



Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 07:17 pm BST

PDB ID : 3Q66
Title : Structure of the Vps75-Rtt109 histone chaperone-lysine acetyltransferase complex (Full-length proteins in space group P6122)
Authors : Su, D.; Thompson, J.R.; Mer, G.
Deposited on : 2010-12-30
Resolution : 2.71 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 : 2.11
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) : 2.11

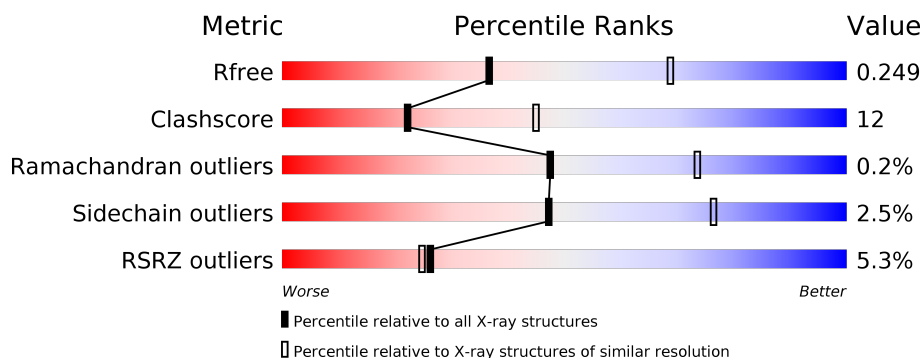
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.71 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	264	<div> <div>5%</div> <div> <div></div> <div>69%</div> <div>20%</div> <div>• 11%</div> </div> </div>
1	B	264	<div> <div>5%</div> <div> <div></div> <div>65%</div> <div>17%</div> <div>18%</div> </div> </div>
2	C	442	<div> <div>5%</div> <div> <div></div> <div>71%</div> <div>26%</div> <div>••</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7471 atoms, of which 58 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 Vacuolar protein sorting-associated protein 75.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	236	Total	C	H	N	O	S	0	2	0
			1988	1258	24	315	385	6			
1	B	217	Total	C	H	N	O	S	0	1	0
			1842	1173	26	295	343	5			

- Molecule 2 is a protein called Histone acetyltransferase RTT109.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	432	Total	C	H	N	O	S	0	1	0
			3513	2251	8	594	649	11			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	GLY	-	EXPRESSION TAG	UNP Q07794
C	-4	MET	-	EXPRESSION TAG	UNP Q07794
C	-3	ASP	-	EXPRESSION TAG	UNP Q07794
C	-2	PRO	-	EXPRESSION TAG	UNP Q07794
C	-1	ASN	-	EXPRESSION TAG	UNP Q07794
C	0	SER	-	EXPRESSION TAG	UNP Q07794

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

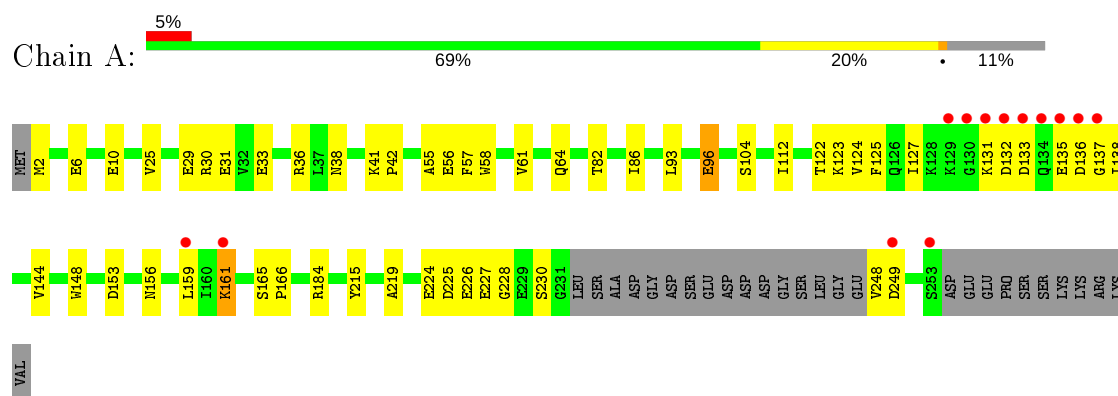
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	37	Total	O	0	0
			37	37		
4	C	58	Total	O	0	0
			58	58		
4	B	23	Total	O	0	0
			23	23		

