Full wwPDB X-ray Structure Validation Report ⓘ

Apr 21, 2024 – 11:55 am BST

PDB ID	:	6I3Q
Title	:	The structure of thiocyanate dehydrogenase from Thioalkalivibrio paradoxus complex with acetate ions.
Authors	:	Polyakov, K.M.; Popov, A.N.; Tikhkonova, T.V.; Popov, V.O.; Trofimov, A.A.
Deposited on	:	2018-11-07
Resolution	:	1.45 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:

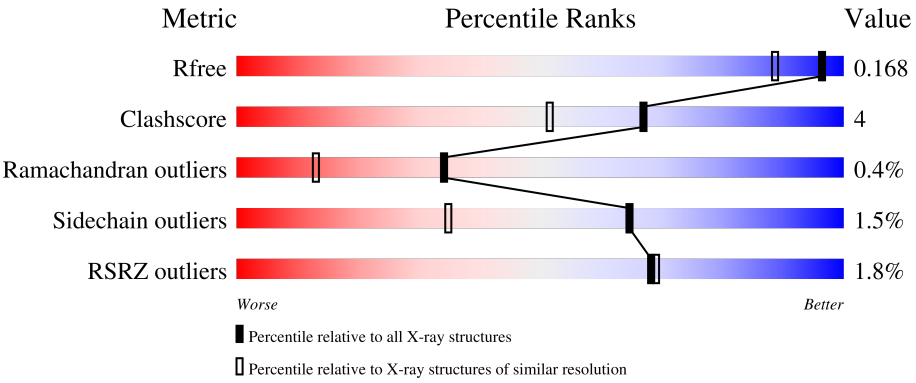
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.45 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	1156 (1.46-1.46)
Clashscore	141614	1202 (1.46-1.46)
Ramachandran outliers	138981	1178 (1.46-1.46)
Sidechain outliers	138945	1178 (1.46-1.46)
RSRZ outliers	127900	1139 (1.46-1.46)

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 <=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	548	79% 5% 15%
1	B	548	3% 77% 7% 15%
1	C	548	79% 6% 15%
1	D	548	78% 7% 15%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ACT	C	604	-	-	X	-
3	ACT	D	603	-	-	X	-
3	ACT	D	604	-	-	X	-
4	GOL	D	606	-	-	X	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 16357 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.

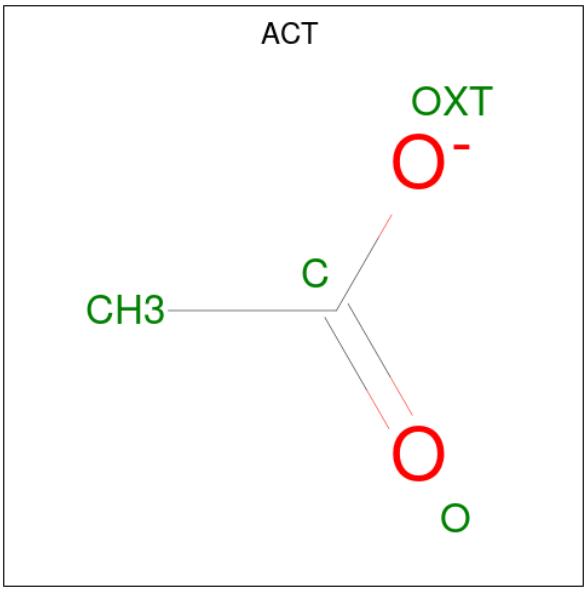
- Molecule 1 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	467	Total 3663	C 2337	N 607	O 699	S 20	0	11	0
1	B	467	Total 3653	C 2329	N 607	O 696	S 21	0	8	0
1	C	466	Total 3645	C 2327	N 604	O 695	S 19	0	7	0
1	D	467	Total 3671	C 2343	N 610	O 699	S 19	0	13	0

