



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 01:12 am GMT

PDB ID : 2X24
Title : BOVINE ACC2 CT DOMAIN IN COMPLEX WITH INHIBITOR
Authors : Oster, L.; Folmer, R.; Blaho, S.; Wiberg, F.; Hallberg, K.
Deposited on : 2010-01-11
Resolution : 2.40 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

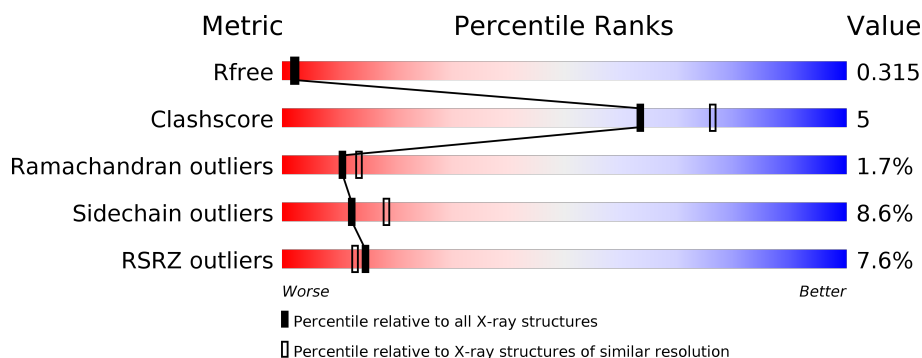
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	100719	3166 (2.40-2.40)
Clashscore	112137	3674 (2.40-2.40)
Ramachandran outliers	110173	3616 (2.40-2.40)
Sidechain outliers	110143	3617 (2.40-2.40)
RSRZ outliers	101464	3195 (2.40-2.40)

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	793	<div> <div>6%</div> <div> <div></div> <div>66%</div> <div>16%</div> <div>•</div> <div>18%</div> </div> </div>
1	B	793	<div> <div>7%</div> <div> <div></div> <div>67%</div> <div>15%</div> <div>•</div> <div>16%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10763 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.

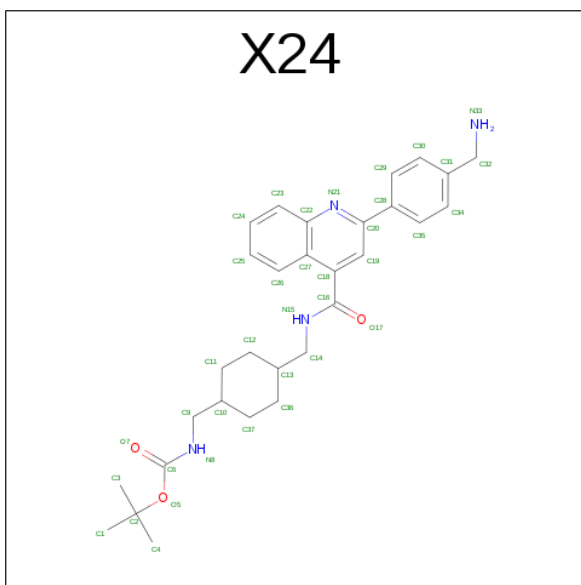
- Molecule 1 is a protein called ACETYL-COA CARBOXYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	654	Total	C	N	O	S	0	0	0
			5219	3339	899	958	23			
1	B	667	Total	C	N	O	S	0	0	0
			5324	3404	919	976	25			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	MET	-	EXPRESSION TAG	PDB 2X24
A	-8	GLY	-	EXPRESSION TAG	PDB 2X24
A	-7	SER	-	EXPRESSION TAG	PDB 2X24
A	-6	SER	-	EXPRESSION TAG	PDB 2X24
A	-5	HIS	-	EXPRESSION TAG	PDB 2X24
A	-4	HIS	-	EXPRESSION TAG	PDB 2X24
A	-3	HIS	-	EXPRESSION TAG	PDB 2X24
A	-2	HIS	-	EXPRESSION TAG	PDB 2X24
A	-1	HIS	-	EXPRESSION TAG	PDB 2X24
A	0	HIS	-	EXPRESSION TAG	PDB 2X24
B	-9	MET	-	EXPRESSION TAG	PDB 2X24
B	-8	GLY	-	EXPRESSION TAG	PDB 2X24
B	-7	SER	-	EXPRESSION TAG	PDB 2X24
B	-6	SER	-	EXPRESSION TAG	PDB 2X24
B	-5	HIS	-	EXPRESSION TAG	PDB 2X24
B	-4	HIS	-	EXPRESSION TAG	PDB 2X24
B	-3	HIS	-	EXPRESSION TAG	PDB 2X24
B	-2	HIS	-	EXPRESSION TAG	PDB 2X24
B	-1	HIS	-	EXPRESSION TAG	PDB 2X24
B	0	HIS	-	EXPRESSION TAG	PDB 2X24