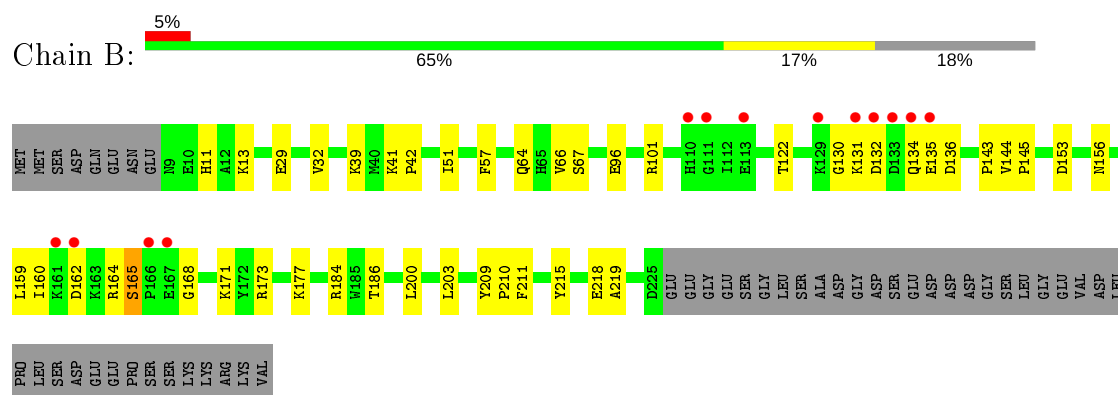
3 Residue-property plots [i](#)

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

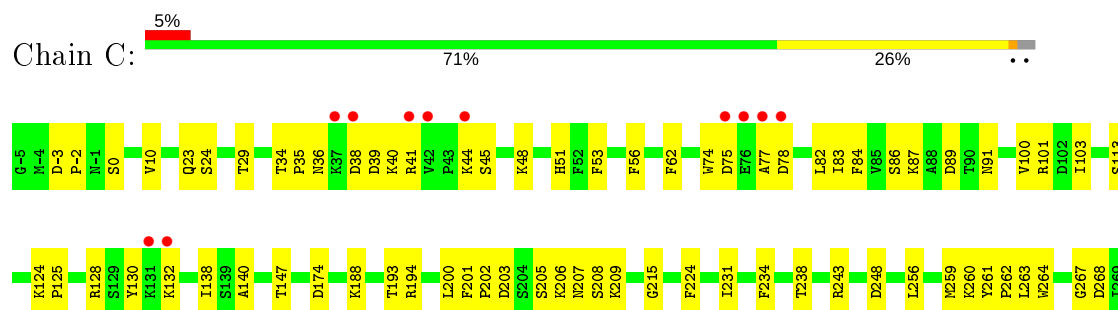
- Molecule 1: Vacuolar protein sorting-associated protein 75

