



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 11:53 AM GMT

PDB ID : 1JDP
Title : Crystal Structure of Hormone/Receptor Complex
Authors : He, X.-L.; Chow, D.-C.; Martick, M.M.; Garcia, K.C.
Deposited on : 2001-06-14
Resolution : 2.00 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

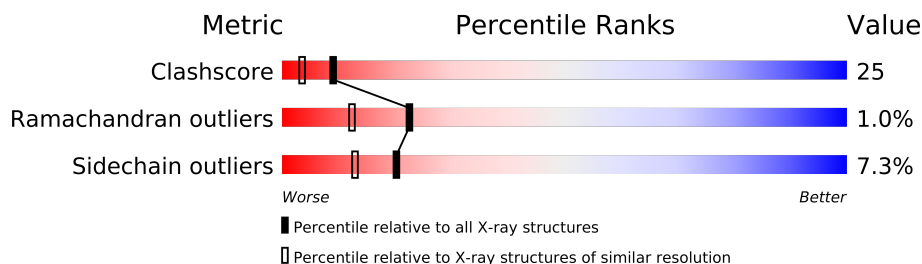
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.00 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))
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	441	
1	B	441	
2	H	22	

2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 7041 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

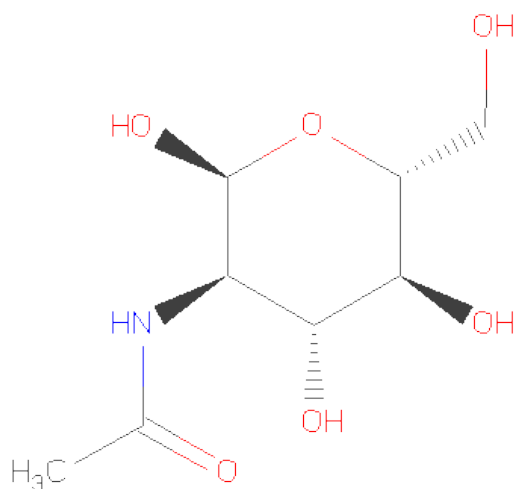
- Molecule 1 is a protein called ATRIAL NATRIURETIC PEPTIDE CLEARANCE RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	396	Total	C	N	O	S	0	0	0
			3130	1983	537	594	16			
1	B	395	Total	C	N	O	S	0	0	0
			3121	1978	536	591	16			

- Molecule 2 is a protein called C-TYPE NATRIURETIC PEPTIDE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	18	Total	C	N	O	S	0	18	0
			248	152	44	46	6			

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NDG) (formula: $C_8H_{15}NO_6$).

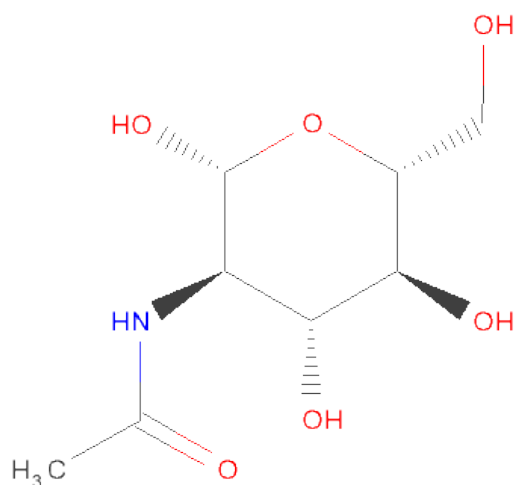


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Cl	0	0
			1	1		
6	A	1	Total	Cl	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	217	Total 217	O 217	0	0
7	B	238	Total 238	O 238	0	0
7	H	15	Total 15	O 15	0	0

Chain H: 

GLY	LEU	SER	LYS	G5	C6	F7	G8	L9	K10	L11	D12	R13	I14	G15	S16	S17	S18	G19	L20	G21	C22
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4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	56.80Å 136.46Å 137.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.00	Depositor
% Data completeness (in resolution range)	97.7 (50.00-2.00)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.227 , 0.248	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7041	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, NDG, CL

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	0.45	0/3199	0.70	2/4323 (0.0%)
1	B	0.46	0/3190	0.71	2/4311 (0.0%)
2	H	0.45	0/248	0.88	2/320 (0.6%)
All	All	0.46	0/6637	0.71	6/8954 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	166	ARG	NE-CZ-NH1	-7.79	116.41	120.30
1	A	127	SER	N-CA-C	-5.48	96.21	111.00
2	H	11[A]	LEU	CA-CB-CG	5.39	127.69	115.30
2	H	11[B]	LEU	CA-CB-CG	5.39	127.69	115.30
1	A	100	ARG	NE-CZ-NH1	-5.08	117.76	120.30
1	B	274	LEU	CA-CB-CG	5.08	126.99	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3130	0	3035	144	0
1	B	3121	0	3027	128	0
2	H	248	0	248	115	0
3	A	28	0	26	8	0
4	B	28	0	25	0	0
5	B	14	0	13	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	217	0	0	17	0
7	B	238	0	0	9	0
7	H	15	0	0	5	0
All	All	7041	0	6374	326	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 25.

