



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:23 PM GMT

PDB ID : 4XNU
Title : X-ray structure of Drosophila dopamine transporter in complex with nisoxetine
Authors : Aravind, P.; Wang, K.; Gouaux, E.
Deposited on : 2015-01-16
Resolution : 2.98 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

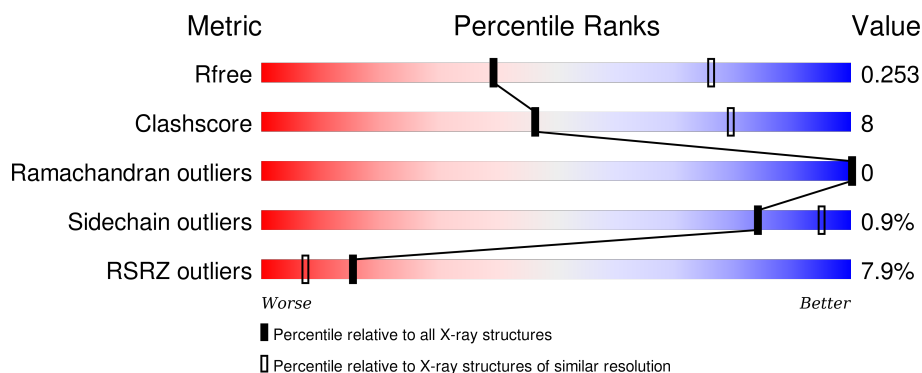
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.98 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	1992 (3.00-2.96)
Clashscore	102246	2349 (3.00-2.96)
Ramachandran outliers	100387	2274 (3.00-2.96)
Sidechain outliers	100360	2277 (3.00-2.96)
RSRZ outliers	91569	2007 (3.00-2.96)

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	532	<div> <div>6%</div> <div>84%</div> <div>16%</div> </div>
2	L	214	<div> <div>12%</div> <div>86%</div> <div>14%</div> </div>
3	H	240	<div> <div>8%</div> <div>72%</div> <div>18%</div> <div>10%</div> </div>

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
4	NA	A	601	-	-	-	X
6	CLR	A	604	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7470 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 Integral membrane protein-dopamine transporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	532	Total	C	N	O	S	0	2	0
			4192	2814	647	713	18			

- Molecule 2 is a protein called antibody fragment light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	214	Total	C	N	O	S	0	0	0
			1621	1007	270	336	8			

- Molecule 3 is a protein called antibody fragment heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	216	Total	C	N	O	S	0	0	0
			1598	1009	270	312	7			

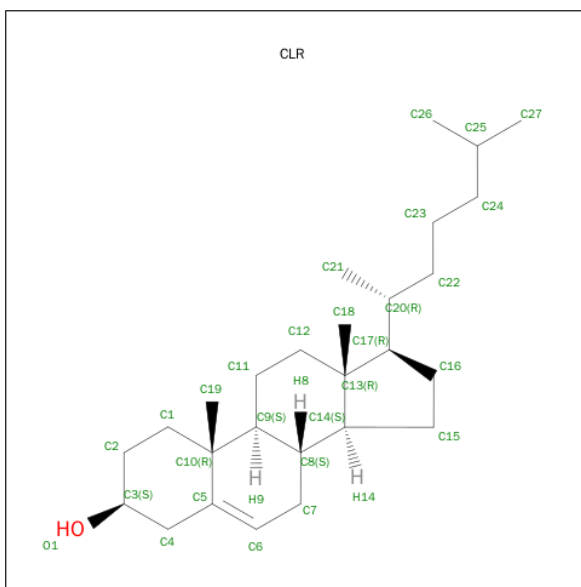
- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Na	0	0
			2	2		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

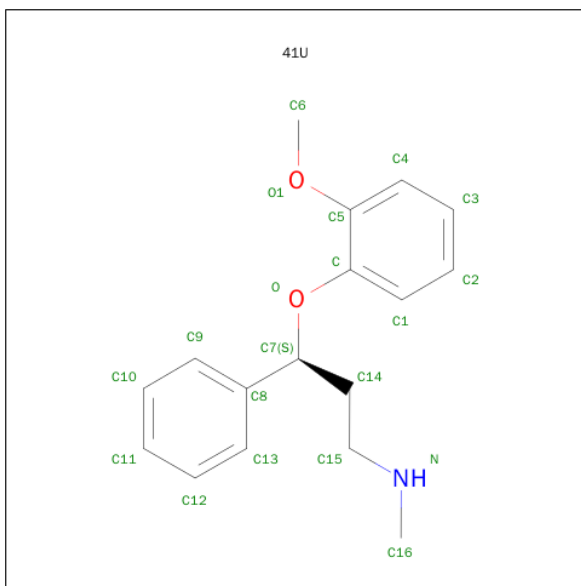
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Cl	0	0
			1	1		