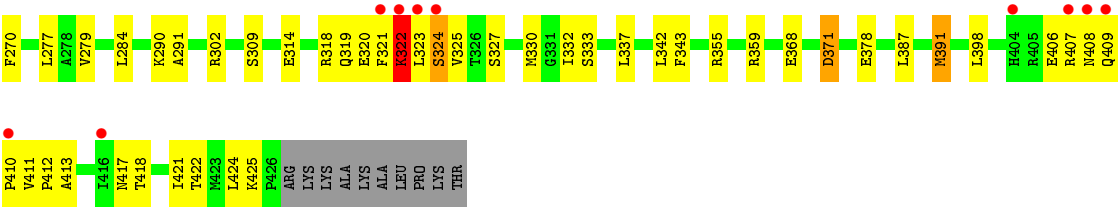


- Molecule 1: Vacuolar protein sorting-associated protein 75



- Molecule 2: Histone acetyltransferase RTT109





4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	99.39 Å 99.39 Å 479.61 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.51 – 2.71 40.50 – 2.71	Depositor EDS
% Data completeness (in resolution range)	94.7 (40.51-2.71) 94.7 (40.50-2.71)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.83 (at 2.69 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.1_357)	Depositor
R, R_{free}	0.206 , 0.247 0.206 , 0.249	Depositor DCC
R_{free} test set	531 reflections (1.34%)	wwPDB-VP
Wilson B-factor (Å ²)	60.8	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 57.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7471	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.30% 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: SO4, ALY

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	0.58	0/2018	0.59	0/2718
1	B	0.53	0/1867	0.58	0/2514
2	C	0.54	0/3574	0.60	0/4838
All	All	0.55	0/7459	0.59	0/10070

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

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	1964	24	1882	41	0
1	B	1816	26	1764	38	0
2	C	3505	8	3558	97	0
3	A	5	0	0	1	0
3	C	5	0	0	0	0
4	A	37	0	0	1	0
4	B	23	0	0	0	0
4	C	58	0	0	2	0
All	All	7413	58	7204	170	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 12.