All (326) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:21:LEU:HD21	3:A:501:NDG:C8	1.82	1.10
1:A:21:LEU:HD21	3:A:501:NDG:H8C2	1.14	1.07
1:A:163:LYS:HE2	2:H:10[B]:LYS:HG3	1.05	1.04
1:B:163:LYS:HG3	2:H:10[A]:LYS:HB2	1.40	1.03
1:B:163:LYS:NZ	2:H:10[A]:LYS:HE2	1.76	1.00
1:A:163:LYS:CE	2:H:10[B]:LYS:HG3	1.91	0.99
1:B:100:ARG:HH22	2:H:16[A]:SER:HB2	1.32	0.94
1:A:163:LYS:HG3	2:H:10[B]:LYS:HB2	1.50	0.93
1:A:21:LEU:CD2	3:A:501:NDG:H8C2	2.00	0.91
1:B:100:ARG:HH22	2:H:16[A]:SER:CB	1.84	0.91
1:A:163:LYS:HE2	2:H:10[B]:LYS:CG	1.97	0.90
1:A:248:ASN:ND2	3:A:501:NDG:H8C1	1.87	0.88
1:A:204:ARG:HH12	1:A:232:HIS:HE1	1.21	0.88
1:B:100:ARG:HH12	2:H:16[A]:SER:C	1.77	0.87
1:B:163:LYS:HZ1	2:H:10[A]:LYS:HE2	1.40	0.87
1:B:38:VAL:HG21	1:B:324:VAL:HG21	1.55	0.86
1:A:100:ARG:HH12	2:H:16[B]:SER:CA	1.87	0.86
1:A:100:ARG:HH12	2:H:16[B]:SER:CB	1.89	0.85
2:H:11[A]:LEU:CD2	2:H:14[A]:ILE:HB	2.06	0.85
2:H:11[B]:LEU:CD2	2:H:14[B]:ILE:HB	2.07	0.85
1:A:100:ARG:HH12	2:H:16[B]:SER:HA	1.46	0.81
1:B:163:LYS:HA	1:B:166:ARG:HD3	1.63	0.80
1:B:163:LYS:HG3	2:H:10[A]:LYS:CB	2.11	0.80
1:A:100:ARG:HD3	1:A:125:GLU:OE2	1.81	0.79
1:B:163:LYS:CE	2:H:10[A]:LYS:HG3	2.13	0.79