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

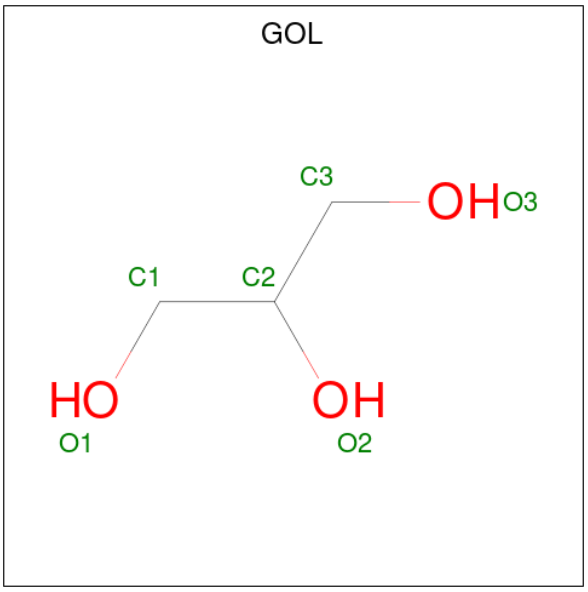
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total 2	Cu 2	0	0
2	B	2	Total 2	Cu 2	0	0
2	C	2	Total 2	Cu 2	0	0
2	D	2	Total 2	Cu 2	0	0

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



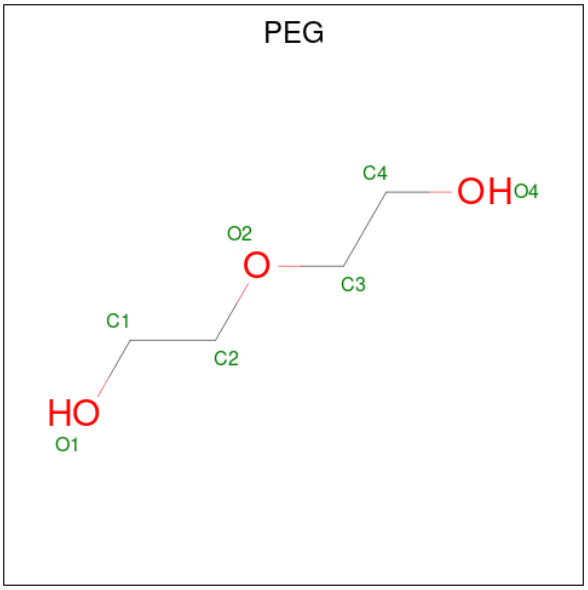
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total C O 6 3 3	0	0
4	D	1	Total C O 6 3 3	0	0

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	D	1	Total C O 5 3 2	0	0

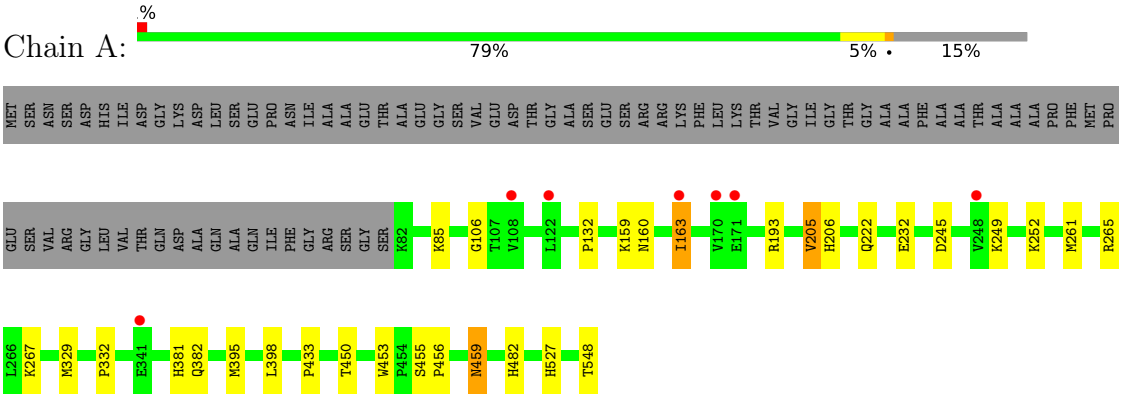
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	412	Total O 412 412	0	0
6	B	401	Total O 401 401	0	0
6	C	436	Total O 436 436	0	0
6	D	415	Total O 415 415	0	0