- Molecule 6 is CHOLESTEROL (three-letter code: CLR) (formula: C₂₇H₄₆O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			28	27	1		

- Molecule 7 is nisoxetine (three-letter code: 41U) (formula: $C_{17}H_{21}NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			20	17	1	2		

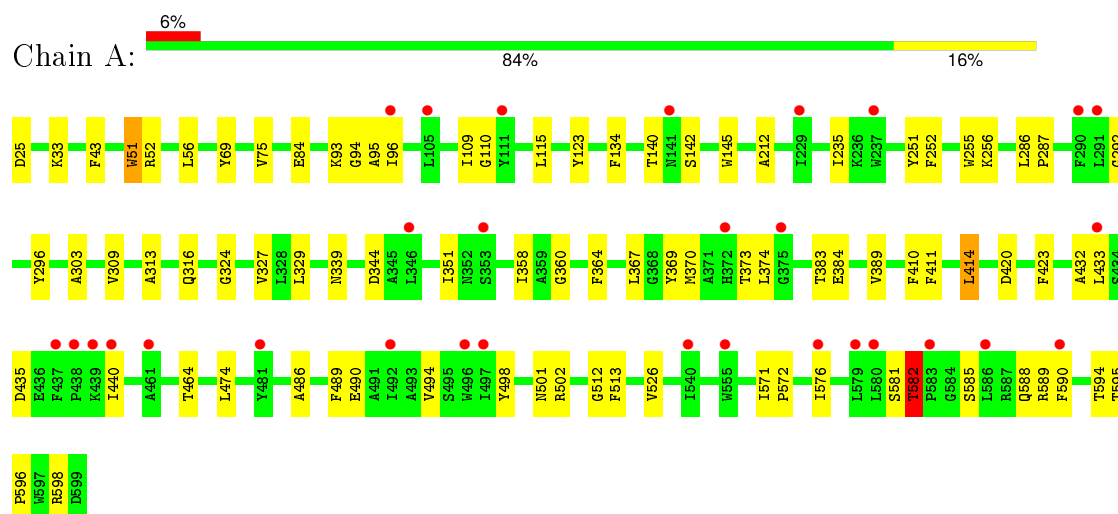
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	8	Total	O	0	0
			8	8		

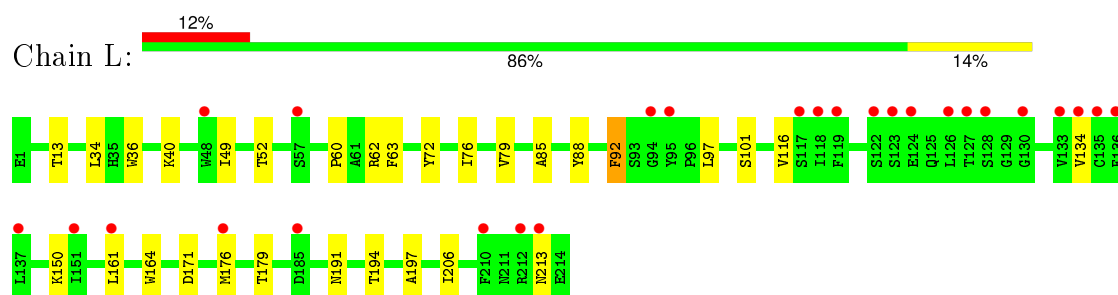
3 Residue-property plots [i](#)

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.