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:100:ARG:HH12	2:H:16[B]:SER:HB2	1.47	0.79
1:A:128:HIS:HA	1:A:344:ILE:HG13	1.65	0.79
1:B:148:ARG:HG3	1:B:148:ARG:HH21	1.48	0.78
1:A:284:LYS:HE3	1:A:357:GLY:HA2	1.67	0.77
2:H:11[B]:LEU:HD22	2:H:14[B]:ILE:HB	1.68	0.75
2:H:13[A]:ARG:HH21	2:H:13[A]:ARG:HG2	1.50	0.75
2:H:13[B]:ARG:HG2	2:H:13[B]:ARG:HH21	1.51	0.74
1:B:130:THR:HG21	1:B:347:THR:OG1	1.88	0.74
1:A:163:LYS:HB3	2:H:11[B]:LEU:H	1.52	0.74
2:H:11[A]:LEU:HD22	2:H:14[A]:ILE:HB	1.68	0.73
1:A:31:ILE:HG23	1:A:320:ILE:CD1	2.17	0.73
2:H:20[A]:LEU:HG	2:H:21[A]:GLY:N	2.04	0.73
1:A:159:TYR:HB3	1:A:172:LEU:HD22	1.71	0.73
2:H:20[B]:LEU:HG	2:H:21[B]:GLY:N	2.03	0.72
1:A:193:GLU:HA	1:A:197:LEU:HD21	1.72	0.71
1:A:127:SER:O	1:A:128:HIS:HB2	1.89	0.71
1:B:163:LYS:CD	2:H:10[A]:LYS:HG3	2.20	0.71
1:B:130:THR:HG22	1:B:348:TRP:HE1	1.56	0.70
1:A:100:ARG:NH1	2:H:16[B]:SER:HA	2.05	0.70
1:B:230:HIS:CD2	1:B:266:GLU:HG3	2.27	0.70
1:A:198:ASP:OD2	1:A:201:ASP:HB2	1.91	0.70
1:A:3:LEU:HB3	1:A:4:PRO:HD2	1.74	0.69
1:B:215:MET:CE	1:B:225:ILE:HG21	2.23	0.69
1:B:161:ASP:OD2	1:B:166:ARG:HD2	1.93	0.68
1:B:290:PHE:O	1:B:294:VAL:HG23	1.93	0.68
1:B:202:ILE:HG21	1:B:225:ILE:HD12	1.74	0.68
1:A:47:LEU:O	1:A:328:HIS:ND1	2.20	0.68
1:A:289:LYS:HE2	1:A:293:GLU:OE2	1.94	0.68
1:A:163:LYS:NZ	2:H:10[B]:LYS:HE2	2.09	0.67
1:B:40:GLY:O	1:B:46:ARG:HG2	1.95	0.67
1:B:325:LEU:O	1:B:329:GLU:HG2	1.94	0.67
1:A:258:LYS:HD3	1:A:259:ARG:N	2.09	0.67
1:A:187:SER:C	1:A:188:ILE:HD12	2.16	0.67
1:B:327:LEU:O	1:B:330:VAL:HG12	1.95	0.66
1:B:100:ARG:HH22	2:H:16[A]:SER:CA	2.08	0.66
1:A:48:LEU:HD13	1:A:324:VAL:HG13	1.76	0.66
1:B:166:ARG:HH11	2:H:14[B]:ILE:HD11	1.60	0.66
1:A:100:ARG:NH1	2:H:16[B]:SER:HB2	2.09	0.66
1:A:188:ILE:HB	2:H:5[A]:GLY:HA2	1.78	0.66
1:A:10:VAL:CG2	1:A:56:VAL:HG22	2.26	0.65
1:A:177:GLU:OE1	2:H:9[A]:LEU:HB3	1.96	0.65
1:A:306:GLU:CD	1:A:306:GLU:H	1.98	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:163:LYS:HG3	2:H:10[A]:LYS:HG3	1.79	0.65
1:A:31:ILE:HG23	1:A:320:ILE:HD11	1.79	0.65
1:B:227:LEU:HD22	1:B:266:GLU:HG2	1.79	0.64
1:A:204:ARG:HH11	1:A:204:ARG:HG3	1.62	0.64
1:B:148:ARG:NH2	1:B:148:ARG:HG3	2.10	0.64
1:A:401:PRO:HD2	7:A:648:HOH:O	1.97	0.63
1:B:161:ASP:OD1	1:B:163:LYS:HE3	1.99	0.63
1:B:166:ARG:NH1	2:H:14[B]:ILE:HD11	2.12	0.63
1:B:3:LEU:HD23	1:B:4:PRO:HD2	1.79	0.62
1:B:227:LEU:CD2	1:B:266:GLU:HG2	2.30	0.62
1:A:48:LEU:HD23	1:A:52:THR:HG21	1.80	0.62
3:A:501:NDG:H8C1	3:A:501:NDG:C1	2.28	0.62