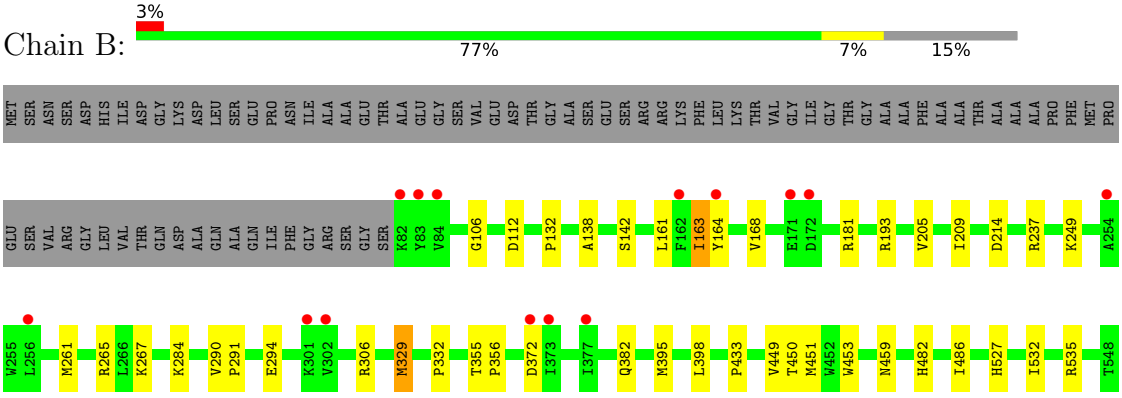
3 Residue-property plots (i)

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.