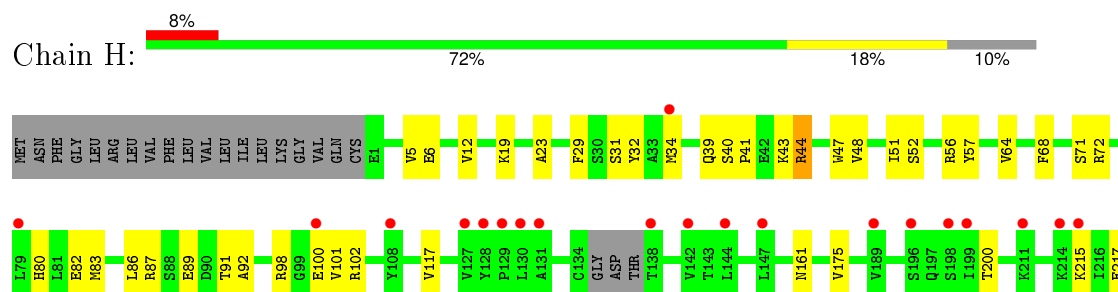
- Molecule 1: Integral membrane protein-dopamine transporter



- Molecule 2: antibody fragment light chain



- Molecule 3: antibody fragment heavy chain



P218	R219
	GLY
	PRO

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	96.90Å 133.67Å 161.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.10 – 2.98 47.10 – 2.97	Depositor EDS
% Data completeness (in resolution range)	98.6 (47.10-2.98) 93.3 (47.10-2.97)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.90 (at 2.96Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.226 , 0.251 0.237 , 0.253	Depositor DCC
R_{free} test set	1971 reflections (5.04%)	DCC
Wilson B-factor (Å ²)	86.7	Xtriage
Anisotropy	0.469	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 36.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 43369 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	7470	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.98% 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, 0.375 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: 41U, CL, CLR, NA

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	0.29	0/4340	0.44	2/5932 (0.0%)
2	L	0.25	0/1659	0.46	0/2257
3	H	0.28	0/1636	0.47	0/2230
All	All	0.28	0/7635	0.45	2/10419 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	414	LEU	CB-CG-CD2	-7.48	98.28	111.00
1	A	582	THR	C-N-CD	5.72	140.41	128.40

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	4192	0	4087	62	0
2	L	1621	0	1523	23	0
3	H	1598	0	1524	35	0
4	A	2	0	0	0	0
5	A	1	0	0	1	0
6	A	28	0	46	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	20	0	21	1	0
8	A	8	0	0	4	0
All	All	7470	0	7201	112	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 8.