1:A:163:LYS:HG3	2:H:10[B]:LYS:CB	2.29	0.62
1:B:100:ARG:HH12	2:H:17[A]:MET:N	1.97	0.61
1:A:35:LEU:HD13	1:A:320:ILE:HG21	1.81	0.61
1:B:176:HIS:CD2	2:H:7[B]:PHE:HB3	2.35	0.61
1:A:170:PHE:CE1	2:H:14[A]:ILE:HD13	2.34	0.61
1:B:100:ARG:HH12	2:H:16[A]:SER:CA	2.13	0.61
1:A:325:LEU:O	1:A:329:GLU:HG3	2.00	0.61
2:H:18[B]:SER:HB3	7:H:152:HOH:O	2.00	0.61
1:B:28:ARG:HB3	1:B:29:PRO:HD3	1.82	0.60
2:H:8[A]:GLY:C	2:H:10[A]:LYS:HD2	2.21	0.60
1:B:96:ALA:HB3	1:B:97:PRO:HD3	1.83	0.60
1:A:262:LYS:HG2	1:A:262:LYS:O	2.00	0.60
1:B:163:LYS:HG3	2:H:10[A]:LYS:CG	2.31	0.60
1:B:215:MET:HE1	1:B:225:ILE:HG21	1.84	0.60
1:B:18:ASP:OD1	1:B:303:LEU:HD11	2.00	0.60
1:B:295:LYS:O	1:B:299:GLU:HG3	2.02	0.60
1:A:394:GLU:OE1	1:A:396:ARG:NH1	2.35	0.59
2:H:8[B]:GLY:C	2:H:10[B]:LYS:HD2	2.21	0.59
1:B:163:LYS:CG	2:H:10[A]:LYS:HG3	2.33	0.58
1:A:10:VAL:HG23	1:A:56:VAL:HG13	1.85	0.58
1:A:163:LYS:HZ3	2:H:10[B]:LYS:HE2	1.67	0.58
1:B:3:LEU:HD22	1:B:49:PRO:HG2	1.85	0.58
1:B:117:ALA:O	1:B:120:GLN:HB2	2.03	0.58
1:B:161:ASP:OD2	1:B:166:ARG:CD	2.51	0.58
1:B:192:ASP:OD1	1:B:194:THR:HB	2.03	0.58
1:B:100:ARG:NH2	2:H:16[A]:SER:HB2	2.11	0.58
1:B:215:MET:HE3	1:B:225:ILE:HG21	1.85	0.58
1:A:25:THR:HG23	7:A:603:HOH:O	2.03	0.58
1:B:309:VAL:HG11	1:B:313:VAL:HG11	1.86	0.58
1:B:100:ARG:NH1	2:H:16[A]:SER:HA	2.19	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:100:ARG:NH2	2:H:16[A]:SER:HA	2.18	0.58
1:B:39:GLU:OE1	1:B:53:ARG:NH1	2.36	0.58
1:A:330:VAL:CG1	1:A:335:TYR:HB2	2.33	0.58
7:A:621:HOH:O	2:H:9[A]:LEU:HD13	2.03	0.57
1:A:176:HIS:CD2	2:H:7[A]:PHE:HB3	2.39	0.57
1:A:100:ARG:NH1	2:H:16[B]:SER:CB	2.62	0.57
1:B:123:ASP:HB2	7:B:660:HOH:O	2.04	0.57
1:B:394:GLU:HG3	7:B:667:HOH:O	2.04	0.57
1:A:7:LYS:HE3	1:A:53:ARG:HD2	1.85	0.57
1:B:170:PHE:CE1	2:H:14[B]:ILE:HD13	2.39	0.57
1:B:38:VAL:CG2	1:B:324:VAL:HG21	2.29	0.57
1:B:3:LEU:HD23	1:B:4:PRO:CD	2.34	0.57
2:H:14[A]:ILE:HG23	2:H:14[A]:ILE:O	2.05	0.57
1:A:204:ARG:HH12	1:A:232:HIS:CE1	2.12	0.56
2:H:14[B]:ILE:O	2:H:14[B]:ILE:HG23	2.05	0.56
1:A:290:PHE:O	1:A:294:VAL:HG23	2.04	0.56
1:A:68:LEU:HD23	7:A:659:HOH:O	2.04	0.56
2:H:13[A]:ARG:NH2	7:H:310:HOH:O	2.38	0.56
1:A:10:VAL:HG22	1:A:56:VAL:HG22	1.88	0.56
2:H:18[A]:SER:HB3	7:H:269:HOH:O	2.06	0.56
1:A:284:LYS:CE	1:A:357:GLY:HA2	2.34	0.55
1:A:132:VAL:O	1:A:367:ARG:HD2	2.06	0.55
1:A:298:VAL:HG12	1:A:303:LEU:HB2	1.88	0.55
7:B:640:HOH:O	2:H:17[A]:MET:HA	2.07	0.55
1:A:163:LYS:HD3	7:A:641:HOH:O	2.07	0.55