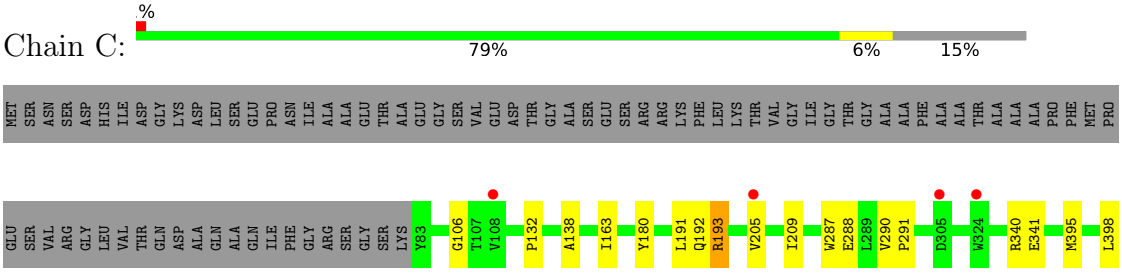
• Molecule 1: Uncharacterized protein

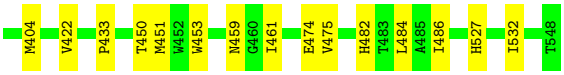


• Molecule 1: Uncharacterized protein



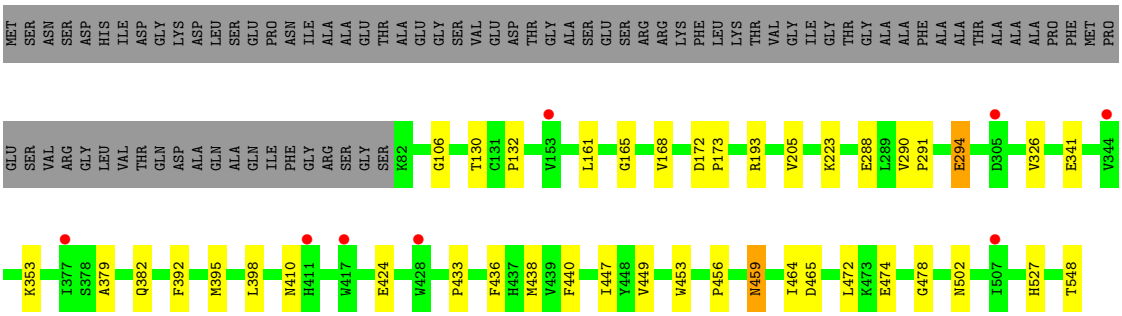
• Molecule 1: Uncharacterized protein





• Molecule 1: Uncharacterized protein

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	90.96Å 162.70Å 90.94Å 90.00° 119.93° 90.00°	Depositor
Resolution (Å)	45.48 – 1.45 45.48 – 1.45	Depositor EDS
% Data completeness (in resolution range)	97.1 (45.48-1.45) 99.7 (45.48-1.45)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.58 (at 1.45Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.142 , 0.165 0.146 , 0.168	Depositor DCC
R_{free} test set	20017 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å^2)	13.9	Xtriage
Anisotropy	0.005	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 45.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.015 for l,k,-h-l 0.015 for -h-l,k,h 0.046 for -h-l,-k,l 0.013 for h,-k,-h-l 0.148 for l,-k,h	Xtriage
Reported twinning fraction	0.439 for H, K, L 0.561 for L, -K, H	Depositor
Outliers	0 of 402549 reflections	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	16357	wwPDB-VP
Average B, all atoms (Å^2)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.64% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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, PEG, CU, GOL

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	0.66	0/3827	0.87	2/5219 (0.0%)
1	B	0.66	0/3799	0.88	6/5183 (0.1%)
1	C	0.67	0/3786	0.87	2/5167 (0.0%)
1	D	0.66	0/3842	0.89	2/5244 (0.0%)
All	All	0.66	0/15254	0.88	12/20813 (0.1%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	329[A]	MET	CG-SD-CE	-7.98	87.43	100.20
1	B	329[B]	MET	CG-SD-CE	-7.98	87.43	100.20
1	C	340	ARG	NE-CZ-NH2	-6.52	117.04	120.30
1	A	193	ARG	NE-CZ-NH1	6.49	123.54	120.30
1	B	237	ARG	NE-CZ-NH2	-6.32	117.14	120.30
1	B	181	ARG	NE-CZ-NH2	-5.95	117.33	120.30
1	C	193	ARG	NE-CZ-NH1	5.65	123.12	120.30
1	A	193	ARG	NE-CZ-NH2	-5.42	117.59	120.30
1	D	193[A]	ARG	NE-CZ-NH1	5.28	122.94	120.30
1	D	193[B]	ARG	NE-CZ-NH1	5.28	122.94	120.30
1	B	214	ASP	CB-CG-OD1	5.08	122.87	118.30
1	B	112	ASP	CB-CG-OD2	-5.03	113.78	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	3663	0	3521	18	0
1	B	3653	0	3518	17	0
1	C	3645	0	3510	21	0
1	D	3671	0	3514	32	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	8	0	1	1	0
3	B	8	0	2	1	0
3	C	8	0	2	2	0
3	D	12	0	9	17	0
4	C	6	0	8	1	0
4	D	6	0	8	5	0
5	D	5	0	5	3	0
6	A	412	0	0	4	0
6	B	401	0	0	2	0
6	C	436	0	0	6	0
6	D	415	0	0	6	0
All	All	16357	0	14098	110	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 4.