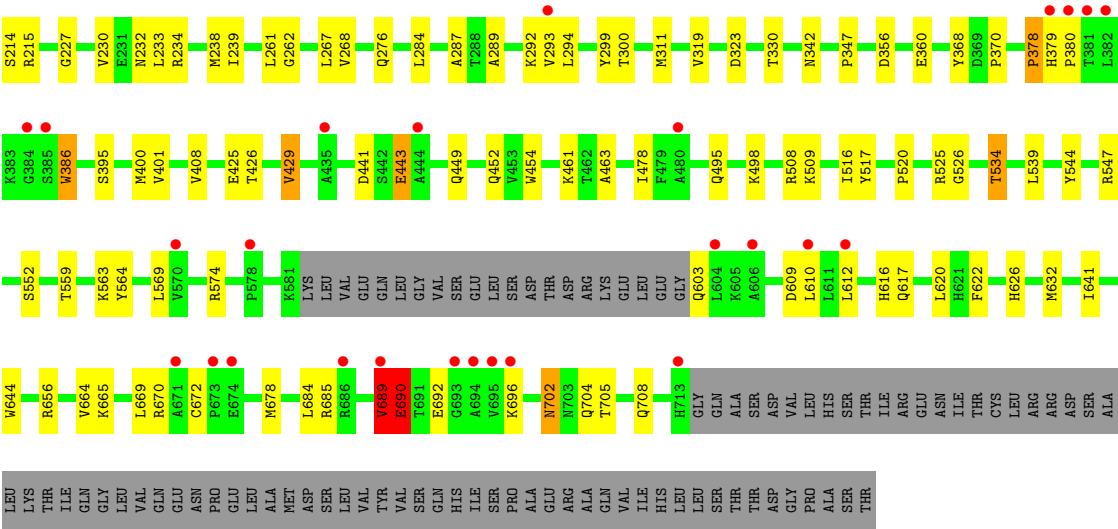
- Molecule 2 is TERT-BUTYL [(TRANS-4-{{(2-[4-(AMINOMETHYL)PHENYL]QUINOLIN-4-YL)CARBONYL)AMINO}METHYL}CYCLOHEXYL)METHYL]CARBAMATE (three-letter code: X24) (formula: C₃₀H₃₈N₄O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 37	C 30	N 4	O 3	0	0
2	B	1	Total 37	C 30	N 4	O 3	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	62	Total O 62 62	0	0
3	B	84	Total O 84 84	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	225.19Å 104.87Å 85.08Å 90.00° 95.67° 90.00°	Depositor
Resolution (Å)	29.70 – 2.40 29.49 – 2.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) (29.70-2.40) 93.9 (29.49-2.40)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 2.39Å)	Xtriage
Refinement program	BUSTER 2.9.2	Depositor
R, R_{free}	0.232 , 0.283 0.251 , 0.315	Depositor DCC
R_{free} test set	3643 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	31.5	Xtriage
Anisotropy	0.144	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 61.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	10763	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.99% 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: X24

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	0.53	0/5342	0.77	2/7245 (0.0%)
1	B	0.54	0/5451	0.78	3/7395 (0.0%)
All	All	0.54	0/10793	0.78	5/14640 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	689	VAL	C-N-CA	7.91	141.48	121.70
1	A	178	GLU	C-N-CA	7.00	139.19	121.70
1	A	198	SER	C-N-CA	6.99	139.17	121.70
1	B	178	GLU	C-N-CA	6.58	138.14	121.70
1	B	198	SER	C-N-CA	6.37	137.62	121.70

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	5219	0	5207	56	0
1	B	5324	0	5308	56	0
2	A	37	0	38	1	0
2	B	37	0	38	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	62	0	0	0	0
3	B	84	0	0	6	0
All	All	10763	0	10591	103	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 5.