All (170) 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)
2:C:324:SER:O	4:C:477:HOH:O	1.95	0.84
1:A:6:GLU:O	1:A:10:GLU:HG2	1.84	0.78
2:C:270:PHE:HZ	2:C:290:ALY:HH31	1.50	0.77
1:A:133:ASP:HB3	1:A:135:GLU:HG2	1.71	0.73
2:C:410:PRO:HG2	2:C:413:ALA:HB3	1.73	0.70
2:C:-3:ASP:HB2	2:C:-2:PRO:HD2	1.75	0.68
2:C:342:LEU:HD12	2:C:343:PHE:N	2.09	0.68
1:A:31:GLU:CD	1:B:39[B]:LYS:HE2	2.15	0.67
1:A:96:GLU:H	1:A:96:GLU:CD	2.00	0.64
2:C:40:LYS:HG3	2:C:41:ARG:N	2.13	0.63
1:A:33:GLU:HA	1:A:33:GLU:OE1	1.99	0.63
1:B:41:LYS:HB3	1:B:42:PRO:HD3	1.79	0.63
1:B:131:LYS:HD2	1:B:131:LYS:N	2.14	0.63
2:C:407:ARG:HD2	2:C:411:VAL:HG22	1.81	0.63
1:A:133:ASP:HB3	1:A:135:GLU:CG	2.29	0.62
1:A:165:SER:HB2	1:A:166:PRO:HD2	1.82	0.62
2:C:262:PRO:HB2	2:C:263:LEU:CD1	2.30	0.62
1:B:29:GLU:HA	1:B:29:GLU:OE1	2.00	0.62
2:C:398:LEU:C	2:C:398:LEU:HD12	2.20	0.61
1:B:96:GLU:H	1:B:96:GLU:CD	2.03	0.61
2:C:270:PHE:CZ	2:C:290:ALY:HH31	2.34	0.61
2:C:411:VAL:N	2:C:412:PRO:HD2	2.16	0.60
1:B:135:GLU:O	1:B:136:ASP:HB2	2.02	0.59
1:A:184:ARG:HD3	3:A:265:SO4:O1	2.03	0.59
2:C:421:ILE:HG13	2:C:422:THR:N	2.17	0.59
1:A:135:GLU:O	1:A:136:ASP:HB2	2.02	0.59
2:C:318:ARG:HD2	2:C:321:PHE:HE2	1.68	0.58
2:C:206:LYS:HD3	2:C:371:ASP:HB3	1.83	0.58
2:C:194:ARG:HD2	2:C:322:LYS:HB2	1.85	0.58
2:C:231:ILE:HD11	2:C:260:LYS:HB2	1.87	0.57
2:C:323:LEU:HG	2:C:327:SER:OG	2.05	0.56
1:A:64:GLN:HG3	1:A:215:TYR:O	2.05	0.55
1:A:64:GLN:HG2	1:A:219:ALA:HB2	1.88	0.55
2:C:125:PRO:HG2	2:C:128:ARG:HG3	1.89	0.55
1:B:134:GLN:HG2	1:B:135:GLU:N	2.21	0.55
2:C:10:VAL:CG1	2:C:10:VAL:O	2.54	0.55
1:A:224:GLU:O	1:A:227:GLU:HG2	2.06	0.55
1:A:30:ARG:NH1	4:A:287:HOH:O	2.30	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:PHE:HB2	1:B:215:TYR:CE2	2.42	0.54
1:A:55:ALA:O	1:A:56:GLU:HB2	2.08	0.54
1:A:226:GLU:OE2	2:C:130:TYR:OH	2.25	0.54
2:C:421:ILE:HG13	2:C:422:THR:HG23	1.90	0.54
2:C:101:ARG:HD2	2:C:224:PHE:CD2	2.43	0.54
2:C:262:PRO:HB2	2:C:263:LEU:HD13	1.89	0.54
2:C:368:GLU:OE2	2:C:378:GLU:HB3	2.08	0.54
2:C:322:LYS:O	2:C:323:LEU:HB2	2.07	0.53
2:C:215:GLY:HA3	2:C:325:VAL:O	2.08	0.53
2:C:82:LEU:HD23	2:C:82:LEU:C	2.28	0.53
2:C:387:LEU:HA	2:C:391:MET:HG3	1.91	0.53
2:C:125:PRO:HG2	2:C:128:ARG:CG	2.39	0.52
1:B:143:PRO:HD3	1:B:186:THR:HG22	1.90	0.52
1:B:156:ASN:O	1:B:160:ILE:HG13	2.09	0.52
2:C:302:ARG:NH2	2:C:314:GLU:OE1	2.43	0.52
2:C:330:MET:O	4:C:475:HOH:O	2.18	0.51
1:A:148:TRP:HB2	1:A:156:ASN:ND2	2.25	0.51
1:B:131:LYS:O	1:B:132:ASP:HB2	2.10	0.51
2:C:138:ILE:HG21	2:C:147:THR:HG23	1.93	0.50
1:A:64:GLN:CG	1:A:219:ALA:HB2	2.41	0.50