All (110) 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)
3:D:603:ACT:C	3:D:604:ACT:H2	1.12	1.58
3:D:603:ACT:H1	3:D:604:ACT:C	1.10	1.54
1:A:382:GLN:HG3	6:A:758:HOH:O	1.43	1.15
1:D:436[A]:PHE:CD2	4:D:606:GOL:H31	1.85	1.11
5:D:607:PEG:H32	6:D:877:HOH:O	1.51	1.09
3:D:603:ACT:C	3:D:604:ACT:CH3	1.85	1.09
1:D:436[A]:PHE:HD2	4:D:606:GOL:H31	0.95	1.07
3:A:604:ACT:O	6:A:702:HOH:O	1.72	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:436[A]:PHE:HD2	4:D:606:GOL:C3	1.73	1.01
1:C:288[A]:GLU:OE1	6:C:701:HOH:O	1.78	1.00
1:D:290:VAL:HG22	1:D:291:PRO:HD2	1.47	0.96
1:D:290:VAL:HG22	1:D:291:PRO:CD	1.96	0.95
3:D:603:ACT:H2	3:D:604:ACT:CH3	1.44	0.94
1:B:372[B]:ASP:OD1	6:B:701:HOH:O	1.89	0.90
3:C:604:ACT:OXT	6:C:702:HOH:O	1.90	0.88
1:C:475[A]:VAL:HG13	6:C:1019:HOH:O	1.73	0.85
1:C:451:MET:HG3	1:C:474:GLU:OE1	1.79	0.82
3:C:604:ACT:C	6:C:702:HOH:O	2.29	0.81
1:D:438:MET:SD	1:D:447[A]:ILE:HD11	2.22	0.80
3:D:603:ACT:CH3	3:D:604:ACT:C	1.95	0.80
1:C:461[A]:ILE:HD12	1:C:484:LEU:HD11	1.63	0.78
3:D:603:ACT:H2	3:D:604:ACT:H1	1.17	0.78
1:A:265:ARG:HD2	1:A:267:LYS:HE2	1.67	0.77
1:D:438:MET:HB2	1:D:447[A]:ILE:HD11	1.68	0.76
3:D:603:ACT:H3	3:D:604:ACT:H3	0.75	0.74
1:B:433:PRO:HD3	1:B:453:TRP:CZ2	2.24	0.73
1:B:265:ARG:HD2	1:B:267:LYS:HE3	1.70	0.73
3:D:603:ACT:CH3	3:D:604:ACT:H3	1.31	0.70
1:A:381:HIS:HB3	6:A:703:HOH:O	1.93	0.69
3:D:603:ACT:H2	3:D:604:ACT:H2	1.20	0.68
1:D:130[B]:THR:O	6:D:702:HOH:O	2.12	0.68
1:A:232:GLU:HG2	6:A:714:HOH:O	1.97	0.65
1:D:410:ASN:HB2	5:D:607:PEG:H42	1.80	0.64
1:C:486:ILE:C	1:C:532[B]:ILE:HD12	2.19	0.62
1:D:341:GLU:HG2	6:D:719:HOH:O	1.97	0.62
3:D:603:ACT:C	3:D:604:ACT:H3	1.94	0.60
1:D:438:MET:SD	1:D:447[A]:ILE:CD1	2.90	0.59
3:D:603:ACT:CH3	3:D:604:ACT:CH3	0.60	0.59
1:D:290:VAL:HG22	1:D:291:PRO:HD3	1.83	0.58
1:C:290:VAL:HB	1:C:291:PRO:HD2	1.84	0.58
1:B:161:LEU:HG	1:B:168:VAL:HG11	1.85	0.58
3:D:603:ACT:CH3	3:D:604:ACT:H1	1.06	0.57
1:A:160:ASN:HD21	1:A:222:GLN:HE22	1.53	0.57
3:D:603:ACT:H3	3:D:604:ACT:CH3	0.79	0.56
4:D:606:GOL:O1	6:D:701:HOH:O	0.56	0.56
1:C:475[A]:VAL:CG1	6:C:1019:HOH:O	2.41	0.56
1:C:341:GLU:HB3	6:C:703:HOH:O	2.06	0.55
1:D:436[A]:PHE:CD2	4:D:606:GOL:C3	2.66	0.55
1:C:163:ILE:HD11	1:C:287:TRP:CD1	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:261:MET:SD	1:B:329[B]:MET:HG2	2.48	0.54
3:D:603:ACT:OXT	3:D:604:ACT:H2	1.89	0.53
1:A:450:THR:HG21	1:A:482:HIS:O	2.07	0.53
3:D:603:ACT:CH3	3:D:604:ACT:H2	0.55	0.53