All (103) 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:626:HIS:HE1	1:B:163:ALA:H	1.29	0.81
1:A:118:ASN:HD22	1:A:154:ALA:H	1.32	0.77
1:A:198:SER:HB3	1:A:199:SER:HB2	1.73	0.71
1:B:289:ALA:O	1:B:293:VAL:HG23	1.91	0.70
1:B:429:VAL:HG22	1:B:449:GLN:HB2	1.74	0.69
1:A:276:GLN:HE22	1:A:311:MET:HB2	1.57	0.68
1:B:155:ASN:HD22	1:B:157:GLY:H	1.44	0.66
1:A:163:ALA:H	1:B:626:HIS:HE1	1.45	0.65
1:A:198:SER:HB3	1:A:199:SER:CB	2.30	0.60
1:B:102:LEU:HD11	1:B:113:ILE:HG12	1.84	0.60
1:B:443:GLU:HA	3:B:2054:HOH:O	2.01	0.59
1:A:702:ASN:HD22	1:A:705:THR:H	1.52	0.58
1:B:64:PRO:HD2	1:B:67:ILE:HD12	1.85	0.57
1:A:71:THR:HA	1:A:85:ASN:HD21	1.70	0.56
1:B:37:LEU:HD13	1:B:120:ILE:HG12	1.88	0.56
1:A:404:ALA:HB3	1:A:461:LYS:HD3	1.87	0.56
1:B:378:PRO:HA	1:B:386:TRP:HA	1.87	0.56
1:B:65:LYS:H	1:B:65:LYS:HD3	1.71	0.56
1:A:155:ASN:HD22	1:A:157:GLY:H	1.54	0.55
1:A:370:PRO:O	1:A:373:LEU:HB3	2.07	0.55
1:A:374:LEU:HD22	1:A:391:PHE:HE2	1.71	0.55
1:B:276:GLN:HE22	1:B:311:MET:HB2	1.72	0.55
1:A:319:VAL:HG21	1:A:330:THR:HG21	1.88	0.55
1:B:664:VAL:HG11	1:B:684:LEU:HD21	1.89	0.54
1:B:136:LEU:HD13	1:B:238:MET:HG2	1.89	0.54
1:B:175:VAL:HG22	1:B:182:LYS:HB3	1.90	0.53
1:A:39:THR:HG21	1:A:120:ILE:HG21	1.91	0.53
1:A:462:THR:O	1:A:466:ILE:HG13	2.10	0.52
1:A:163:ALA:H	1:B:626:HIS:CE1	2.27	0.52
1:B:517:TYR:HA	1:B:544:TYR:O	2.11	0.51
1:A:181:HIS:O	1:A:182:LYS:HB2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:547:ARG:HG2	1:B:641:ILE:HG22	1.93	0.50
1:A:251:VAL:HG11	1:A:338:MET:SD	2.51	0.50
1:B:370:PRO:HG2	1:B:408:VAL:HG21	1.93	0.49
1:A:146:GLY:HA2	1:A:250:ILE:CG2	2.43	0.49
1:B:520:PRO:HG3	1:B:644:TRP:HB2	1.93	0.49
1:A:172:VAL:HG13	1:A:184:ILE:HD12	1.95	0.49
1:B:239:ILE:HD12	1:B:267:LEU:HD11	1.94	0.48
1:A:574:ARG:HD3	1:A:604:LEU:HD21	1.94	0.48
1:B:401:VAL:HG23	3:B:2030:HOH:O	2.12	0.48
1:B:227:GLY:HA2	1:B:232:ASN:HD21	1.78	0.48
1:B:622:PHE:O	1:B:626:HIS:HD2	1.97	0.48
1:A:64:PRO:HD2	1:A:67:ILE:HD12	1.95	0.47
1:B:525:ARG:NH1	1:B:552:SER:OG	2.47	0.47
1:A:417:ILE:HD11	1:A:656:ARG:HG2	1.96	0.46
1:A:198:SER:HB3	1:A:199:SER:CA	2.45	0.46
1:B:508:ARG:HH22	1:B:509:LYS:HE3	1.80	0.46
1:B:692:GLU:HB3	1:B:696:LYS:HD2	1.97	0.46
1:A:102:LEU:O	1:A:110:GLY:HA2	2.15	0.46
1:A:269:ARG:HD2	1:A:269:ARG:HA	1.79	0.46
1:A:269:ARG:CZ	1:B:498:LYS:HG2	2.46	0.46
1:A:702:ASN:ND2	1:A:705:THR:H	2.12	0.46
1:B:478:ILE:HD12	1:B:516:ILE:HG12	1.97	0.46