1:B:131:LYS:O	1:B:132:ASP:CB	2.59	0.50
1:B:51:ILE:HG23	1:B:57:PHE:CD2	2.46	0.50
2:C:188:LYS:HA	2:C:332:ILE:O	2.11	0.50
1:B:153:ASP:HB2	1:B:159:LEU:HD23	1.94	0.50
1:A:153:ASP:HA	1:A:159:LEU:HD12	1.93	0.50
2:C:355:ARG:HD2	2:C:359:ARG:NH1	2.27	0.50
2:C:270:PHE:HZ	2:C:290:ALY:CH3	2.23	0.49
2:C:36:ASN:HB3	2:C:39:ASP:HB2	1.94	0.49
2:C:409:GLN:HB3	2:C:410:PRO:HD2	1.95	0.49
2:C:82:LEU:HD23	2:C:83:ILE:N	2.28	0.49
1:A:38:ASN:OD1	1:A:93:LEU:HD22	2.13	0.49
2:C:355:ARG:HD2	2:C:359:ARG:CZ	2.42	0.49
1:A:36:ARG:HG3	1:B:32:VAL:HG21	1.94	0.48
2:C:238:THR:HG23	2:C:333:SER:O	2.14	0.48
2:C:91:ASN:HB3	2:C:201:PHE:CG	2.49	0.48
2:C:318:ARG:HB2	2:C:321:PHE:CD2	2.48	0.48
2:C:40:LYS:HE2	2:C:41:ARG:HB3	1.96	0.48
2:C:408:ASN:C	2:C:409:GLN:HG3	2.34	0.48
2:C:40:LYS:CG	2:C:41:ARG:N	2.76	0.47
1:B:130:GLY:C	1:B:131:LYS:HD2	2.34	0.47
1:A:29:GLU:OE1	1:A:29:GLU:HA	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:256:LEU:HD22	2:C:264:TRP:HB3	1.95	0.47
1:A:248:VAL:HG12	1:A:249:ASP:H	1.80	0.47
2:C:243:ARG:NH1	2:C:268:ASP:OD2	2.47	0.47
2:C:36:ASN:HB3	2:C:39:ASP:OD2	2.15	0.47
2:C:411:VAL:N	2:C:412:PRO:CD	2.77	0.47
1:B:131:LYS:CD	1:B:131:LYS:N	2.78	0.46
1:B:143:PRO:HD3	1:B:186:THR:CG2	2.45	0.46
1:B:153:ASP:HB2	1:B:159:LEU:CD2	2.45	0.46
1:B:173:ARG:HG2	1:B:177:LYS:HE3	1.97	0.46
1:A:123:LYS:HE3	1:A:125:PHE:CZ	2.50	0.46
1:A:127:ILE:HA	1:A:138:ILE:O	2.16	0.46
1:A:225:ASP:OD1	2:C:124:LYS:HE2	2.15	0.46
1:B:135:GLU:O	1:B:136:ASP:CB	2.63	0.46
2:C:321:PHE:O	2:C:322:LYS:HB2	2.16	0.46
1:A:131:LYS:O	1:A:132:ASP:HB3	2.17	0.45
1:A:135:GLU:C	1:A:137:GLY:H	2.20	0.45
2:C:424:LEU:O	2:C:425:LYS:C	2.54	0.45
1:A:25:VAL:O	1:A:29:GLU:HG2	2.15	0.45
1:B:101:ARG:HH22	1:B:136:ASP:HB3	1.80	0.45
2:C:51:HIS:HB3	2:C:53:PHE:CE2	2.51	0.45
1:B:209:TYR:N	1:B:210:PRO:CD	2.80	0.45
2:C:321:PHE:C	2:C:322:LYS:HD3	2.36	0.45
2:C:319:GLN:HA	2:C:319:GLN:OE1	2.16	0.45
1:B:134:GLN:HG2	1:B:135:GLU:H	1.82	0.45
1:B:153:ASP:HA	1:B:156:ASN:HB2	1.99	0.45
1:B:200:LEU:O	1:B:203:LEU:HB3	2.17	0.45
2:C:193:THR:O	2:C:327:SER:HB2	2.16	0.45
2:C:408:ASN:O	2:C:409:GLN:HG3	2.17	0.45
1:B:143:PRO:HA	1:B:184:ARG:HA	1.99	0.45
2:C:41:ARG:HG3	2:C:74:TRP:CE3	2.51	0.45
1:A:58:TRP:CE3	1:A:86:ILE:HD12	2.52	0.44
2:C:56:PHE:CD2	2:C:56:PHE:N	2.85	0.44
1:A:57:PHE:O	1:A:61:VAL:HG23	2.17	0.44
2:C:259:MET:HB3	2:C:264:TRP:CD1	2.52	0.44
2:C:29:THR:HG21	2:C:48:LYS:HB2	1.99	0.44
2:C:10:VAL:O	2:C:10:VAL:HG12	2.17	0.44
2:C:410:PRO:HG2	2:C:413:ALA:CB	2.45	0.44
1:B:122:THR:O	1:B:144:VAL:HG21	2.18	0.44
1:A:41:LYS:N	1:A:42:PRO:HD2	2.32	0.44