1:A:329[B]:MET:HB3	1:A:332:PRO:HD2	1.90	0.53
1:A:382:GLN:HE22	1:A:548:THR:H	1.56	0.53
1:B:355:THR:HB	1:B:356:PRO:HD2	1.90	0.53
1:B:290:VAL:HB	1:B:291:PRO:CD	2.39	0.52
1:C:106:GLY:HA2	1:C:132:PRO:O	2.10	0.51
1:D:447[A]:ILE:HG23	1:D:464[A]:ILE:HD12	1.93	0.51
1:D:438:MET:CB	1:D:447[A]:ILE:HD11	2.41	0.50
1:B:450:THR:HG21	1:B:482:HIS:O	2.12	0.50
1:D:382:GLN:HE21	1:D:548:THR:H	1.58	0.50
1:D:165[A]:GLY:O	1:D:502:ASN:ND2	2.44	0.49
1:C:450:THR:HG22	1:C:461[A]:ILE:CD1	2.42	0.49
1:B:106:GLY:HA2	1:B:132:PRO:O	2.12	0.49
3:B:604:ACT:C	6:B:702:HOH:O	2.59	0.49
1:D:173:PRO:HA	6:D:702:HOH:O	2.11	0.49
1:C:474:GLU:OE1	4:C:605:GOL:H2	2.13	0.48
1:D:449:VAL:HG11	1:D:464[A]:ILE:HD11	1.96	0.48
3:D:603:ACT:H3	3:D:604:ACT:H1	0.94	0.48
1:D:326:VAL:HG11	1:D:392:PHE:CZ	2.49	0.47
1:C:290:VAL:HB	1:C:291:PRO:CD	2.45	0.47
1:A:106:GLY:HA2	1:A:132:PRO:O	2.14	0.47
1:C:192:GLN:O	1:C:193:ARG:HB3	2.15	0.47
1:B:329[B]:MET:HB3	1:B:332:PRO:HD2	1.97	0.46
1:D:353:LYS:HE3	1:D:424:GLU:OE1	2.15	0.46
1:C:433:PRO:HD3	1:C:453:TRP:CZ2	2.50	0.46
1:B:449:VAL:HG23	1:B:451[A]:MET:HE2	1.96	0.46
1:C:138:ALA:HB1	1:C:209:ILE:HG12	1.96	0.45
1:B:267:LYS:HD2	1:D:172:ASP:HB2	1.97	0.45
1:D:161:LEU:HG	1:D:168[B]:VAL:HG11	1.97	0.45
1:A:160:ASN:HD21	1:A:222:GLN:NE2	2.15	0.45
1:A:85:LYS:HB3	1:A:85:LYS:HE2	1.59	0.45
1:D:290:VAL:CG2	1:D:291:PRO:CD	2.83	0.45
1:A:261:MET:SD	1:A:329[B]:MET:HG2	2.57	0.45
1:C:180:TYR:CD1	1:C:191:LEU:HD11	2.52	0.45
1:A:459:ASN:HD22	1:A:459:ASN:N	2.15	0.44
1:D:440:PHE:CE1	1:D:447[A]:ILE:HD12	2.53	0.44
1:D:288[B]:GLU:OE1	3:D:604:ACT:OXT	2.36	0.44
1:C:404:MET:SD	1:C:422:VAL:HG22	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:138:ALA:HB1	1:B:209:ILE:HG12	2.01	0.43
1:A:433:PRO:HD3	1:A:453:TRP:CZ2	2.53	0.43
1:A:455:SER:HA	1:A:456:PRO:HA	1.84	0.43
1:A:245:ASP:OD1	1:A:249:LYS:NZ	2.49	0.42
1:B:142:SER:O	1:B:535:ARG:HA	2.19	0.42
1:B:284:LYS:HG2	1:B:306:ARG:CZ	2.49	0.42
1:C:461[A]:ILE:CD1	1:C:484:LEU:HD21	2.49	0.42
5:D:607:PEG:C3	6:D:877:HOH:O	2.33	0.42
1:A:205:VAL:HG12	1:A:206:HIS:N	2.34	0.42
1:B:163:ILE:HG22	1:B:164:TYR:CE1	2.54	0.42
1:D:106:GLY:HA2	1:D:132:PRO:O	2.20	0.42
1:D:294:GLU:HG2	1:D:379:ALA:HB2	2.02	0.41
1:C:486:ILE:O	1:C:532[B]:ILE:HD12	2.20	0.41
1:D:465:ASP:HB2	1:D:472:LEU:HD21	2.03	0.41
1:A:159:LYS:O	1:A:163[A]:ILE:HD13	2.21	0.41
1:C:450:THR:HG21	1:C:482:HIS:O	2.21	0.41
1:D:459:ASN:HB2	1:D:478:GLY:O	2.21	0.40
1:D:433:PRO:HD3	1:D:453:TRP:CZ2	2.56	0.40
1:B:486:ILE:C	1:B:532[A]:ILE:HD12	2.42	0.40