1:B:617:GLN:HA	1:B:620:LEU:HD12	1.98	0.46
1:A:118:ASN:ND2	1:A:153:ALA:HA	2.30	0.46
1:B:198:SER:HB3	1:B:199:SER:HB3	1.96	0.46
1:B:704:GLN:HE21	1:B:708:GLN:NE2	2.13	0.46
1:B:370:PRO:HG3	1:B:425:GLU:HA	1.99	0.45
1:A:82:VAL:HG13	1:A:84:MET:HG2	1.97	0.45
1:A:687:TRP:CD1	1:A:709:TRP:HZ2	2.34	0.45
1:B:569:LEU:HD23	1:B:612:LEU:HD23	1.99	0.45
1:B:689:VAL:HB	1:B:690:GLU:HB2	1.99	0.45
1:A:626:HIS:CE1	1:B:163:ALA:H	2.20	0.45
1:A:160:ILE:HG22	1:B:563:LYS:HG3	1.99	0.44
1:B:702:ASN:HD22	1:B:705:THR:H	1.66	0.44
1:A:53:LEU:HD11	1:A:102:LEU:HD23	2.00	0.44
1:A:230:VAL:HG21	1:B:632:MET:HG2	1.98	0.44
1:A:358:GLU:HA	1:A:645:LYS:O	2.18	0.44
1:A:293:VAL:HG11	2:B:1714:X24:H361	2.00	0.44
1:A:622:PHE:O	1:A:626:HIS:HD2	2.00	0.43
1:B:463:ALA:HB3	3:B:2013:HOH:O	2.19	0.43
2:A:1715:X24:H19	2:A:1715:X24:H29	1.76	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:452:GLN:OE1	1:A:483:ARG:HD2	2.19	0.43
1:B:400:MET:HB2	1:B:461:LYS:HE3	2.01	0.43
1:A:50:ARG:HG3	1:A:68:LEU:HB3	2.00	0.43
1:A:632:MET:HG2	1:B:230:VAL:HG11	1.99	0.43
1:B:426:THR:HG22	1:B:452:GLN:CG	2.49	0.43
1:A:425:GLU:OE1	1:A:427:ARG:NH2	2.32	0.42
1:A:173:ALA:HB1	1:A:185:LYS:HE3	2.01	0.42
1:A:699:LEU:HB3	1:A:705:THR:HG21	2.01	0.42
1:A:272:GLN:OE1	1:A:464:GLN:NE2	2.53	0.42
1:B:287:ALA:HB1	1:B:299:TYR:HB2	2.01	0.42
1:A:200:LEU:HD13	1:A:224:LYS:HD3	2.01	0.42
1:B:227:GLY:CA	1:B:232:ASN:HD21	2.32	0.42
1:B:319:VAL:HG21	1:B:330:THR:HG21	2.00	0.42
1:A:605:LYS:HA	1:A:608:GLU:HG2	2.02	0.42
1:B:106:GLU:HB3	1:B:347:PRO:HB2	2.01	0.42
1:A:553:VAL:HG22	1:B:233:LEU:HD21	2.01	0.41
1:B:176:ASP:HB2	1:B:182:LYS:HG3	2.02	0.41
1:A:617:GLN:HA	1:A:620:LEU:HD12	2.02	0.41
1:B:191:PRO:HD3	1:B:214:SER:O	2.20	0.41
1:B:368:TYR:HA	3:B:2037:HOH:O	2.20	0.41
1:A:239:ILE:HD12	1:A:267:LEU:HD11	2.03	0.41
1:B:174:TRP:HB3	3:B:2011:HOH:O	2.20	0.41
1:A:637:VAL:HG23	1:A:638:ILE:HG23	2.03	0.41
1:A:67:ILE:HG13	1:A:103:LYS:HB2	2.03	0.40
1:A:146:GLY:HA2	1:A:250:ILE:HG22	2.02	0.40
1:B:569:LEU:HD11	1:B:616:HIS:HA	2.03	0.40
1:A:207:HIS:HB2	1:A:216:TYR:CE1	2.56	0.40
1:A:289:ALA:O	1:A:293:VAL:HG13	2.21	0.40
1:B:185:LYS:HD2	1:B:186:TYR:HD2	1.87	0.40
1:A:485:PHE:HB2	1:B:284:LEU:HD13	2.03	0.40
1:B:534:THR:HG21	3:B:2073:HOH:O	2.21	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	648/793 (82%)	610 (94%)	29 (4%)	9 (1%)	13	18
1	B	663/793 (84%)	614 (93%)	36 (5%)	13 (2%)	9	10
All	All	1311/1586 (83%)	1224 (93%)	65 (5%)	22 (2%)	11	13