1:A:82:THR:HG21	1:A:112:ILE:HG13	2.00	0.44
2:C:100:VAL:HA	2:C:103:ILE:HD12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:132:LYS:O	2:C:132:LYS:HG2	2.16	0.44
1:A:122:THR:O	1:A:144:VAL:HG11	2.17	0.44
1:B:101:ARG:HH12	1:B:136:ASP:CB	2.30	0.44
1:B:171:LYS:N	1:B:171:LYS:HD3	2.33	0.44
2:C:38:ASP:CG	2:C:38:ASP:O	2.56	0.43
1:A:31:GLU:OE1	1:B:39[B]:LYS:HE2	2.17	0.43
2:C:418:THR:O	2:C:421:ILE:HG12	2.18	0.43
1:B:165:SER:HB3	1:B:168:GLY:H	1.84	0.43
2:C:39:ASP:OD1	2:C:40:LYS:HG2	2.18	0.43
1:A:165:SER:HB2	1:A:166:PRO:CD	2.48	0.43
1:B:153:ASP:HA	1:B:156:ASN:CB	2.48	0.43
2:C:277:LEU:HA	2:C:277:LEU:HD23	1.90	0.43
2:C:40:LYS:HG3	2:C:41:ARG:CB	2.49	0.43
2:C:417:ASN:OD1	2:C:417:ASN:C	2.56	0.43
1:B:144:VAL:HG23	1:B:145:PRO:HD2	2.01	0.43
2:C:202:PRO:O	2:C:203:ASP:HB2	2.19	0.42
2:C:290:ALY:HH31	2:C:290:ALY:HE2	1.80	0.42
2:C:77:ALA:O	2:C:78:ASP:HB2	2.19	0.42
1:B:41:LYS:N	1:B:42:PRO:CD	2.82	0.42
2:C:89:ASP:HB3	2:C:200:LEU:HB2	2.01	0.42
1:A:227:GLU:HA	1:A:228:GLY:HA2	1.64	0.42
2:C:113:SER:O	2:C:342:LEU:HB3	2.20	0.42
2:C:86:SER:O	2:C:87:LYS:HG2	2.19	0.42
2:C:62:PHE:HA	2:C:91:ASN:OD1	2.19	0.42
2:C:207:ASN:HD21	2:C:209:LYS:HB2	1.85	0.41
2:C:101:ARG:HD2	2:C:224:PHE:CE2	2.55	0.41
1:A:2:MET:CG	1:A:2:MET:O	2.67	0.41
1:B:162:ASP:O	1:B:168:GLY:HA3	2.20	0.41
2:C:34:THR:HA	2:C:35:PRO:HD3	1.85	0.41
1:A:36:ARG:NH1	1:A:36:ARG:HG2	2.35	0.41
2:C:398:LEU:O	2:C:398:LEU:HD12	2.20	0.41
1:A:104:SER:HB3	1:A:124:VAL:HG22	2.03	0.41
1:B:164:ARG:O	1:B:165:SER:C	2.57	0.41
2:C:261:TYR:CD1	2:C:262:PRO:HD2	2.55	0.41
1:A:230:SER:HA	2:C:140:ALA:O	2.21	0.41
2:C:82:LEU:C	2:C:82:LEU:CD2	2.89	0.41
1:A:161:LYS:H	1:A:161:LYS:HD2	1.86	0.41
2:C:261:TYR:HA	2:C:262:PRO:HD3	1.82	0.41
2:C:268:ASP:OD1	2:C:268:ASP:C	2.59	0.41
2:C:101:ARG:CD	2:C:224:PHE:CD2	3.04	0.40
2:C:243:ARG:HB3	2:C:267:GLY:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:44:LYS:O	2:C:45:SER:HB2	2.21	0.40
1:B:64:GLN:HG3	1:B:219:ALA:CB	2.51	0.40
2:C:284:LEU:HD22	2:C:291:ALA:HA	2.03	0.40
2:C:234:PHE:O	2:C:337:LEU:HD21	2.21	0.40
2:C:23:GLN:HG2	2:C:24:SER:N	2.37	0.40
2:C:321:PHE:C	2:C:322:LYS:CD	2.90	0.40
2:C:206:LYS:CD	2:C:371:ASP:HB3	2.51	0.40
2:C:84:PHE:CE2	2:C:86:SER:HB2	2.56	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	234/264 (89%)	227 (97%)	7 (3%)	0	100	100
1	B	216/264 (82%)	207 (96%)	8 (4%)	1 (0%)	29	54
2	C	430/442 (97%)	406 (94%)	23 (5%)	1 (0%)	47	73
All	All	880/970 (91%)	840 (96%)	38 (4%)	2 (0%)	47	73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	322	LYS
1	B	165	SER