All (112) 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:H:40:SER:HB3	3:H:41:PRO:HD2	1.53	0.91
3:H:91:THR:HG22	3:H:117:VAL:H	1.46	0.78
3:H:31:SER:O	3:H:100:GLU:OE1	2.08	0.72
1:A:585:SER:H	1:A:588:GLN:HB2	1.55	0.71
3:H:89:GLU:N	3:H:89:GLU:OE1	2.24	0.71
2:L:197:ALA:HB3	2:L:206:ILE:HD11	1.72	0.70
3:H:34:MET:SD	3:H:98:ARG:HB2	2.32	0.70
1:A:598:ARG:O	8:A:707:HOH:O	2.09	0.69
1:A:252:PHE:HA	1:A:255:TRP:CD1	2.30	0.67
1:A:502[A]:ARG:NH2	8:A:707:HOH:O	2.22	0.66
1:A:364:PHE:HA	1:A:367:LEU:HB2	1.78	0.66
3:H:39:GLN:O	3:H:92:ALA:HB1	1.95	0.66
1:A:33:LYS:NZ	1:A:339:ASN:OD1	2.30	0.65
3:H:48:VAL:HG13	3:H:64:VAL:HG21	1.79	0.65
1:A:502[B]:ARG:NH2	8:A:707:HOH:O	2.22	0.64
1:A:585:SER:O	1:A:589:ARG:HG2	1.97	0.64
1:A:512:GLY:HA2	3:H:102:ARG:HG3	1.79	0.64
3:H:40:SER:CB	3:H:41:PRO:HD2	2.27	0.62
1:A:513:PHE:HB3	3:H:101:VAL:HG13	1.83	0.60
1:A:94:GLY:HA3	1:A:432:ALA:HA	1.83	0.60
1:A:43:PHE:CZ	1:A:327:VAL:HG11	2.37	0.60
2:L:134:VAL:HG22	2:L:179:THR:HG23	1.85	0.59
2:L:40:LYS:HD3	2:L:85:ALA:HB2	1.83	0.59
1:A:93:LYS:HE3	1:A:435:ASP:HB3	1.84	0.59
2:L:62:ARG:HG3	2:L:76:ILE:HG23	1.84	0.58
3:H:71:SER:HB2	3:H:80:HIS:HB2	1.85	0.58
1:A:94:GLY:N	1:A:435:ASP:OD2	2.36	0.58
1:A:52:ARG:HG3	1:A:52:ARG:HH11	1.69	0.57
1:A:84:GLU:OE1	1:A:324:GLY:N	2.34	0.57
1:A:255:TRP:CZ3	1:A:256:LYS:HE2	2.40	0.56
3:H:64:VAL:HG13	3:H:68:PHE:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:101:SER:O	3:H:44:ARG:HD2	2.04	0.56
1:A:303:ALA:HB1	1:A:309:VAL:HG21	1.87	0.56
1:A:33:LYS:NZ	1:A:344:ASP:OD2	2.38	0.55
2:L:13:THR:HG21	2:L:79:VAL:HG21	1.89	0.55
3:H:39:GLN:O	3:H:92:ALA:CB	2.56	0.54
1:A:96:ILE:HA	1:A:110:GLY:HA3	1.89	0.54
1:A:287:PRO:HG2	1:A:373:THR:HG21	1.90	0.54
3:H:87:ARG:HB3	3:H:89:GLU:OE1	2.07	0.54
2:L:150:LYS:HB2	2:L:194:THR:HB	1.90	0.53
1:A:590:PHE:O	1:A:594:THR:N	2.43	0.52
3:H:51:ILE:HD13	3:H:72:ARG:HG3	1.91	0.52
1:A:235:ILE:HG12	1:A:464:THR:HG22	1.92	0.51
1:A:123:TYR:HB3	1:A:474:LEU:HD12	1.91	0.51
2:L:88:TYR:OH	3:H:43:LYS:O	2.26	0.51
1:A:286:LEU:HD13	1:A:369:TYR:CG	2.46	0.51
1:A:582:THR:O	1:A:589:ARG:NH1	2.44	0.50
2:L:164:TRP:CE2	2:L:176:MET:HG3	2.46	0.50
1:A:433:LEU:HB3	1:A:440:ILE:HD11	1.92	0.50
1:A:358:ILE:HD13	6:A:604:CLR:H263	1.94	0.50
1:A:109:ILE:HG21	1:A:490:GLU:HG2	1.93	0.50
2:L:191:ASN:ND2	2:L:213:ASN:OD1	2.45	0.49
1:A:512:GLY:CA	3:H:102:ARG:HG3	2.42	0.49
2:L:52:THR:HG21	2:L:72:TYR:CD2	2.47	0.49
3:H:32:TYR:CB	3:H:98:ARG:HD2	2.43	0.48
3:H:52:SER:HB3	3:H:57:TYR:HB2	1.95	0.48
2:L:34:LEU:HD13	2:L:72:TYR:CD1	2.49	0.48
2:L:92:PHE:CE1	2:L:97:LEU:HD11	2.49	0.47
1:A:52:ARG:CG	1:A:52:ARG:HH11	2.28	0.47
1:A:51:TRP:CD1	1:A:51:TRP:C	2.88	0.47
1:A:296:TYR:CZ	1:A:360:GLY:HA3	2.50	0.46