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	62	LYS
1	A	179	ASP
1	A	526	GLY
1	B	179	ASP
1	B	526	GLY
1	B	690	GLU
1	B	59	SER
1	B	197	ILE
1	A	182	LYS
1	A	197	ILE
1	A	211	ASP
1	A	258	CYS
1	B	379	HIS
1	B	380	PRO
1	B	689	VAL
1	A	495	GLN
1	B	495	GLN
1	B	669	LEU
1	A	59	SER
1	B	262	GLY
1	B	212	GLY
1	B	378	PRO

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	560/683 (82%)	514 (92%)	46 (8%)	13	20
1	B	572/683 (84%)	521 (91%)	51 (9%)	11	17
All	All	1132/1366 (83%)	1035 (91%)	97 (9%)	12	18

All (97) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	ARG
1	A	35	GLN
1	A	56	MET
1	A	65	LYS
1	A	69	THR
1	A	84	MET
1	A	87	LEU
1	A	91	ASN
1	A	100	MET
1	A	115	LEU
1	A	149	ARG
1	A	184	ILE
1	A	201	ASN
1	A	206	LYS
1	A	214	SER
1	A	215	ARG
1	A	220	ASP
1	A	234	ARG
1	A	259	ARG
1	A	261	LEU
1	A	281	HIS
1	A	297	ASP
1	A	342	ASN
1	A	352	LYS
1	A	356	ASP
1	A	445	LYS
1	A	454	TRP
1	A	458	SER
1	A	460	TYR
1	A	495	GLN
1	A	505	ASP
1	A	510	TYR
1	A	528	SER
1	A	552	SER
1	A	564	TYR

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Mol	Chain	Res	Type
1	A	581	LYS
1	A	603	GLN
1	A	605	LYS
1	A	614	MET
1	A	635	LYS
1	A	649	SER
1	A	656	ARG
1	A	681	GLN
1	A	683	MET
1	A	684	LEU
1	A	702	ASN
1	B	28	GLN
1	B	56	MET
1	B	61	ASP
1	B	65	LYS
1	B	102	LEU
1	B	115	LEU
1	B	120	ILE
1	B	149	ARG
1	B	165	GLU
1	B	175	VAL
1	B	176	ASP
1	B	182	LYS
1	B	192	GLN
1	B	199	SER
1	B	201	ASN
1	B	206	LYS
1	B	209	GLU
1	B	210	GLU
1	B	215	ARG
1	B	234	ARG
1	B	261	LEU
1	B	268	VAL
1	B	292	LYS
1	B	294	LEU
1	B	300	THR
1	B	323	ASP
1	B	342	ASN
1	B	356	ASP
1	B	360	GLU
1	B	386	TRP
1	B	395	SER