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	213/235 (91%)	211 (99%)	2 (1%)	78	92
1	B	195/235 (83%)	190 (97%)	5 (3%)	46	75
2	C	395/402 (98%)	382 (97%)	13 (3%)	38	67
All	All	803/872 (92%)	783 (98%)	20 (2%)	47	76

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	96	GLU
1	A	161	LYS
2	C	0	SER
2	C	75	ASP
2	C	205	SER
2	C	208	SER
2	C	248	ASP
2	C	279	VAL
2	C	309	SER
2	C	320	GLU
2	C	322	LYS
2	C	324	SER
2	C	371	ASP
2	C	391	MET
2	C	406	GLU
1	B	11	HIS
1	B	13	LYS
1	B	66	VAL
1	B	67	SER
1	B	218	GLU

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 ⓘ

1 non-standard protein/DNA/RNA residue is 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	ALY	C	290	2	10,11,12	1.61	1 (10%)	7,12,14	1.31	1 (14%)

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	ALY	C	290	2	-	2/9/10/12	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	290	ALY	CH-NZ	4.47	1.47	1.34

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	290	ALY	CH3-CH-NZ	2.75	120.95	116.09

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	290	ALY	OH-CH-NZ-CE
2	C	290	ALY	CH3-CH-NZ-CE

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	290	ALY	4	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
3	SO4	A	265	-	4,4,4	0.14	0	6,6,6	0.31	0
3	SO4	C	437	-	4,4,4	0.13	0	6,6,6	0.37	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	265	SO4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

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	236/264 (89%)	0.09	13 (5%) 25 24	39, 61, 131, 220	0
1	B	217/264 (82%)	0.16	13 (5%) 21 20	45, 70, 150, 224	0
2	C	431/442 (97%)	0.18	21 (4%) 29 28	38, 68, 141, 247	0
All	All	884/970 (91%)	0.15	47 (5%) 26 25	38, 67, 142, 247	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	132	ASP	10.3
1	A	130	GLY	9.7
1	A	134	GLN	8.6
2	C	42	VAL	7.3
1	A	131	LYS	7.0
1	A	136	ASP	6.3
1	A	133	ASP	6.3
2	C	41	ARG	5.8
1	B	132	ASP	5.6
1	A	135	GLU	5.6
1	B	133	ASP	5.4
1	A	129	LYS	5.4
1	B	131	LYS	5.3
1	A	137	GLY	5.2
2	C	131	LYS	5.1
2	C	407	ARG	4.6
2	C	409	GLN	4.6
1	B	134	GLN	4.3
2	C	132	LYS	4.3
1	B	111	GLY	4.2
1	A	161	LYS	4.1
1	B	166	PRO	4.0
2	C	324	SER	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	135	GLU	3.8
1	B	161	LYS	3.6
2	C	75	ASP	3.4
2	C	321	PHE	3.4
2	C	408	ASN	3.4
1	A	253	SER	3.2
2	C	76	GLU	3.2
1	B	129	LYS	3.1
2	C	404	HIS	2.9
1	B	167	GLU	2.7
1	B	110	HIS	2.7
2	C	37	LYS	2.7
2	C	322	LYS	2.6
1	A	159	LEU	2.5
2	C	78	ASP	2.5
2	C	77	ALA	2.5
2	C	410	PRO	2.4
1	B	113	GLU	2.2
1	B	162	ASP	2.2
2	C	323	LEU	2.2
2	C	44	LYS	2.1
1	A	249	ASP	2.1
2	C	416	ILE	2.1
2	C	38	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(\AA^2)	Q<0.9
2	ALY	C	290	12/13	0.92	0.25	46,58,66,78	0

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. 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(\AA^2)	Q<0.9
3	SO4	A	265	5/5	0.92	0.12	98,107,112,114	0
3	SO4	C	437	5/5	0.97	0.13	66,73,74,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.