)	0.41	18 (7%)	17 18	6, 20, 32, 45	0
All	All	947/1028 (92%)	0.39	73 (7%)	16 17	2, 20, 32, 51	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	203	ALA	9.0
1	D	252	TYR	6.7
1	A	191	GLY	6.2
1	D	191	GLY	5.8
1	A	252	TYR	5.5
1	A	193	ALA	5.3
1	B	0	ALA	5.3
1	B	193	ALA	5.2
1	B	201	GLU	5.2
1	B	252	TYR	4.9
1	A	0	ALA	4.9
1	C	252	TYR	4.8
1	C	204	LYS	4.5
1	D	0	ALA	4.2
1	B	192	GLY	4.1
1	C	0	ALA	3.9
1	D	204	LYS	3.9
1	B	205	ARG	3.8
1	D	-1	ASN	3.8
1	B	191	GLY	3.8
1	D	201	GLU	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	3	GLU	3.7
1	A	90	GLY	3.5
1	C	205	ARG	3.5
1	A	208	GLN	3.4
1	A	-1	ASN	3.3
1	A	190	THR	3.3
1	D	192	GLY	3.3
1	B	253	PRO	3.2
1	D	135	ILE	3.2
1	A	205	ARG	3.2
1	A	84	LEU	3.0
1	D	84	LEU	3.0
1	D	203	ALA	2.9
1	A	192	GLY	2.9
1	D	205	ARG	2.9
1	A	89	ALA	2.9
1	A	135	ILE	2.8
1	B	204	LYS	2.8
1	A	72	GLU	2.7
1	B	206	THR	2.7
1	C	3	GLU	2.7
1	D	206	THR	2.6
1	B	181	ALA	2.6
1	A	85	ILE	2.6
1	B	136	ILE	2.6
1	B	90	GLY	2.6
1	C	203	ALA	2.5
1	B	182	ILE	2.5
1	C	135	ILE	2.5
1	D	128	GLU	2.4
1	A	204	LYS	2.4
1	D	182	ILE	2.4
1	C	89	ALA	2.4
1	C	91	ASN	2.3
1	C	136	ILE	2.3
1	C	188	GLU	2.3
1	C	90	GLY	2.3
1	C	122	ILE	2.3
1	A	136	ILE	2.2
1	D	89	ALA	2.2
1	C	85	ILE	2.2
1	C	181	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	85	ILE	2.1
1	D	136	ILE	2.1
1	C	76	GLU	2.1
1	B	190	THR	2.1
1	C	83	ILE	2.1
1	D	7	ILE	2.1
1	B	194	ASP	2.1
1	B	208	GLN	2.1
1	D	224	LEU	2.0
1	C	207	ILE	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	ACT	B	255	4/4	0.88	0.51	-	53,53,53,53	4
2	ACT	D	255	4/4	0.48	0.42	-	76,77,77,77	0

6.5 Other polymers [i](#)

There are no such residues in this entry.