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Mol	Chain	Res	Type
1	B	429	VAL
1	B	441	ASP
1	B	443	GLU
1	B	454	TRP
1	B	534	THR
1	B	539	LEU
1	B	559	THR
1	B	564	TYR
1	B	574	ARG
1	B	603	GLN
1	B	609	ASP
1	B	610	LEU
1	B	656	ARG
1	B	665	LYS
1	B	670	ARG
1	B	672	CYS
1	B	678	MET
1	B	685	ARG
1	B	690	GLU
1	B	702	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	ASN
1	A	118	ASN
1	A	155	ASN
1	A	204	HIS
1	A	207	HIS
1	A	232	ASN
1	A	276	GLN
1	A	281	HIS
1	A	342	ASN
1	A	448	GLN
1	A	621	HIS
1	A	626	HIS
1	A	702	ASN
1	B	118	ASN
1	B	155	ASN
1	B	232	ASN
1	B	276	GLN
1	B	342	ASN

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Mol	Chain	Res	Type
1	B	362	GLN
1	B	405	GLN
1	B	626	HIS
1	B	702	ASN
1	B	708	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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	$\# Z > 2$
2	X24	A	1715	-	40,40,40	0.73	0	55,56,56	2.14	13 (23%)
2	X24	B	1714	-	40,40,40	0.74	0	55,56,56	2.67	14 (25%)

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	X24	A	1715	-	-	0/25/35/35	0/4/4/4
2	X24	B	1714	-	-	0/25/35/35	0/4/4/4

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1714	X24	C10-C9-N8	-6.73	100.17	112.83
2	B	1714	X24	C13-C14-N15	-6.64	100.35	112.83
2	B	1714	X24	O7-C6-N8	-6.37	114.84	124.98
2	A	1715	X24	C19-C20-C28	-6.19	113.38	121.84
2	A	1715	X24	C13-C14-N15	-4.63	104.12	112.83
2	A	1715	X24	O7-C6-N8	-3.64	119.19	124.98
2	B	1714	X24	C36-C37-C10	-3.55	106.51	112.41
2	B	1714	X24	O17-C16-N15	-3.13	116.13	122.59
2	A	1715	X24	C29-C28-C20	-3.10	116.39	121.30
2	B	1714	X24	C12-C11-C10	-3.01	107.42	112.41
2	B	1714	X24	C27-C22-N21	-2.89	119.86	122.84
2	A	1715	X24	C36-C37-C10	-2.67	107.98	112.41
2	B	1714	X24	O17-C16-C18	-2.61	117.92	121.66
2	A	1715	X24	C27-C22-N21	-2.21	120.56	122.84
2	A	1715	X24	C12-C11-C10	-2.08	108.96	112.41
2	B	1714	X24	O5-C2-C3	2.30	116.35	107.21
2	A	1715	X24	C36-C13-C12	2.50	115.46	109.27
2	B	1714	X24	C36-C13-C12	2.94	116.54	109.27
2	A	1715	X24	C20-N21-C22	3.90	121.03	118.07
2	A	1715	X24	C2-O5-C6	3.98	127.50	121.04
2	B	1714	X24	C2-O5-C6	4.24	127.92	121.04
2	A	1715	X24	C27-C18-C16	4.58	127.43	120.73
2	A	1715	X24	O5-C6-N8	4.96	117.66	109.98
2	A	1715	X24	C28-C20-N21	5.76	125.81	117.15
2	B	1714	X24	C20-N21-C22	5.96	122.59	118.07
2	B	1714	X24	C18-C16-N15	6.75	125.93	116.30
2	B	1714	X24	O5-C6-N8	7.67	121.84	109.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1715	X24	1	0
2	B	1714	X24	1	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, 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	654/793 (82%)	0.38	47 (7%) 16 15	15, 35, 66, 88	0
1	B	667/793 (84%)	0.38	53 (7%) 13 12	14, 34, 64, 92	0
All	All	1321/1586 (83%)	0.38	100 (7%) 15 13	14, 34, 65, 92	0