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	476/548 (87%)	448 (94%)	26 (6%)	2 (0%)	34	13
1	B	473/548 (86%)	448 (95%)	23 (5%)	2 (0%)	34	13
1	C	471/548 (86%)	446 (95%)	23 (5%)	2 (0%)	34	13
1	D	478/548 (87%)	450 (94%)	26 (5%)	2 (0%)	34	13
All	All	1898/2192 (87%)	1792 (94%)	98 (5%)	8 (0%)	34	13

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	398	LEU
1	C	205	VAL
1	C	398	LEU
1	D	205	VAL
1	A	205	VAL
1	B	205	VAL
1	D	398	LEU
1	B	398	LEU

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	402/451 (89%)	396 (98%)	6 (2%)	65	35
1	B	398/451 (88%)	390 (98%)	8 (2%)	55	22
1	C	397/451 (88%)	394 (99%)	3 (1%)	81	62
1	D	402/451 (89%)	395 (98%)	7 (2%)	60	28
All	All	1599/1804 (89%)	1575 (98%)	24 (2%)	65	35

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

Mol	Chain	Res	Type
1	A	163[A]	ILE
1	A	163[B]	ILE
1	A	252	LYS
1	A	395	MET
1	A	459	ASN
1	A	527	HIS
1	B	163	ILE
1	B	193	ARG
1	B	249	LYS
1	B	294	GLU
1	B	382	GLN
1	B	395	MET

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Mol	Chain	Res	Type
1	B	459	ASN
1	B	527	HIS
1	C	395	MET
1	C	459	ASN
1	C	527	HIS
1	D	223	LYS
1	D	294	GLU
1	D	395	MET
1	D	456	PRO
1	D	459	ASN
1	D	474	GLU
1	D	527	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	222	GLN
1	B	126	ASN
1	C	126	ASN
1	C	360	GLN
1	D	126	ASN
1	D	382	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 20 ligands modelled in this entry, 8 are monoatomic - leaving 12 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	B	604	3,2	3,3,3	0.75	0	3,3,3	1.00	0
3	ACT	A	604	3,2	3,3,3	0.66	0	3,3,3	1.85	1 (33%)
4	GOL	C	605	-	5,5,5	0.46	0	5,5,5	0.21	0
3	ACT	C	604	3,2	3,3,3	1.07	0	3,3,3	1.05	0
3	ACT	D	603	2	3,3,3	0.74	0	3,3,3	0.98	0
3	ACT	D	605	-	3,3,3	0.82	0	3,3,3	0.74	0
5	PEG	D	607	-	4,4,6	0.35	0	3,3,5	0.44	0
3	ACT	C	603	3,2	3,3,3	0.69	0	3,3,3	0.64	0
4	GOL	D	606	-	5,5,5	0.23	0	5,5,5	0.59	0
3	ACT	D	604	2	3,3,3	0.81	0	3,3,3	0.46	0
3	ACT	B	603	3,2	3,3,3	0.98	0	3,3,3	0.72	0
3	ACT	A	603	3,2	3,3,3	0.68	0	3,3,3	0.71	0

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
5	PEG	D	607	-	-	2/2/2/4	-
4	GOL	C	605	-	-	0/4/4/4	-
4	GOL	D	606	-	-	0/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	604	ACT	OXT-C-CH3	2.55	125.71	115.18

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	607	PEG	O2-C3-C4-O4
5	D	607	PEG	C4-C3-O2-C2

There are no ring outliers.