2:L:97:LEU:HB2	3:H:47:TRP:CD2	2.51	0.46
1:A:75:VAL:HB	1:A:526:VAL:HG11	1.97	0.46
3:H:6:GLU:OE1	3:H:6:GLU:N	2.49	0.46
1:A:367:LEU:HA	1:A:370:MET:HE2	1.98	0.46
1:A:582:THR:OG1	1:A:589:ARG:HD3	2.17	0.45
1:A:383:THR:OG1	1:A:384:GLU:N	2.50	0.45
1:A:489:PHE:CD2	1:A:571:ILE:HG21	2.52	0.45
1:A:494:VAL:HA	1:A:498:TYR:HB3	1.98	0.45
1:A:590:PHE:O	1:A:594:THR:OG1	2.21	0.45
1:A:351:ILE:HD13	6:A:604:CLR:H71	1.99	0.44
3:H:83:MET:HE2	3:H:86:LEU:HD21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:92:PHE:CD1	3:H:102:ARG:HD3	2.52	0.44
1:A:389:VAL:HB	1:A:414:LEU:HD21	1.98	0.44
1:A:292:GLY:HA3	1:A:364:PHE:O	2.17	0.44
1:A:582:THR:OG1	1:A:589:ARG:CD	2.66	0.44
2:L:92:PHE:CE2	2:L:97:LEU:HD21	2.53	0.43
1:A:69:TYR:HA	1:A:313:ALA:HB1	2.00	0.43
2:L:161:LEU:HD21	3:H:175:VAL:HB	2.01	0.43
3:H:12:VAL:O	3:H:117:VAL:HA	2.18	0.43
1:A:502[B]:ARG:HH21	3:H:56:ARG:HH11	1.66	0.43
1:A:370:MET:HG2	1:A:374:LEU:HD22	2.01	0.43
1:A:51:TRP:HD1	1:A:52:ARG:N	2.16	0.42
2:L:52:THR:HG21	2:L:72:TYR:CE2	2.54	0.42
3:H:29:PHE:O	3:H:72:ARG:NH2	2.52	0.42
1:A:501:ASN:OD1	1:A:501:ASN:N	2.53	0.42
2:L:171:ASP:N	2:L:171:ASP:OD1	2.53	0.42
1:A:410:PHE:CZ	1:A:414:LEU:HD11	2.55	0.42
3:H:44:ARG:NH1	3:H:44:ARG:HG2	2.34	0.42
1:A:140:THR:HG22	1:A:142:SER:H	1.85	0.42
2:L:60:PRO:HG2	2:L:63:PHE:CD2	2.55	0.42
1:A:572:PRO:O	1:A:576:ILE:HG12	2.20	0.42
3:H:217:GLU:HA	3:H:218:PRO:HD3	1.93	0.41
3:H:19:LYS:HG3	3:H:82:GLU:HG3	2.01	0.41
2:L:92:PHE:CE1	3:H:102:ARG:HD3	2.56	0.41
3:H:5:VAL:HG23	3:H:23:ALA:HB3	2.02	0.41
1:A:595:THR:HA	1:A:596:PRO:HD3	1.89	0.41
1:A:56:LEU:HA	1:A:56:LEU:HD23	1.87	0.41
1:A:134:PHE:HB3	1:A:411:PHE:CE2	2.56	0.41
7:A:605:4IU:H8	7:A:605:4IU:H7	1.86	0.41
2:L:116:VAL:HG21	2:L:206:ILE:HD13	2.03	0.41
3:H:19:LYS:NZ	3:H:82:GLU:HB2	2.34	0.41
1:A:95:ALA:HA	1:A:329:LEU:HD23	2.02	0.41
1:A:145:TRP:HB2	1:A:212:ALA:HA	2.03	0.41
1:A:115:LEU:HB3	8:A:706:HOH:O	2.20	0.41
6:A:604:CLR:H211	6:A:604:CLR:H232	1.78	0.41
3:H:161:ASN:OD1	3:H:200:THR:N	2.33	0.41
1:A:486:ALA:O	1:A:490:GLU:HG3	2.20	0.41
1:A:316:GLN:NE2	5:A:603:CL:CL	2.84	0.41
2:L:36:TRP:HB2	2:L:49:ILE:HB	2.01	0.40
1:A:420:ASP:HA	1:A:423:PHE:CD2	2.57	0.40
1:A:251:TYR:O	1:A:255:TRP:HD1	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	532/532 (100%)	516 (97%)	16 (3%)	0	100	100
2	L	212/214 (99%)	205 (97%)	7 (3%)	0	100	100
3	H	212/240 (88%)	203 (96%)	9 (4%)	0	100	100
All	All	956/986 (97%)	924 (97%)	32 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	425/437 (97%)	421 (99%)	4 (1%)	84	95
2	L	182/187 (97%)	181 (100%)	1 (0%)	92	98
3	H	171/205 (83%)	169 (99%)	2 (1%)	78	93
All	All	778/829 (94%)	771 (99%)	7 (1%)	84	95