All (100) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	689	VAL	6.0
1	B	381	THR	5.9
1	B	196	ARG	5.7
1	B	694	ALA	5.6
1	B	671	ALA	5.4
1	A	63	TYR	5.2
1	A	687	TRP	5.0
1	A	713	HIS	4.8
1	B	695	VAL	4.5
1	A	87	LEU	4.4
1	B	211	ASP	4.3
1	B	198	SER	4.2
1	A	712	ALA	4.2
1	A	381	THR	3.9
1	B	293	VAL	3.8
1	B	59	SER	3.8
1	A	61	ASP	3.7
1	B	382	LEU	3.7
1	A	382	LEU	3.7
1	B	713	HIS	3.7
1	A	27	LEU	3.6
1	A	90	GLY	3.6
1	B	77	PRO	3.6
1	B	380	PRO	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	60	PRO	3.5
1	B	61	ASP	3.5
1	B	197	ILE	3.4
1	A	384	GLY	3.4
1	A	42	VAL	3.4
1	B	179	ASP	3.3
1	A	179	ASP	3.3
1	A	681	GLN	3.3
1	A	606	ALA	3.3
1	A	77	PRO	3.2
1	A	175	VAL	3.2
1	A	32	PHE	3.1
1	B	693	GLY	3.1
1	A	293	VAL	3.1
1	B	27	LEU	3.0
1	B	379	HIS	2.9
1	A	64	PRO	2.9
1	B	570	VAL	2.9
1	B	604	LEU	2.9
1	A	683	MET	2.8
1	A	54	PHE	2.8
1	A	198	SER	2.8
1	A	178	GLU	2.8
1	B	208	VAL	2.8
1	A	37	LEU	2.8
1	A	578	PRO	2.8
1	B	696	LYS	2.7
1	B	385	SER	2.7
1	A	666	GLN	2.7
1	B	199	SER	2.7
1	B	62	LYS	2.7
1	A	60	PRO	2.7
1	B	180	PRO	2.7
1	A	690	GLU	2.7
1	B	75	LEU	2.7
1	A	207	HIS	2.7
1	B	686	ARG	2.7
1	A	56	MET	2.7
1	B	612	LEU	2.6
1	A	714	GLY	2.6
1	A	177	PRO	2.6
1	B	178	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	267	LEU	2.5
1	B	578	PRO	2.5
1	B	384	GLY	2.5
1	B	80	GLN	2.4
1	B	28	GLN	2.4
1	A	710	LEU	2.4
1	A	174	TRP	2.3
1	A	680	VAL	2.3
1	A	279	ASN	2.3
1	B	32	PHE	2.3
1	B	57	TRP	2.3
1	A	226	GLU	2.3
1	A	196	ARG	2.2
1	B	191	PRO	2.2
1	B	195	THR	2.2
1	A	366	GLY	2.2
1	B	200	LEU	2.2
1	B	674	GLU	2.2
1	A	38	GLY	2.2
1	A	684	LEU	2.2
1	A	152	LEU	2.1
1	B	79	GLY	2.1
1	B	673	PRO	2.1
1	B	435	ALA	2.1
1	A	144	ALA	2.1
1	B	480	ALA	2.1
1	B	610	LEU	2.1
1	A	57	TRP	2.1
1	B	606	ALA	2.0
1	B	189	LEU	2.0
1	B	29	ALA	2.0
1	B	444	ALA	2.0
1	B	209	GLU	2.0
1	A	58	PRO	2.0

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

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

6.3 Carbohydrates [i](#)

There are no 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(\AA^2)	Q<0.9
2	X24	B	1714	37/37	0.87	0.21	0.76	24,36,47,51	0
2	X24	A	1715	37/37	0.87	0.17	-0.05	29,43,48,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.