8 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	604	ACT	1	0
3	A	604	ACT	1	0
4	C	605	GOL	1	0
3	C	604	ACT	2	0
3	D	603	ACT	16	0
5	D	607	PEG	3	0
4	D	606	GOL	5	0
3	D	604	ACT	17	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

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, 95^{th} 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	467/548 (85%)	0.33	7 (1%) 73 74	11, 17, 25, 40	0
1	B	467/548 (85%)	0.40	14 (2%) 50 53	10, 17, 25, 37	0
1	C	466/548 (85%)	0.41	4 (0%) 84 86	11, 15, 23, 30	0
1	D	467/548 (85%)	0.40	8 (1%) 70 70	10, 16, 23, 34	0
All	All	1867/2192 (85%)	0.39	33 (1%) 68 69	10, 16, 24, 40	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	172	ASP	4.0
1	B	162	PHE	3.4
1	A	171	GLU	3.0
1	B	377	ILE	2.9
1	B	83	TYR	2.8
1	B	256	LEU	2.6
1	D	344	VAL	2.5
1	A	341	GLU	2.5
1	B	302	VAL	2.5
1	C	205	VAL	2.5
1	D	305	ASP	2.5
1	D	417	TRP	2.4
1	A	170[A]	VAL	2.3
1	B	372[A]	ASP	2.3
1	D	411	HIS	2.3
1	A	248	VAL	2.3
1	A	122	LEU	2.2
1	B	171	GLU	2.2
1	D	428	TRP	2.2
1	C	305	ASP	2.2
1	A	108	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	84	VAL	2.2
1	A	163[A]	ILE	2.1
1	C	108	VAL	2.1
1	B	82	LYS	2.1
1	C	324	TRP	2.1
1	D	507	ILE	2.1
1	B	164	TYR	2.1
1	B	254	ALA	2.1
1	B	373	ILE	2.0
1	D	153	VAL	2.0
1	D	377	ILE	2.0
1	B	301	LYS	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, 95^{th} 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
3	ACT	D	603	4/4	0.80	0.33	14,14,14,15	4
3	ACT	D	605	4/4	0.83	0.30	19,20,20,21	4
3	ACT	C	603	4/4	0.85	0.34	12,12,13,14	4
3	ACT	A	603	4/4	0.86	0.21	15,16,16,16	4
3	ACT	D	604	4/4	0.87	0.36	16,18,18,19	4
5	PEG	D	607	5/7	0.87	0.20	17,18,19,19	5
3	ACT	A	604	4/4	0.89	0.20	14,14,15,17	4
3	ACT	B	603	4/4	0.90	0.20	11,12,12,13	4
3	ACT	C	604	4/4	0.90	0.37	12,13,14,15	4
3	ACT	B	604	4/4	0.94	0.26	16,16,16,16	4
4	GOL	D	606	6/6	0.95	0.22	11,12,14,14	6

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	GOL	C	605	6/6	0.97	0.07	15,18,18,19	0
2	CU	C	601	1/1	1.00	0.06	16,16,16,16	0
2	CU	C	602	1/1	1.00	0.09	14,14,14,14	1
2	CU	D	601	1/1	1.00	0.06	16,16,16,16	0
2	CU	D	602	1/1	1.00	0.09	13,13,13,13	1
2	CU	A	601	1/1	1.00	0.06	17,17,17,17	0
2	CU	A	602	1/1	1.00	0.08	15,15,15,15	1
2	CU	B	601	1/1	1.00	0.06	17,17,17,17	0
2	CU	B	602	1/1	1.00	0.08	14,14,14,14	1

6.5 Other polymers (i)

There are no such residues in this entry.