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	ASP
1	A	51	TRP
1	A	581	SER
1	A	582	THR
2	L	92	PHE

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Mol	Chain	Res	Type
3	H	44	ARG
3	H	215	LYS

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

Mol	Chain	Res	Type
2	L	158	ASN

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](#)

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 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	$\# Z > 2$
6	CLR	A	604	-	31,31,31	0.62	0	48,48,48	1.05	3 (6%)
7	41U	A	605	-	20,21,21	0.55	0	23,26,26	1.31	6 (26%)

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
6	CLR	A	604	-	-	0/10/68/68	0/4/4/4
7	41U	A	605	-	-	0/14/14/14	0/2/2/2

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	604	CLR	C14-C8-C9	-2.38	105.93	109.06
7	A	605	41U	C14-C7-C8	-2.27	108.84	112.98
7	A	605	41U	O1-C5-C4	-2.09	120.83	124.35
7	A	605	41U	O-C7-C8	2.24	114.23	110.26
7	A	605	41U	O1-C5-C	2.40	118.83	115.40
7	A	605	41U	O-C7-C14	2.55	110.88	105.40
7	A	605	41U	C16-N-C15	2.66	120.02	112.23
6	A	604	CLR	C4-C5-C10	2.71	120.38	116.43
6	A	604	CLR	C7-C8-C9	2.75	113.46	109.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	604	CLR	3	0
7	A	605	41U	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	H	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	134:CYS	C	138:THR	N	8.43

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	532/532 (100%)	0.47	30 (5%) 28 14	66, 85, 109, 145	0
2	L	214/214 (100%)	0.69	26 (12%) 6 3	57, 77, 110, 146	0
3	H	216/240 (90%)	0.47	20 (9%) 11 5	61, 85, 114, 134	0
All	All	962/986 (97%)	0.52	76 (7%) 15 7	57, 84, 111, 146	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	123	SER	7.2
2	L	126	LEU	5.5
2	L	127	THR	4.7
3	H	129	PRO	4.7
2	L	136	PHE	4.7
2	L	118	ILE	4.6
1	A	439	LYS	4.6
1	A	437	PHE	4.6
1	A	291	LEU	4.5
2	L	119	PHE	4.5
2	L	122	SER	4.3
1	A	290[A]	PHE	4.3
2	L	134	VAL	4.3
3	H	130	LEU	4.0
3	H	144	LEU	3.9
3	H	199	ILE	3.9
2	L	135	CYS	3.9
1	A	540	ILE	3.7
2	L	57	SER	3.7
2	L	213	ASN	3.6
2	L	130	GLY	3.6
3	H	127	VAL	3.5
3	H	79	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
3	H	128	TYR	3.5
1	A	586	LEU	3.3
1	A	375	GLY	3.2
1	A	440	ILE	3.2
3	H	131	ALA	3.1
2	L	124	GLU	3.1
3	H	138	THR	3.1
1	A	492	ILE	3.1
3	H	147	LEU	3.1
1	A	237	TRP	3.0
1	A	590	PHE	3.0
1	A	111	TYR	2.9
1	A	438	PRO	2.9
1	A	105	LEU	2.9
2	L	137	LEU	2.8
3	H	214	LYS	2.8
1	A	496	TRP	2.7
1	A	229	ILE	2.7
1	A	497	ILE	2.7
3	H	100	GLU	2.7
1	A	481	TYR	2.6
1	A	346	LEU	2.6
2	L	151	ILE	2.5
1	A	580	LEU	2.5
3	H	108	TYR	2.5
2	L	95	TYR	2.5
1	A	461	ALA	2.4
3	H	198	SER	2.4
1	A	555	TRP	2.4
2	L	117	SER	2.4
2	L	210	PHE	2.4
2	L	128	SER	2.4
1	A	579	LEU	2.3
1	A	433	LEU	2.3
2	L	176	MET	2.3
3	H	211	LYS	2.3
3	H	142	VAL	2.3
1	A	372	HIS	2.3
1	A	576	ILE	2.3
3	H	215	LYS	2.3
2	L	212	ARG	2.2
2	L	161	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
2	L	94	GLY	2.1
3	H	189	VAL	2.1
1	A	353	SER	2.1
1	A	96	ILE	2.1
1	A	583	PRO	2.0
2	L	48	TRP	2.0
3	H	34	MET	2.0
2	L	185	ASP	2.0
2	L	133	VAL	2.0
3	H	196	SER	2.0
1	A	141	ASN	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
6	CLR	A	604	28/28	0.88	0.72	9.23	84,97,109,113	0
4	NA	A	601	1/1	0.94	0.33	2.34	84,84,84,84	0
7	41U	A	605	20/20	0.93	0.33	1.48	88,94,111,113	0
4	NA	A	602	1/1	0.90	0.23	-2.76	70,70,70,70	0
5	CL	A	603	1/1	0.96	0.15	-4.44	74,74,74,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.