1:B:100:ARG:HH22	2:H:16[A]:SER:HA	1.72	0.55
1:A:100:ARG:HD2	1:B:65:ASN:ND2	2.23	0.54
1:B:386:VAL:HG11	1:B:400:ARG:CZ	2.38	0.54
1:B:231:ARG:HG3	7:B:681:HOH:O	2.07	0.54
1:B:46:ARG:NH1	1:B:50:PRO:HB3	2.23	0.54
1:A:258:LYS:HD3	1:A:260:GLY:H	1.73	0.54
1:A:48:LEU:CD1	1:A:324:VAL:HG13	2.38	0.54
1:B:163:LYS:CE	2:H:10[A]:LYS:HE2	2.36	0.53
1:A:166:ARG:NH2	2:H:14[A]:ILE:HD11	2.24	0.53
1:B:163:LYS:NZ	2:H:10[A]:LYS:CE	2.64	0.53
1:A:352:PHE:HE1	1:A:361:ILE:HD11	1.72	0.53
1:B:163:LYS:HZ3	2:H:10[A]:LYS:HE2	1.68	0.53
1:A:204:ARG:HG3	1:A:204:ARG:NH1	2.24	0.53
1:B:330:VAL:HG22	1:B:335:TYR:HB2	1.89	0.53
1:A:215:MET:CE	1:A:225:ILE:HG21	2.39	0.53
1:A:127:SER:O	1:A:128:HIS:CB	2.57	0.52
1:B:134:PRO:HD2	7:B:549:HOH:O	2.10	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:501:NDG:C8	3:A:501:NDG:C1	2.85	0.52
1:B:331:LEU:HD12	1:B:335:TYR:O	2.10	0.52
1:B:31:ILE:HG22	1:B:35:LEU:HD22	1.92	0.52
1:B:130:THR:HG22	1:B:344:ILE:HG23	1.91	0.52
1:B:275:GLN:HG2	1:B:375:ALA:HB2	1.90	0.52
1:A:295:LYS:HE3	1:A:299:GLU:OE1	2.09	0.52
1:B:100:ARG:HH12	2:H:16[A]:SER:HA	1.73	0.52
1:A:252:TYR:C	1:A:254:ASP:H	2.13	0.51
1:B:200:GLU:HG3	1:B:204:ARG:NE	2.24	0.51
1:A:159:TYR:HB3	1:A:172:LEU:CD2	2.40	0.51
1:A:132:VAL:O	1:A:367:ARG:CD	2.58	0.51
1:A:284:LYS:HE3	1:A:357:GLY:CA	2.39	0.51
1:A:10:VAL:CG2	1:A:56:VAL:HG13	2.40	0.51
1:B:163:LYS:HE2	2:H:10[A]:LYS:HG3	1.90	0.51
1:A:35:LEU:HA	1:A:38:VAL:HG22	1.92	0.51
1:A:204:ARG:NH1	1:A:232:HIS:HE1	2.00	0.50
1:A:295:LYS:HG3	1:A:305:MET:HE2	1.93	0.50
1:A:275:GLN:HG2	1:A:375:ALA:HB2	1.93	0.50
1:A:10:VAL:HG21	1:A:56:VAL:HG22	1.93	0.50
1:B:130:THR:HG23	1:B:344:ILE:HD12	1.93	0.50
1:A:85:LEU:HG	1:A:323:TYR:CD1	2.47	0.50
1:A:39:GLU:O	1:A:39:GLU:HG3	2.12	0.50
2:H:16[A]:SER:O	2:H:17[A]:MET:CB	2.60	0.50
1:A:144:LEU:HD11	1:A:182:GLU:HG3	1.94	0.50
1:A:74:ARG:HD3	7:A:596:HOH:O	2.11	0.50
2:H:13[A]:ARG:HH21	2:H:13[A]:ARG:CG	2.24	0.49
1:A:173:GLU:HB2	2:H:7[A]:PHE:CE1	2.47	0.49
1:A:142:MET:HB2	1:A:390:TYR:CD2	2.46	0.49
1:A:317:HIS:HE1	1:A:321:LEU:HD11	1.78	0.49
1:B:28:ARG:HG3	1:B:58:TYR:CZ	2.47	0.49
1:A:233:GLY:HA2	7:A:551:HOH:O	2.12	0.49
2:H:16[B]:SER:O	2:H:17[B]:MET:CB	2.60	0.49
1:A:335:TYR:HB3	1:A:339:ASP:OD1	2.13	0.49
1:B:73:ASP:O	1:B:77:ALA:HB2	2.13	0.49
1:B:100:ARG:CZ	2:H:16[A]:SER:HA	2.43	0.49
1:A:330:VAL:HG12	1:A:335:TYR:HB2	1.95	0.49
1:A:21:LEU:HD21	3:A:501:NDG:H8C3	1.87	0.48
1:B:46:ARG:CZ	1:B:50:PRO:HB3	2.43	0.48
1:A:261:ASP:OD2	1:A:262:LYS:N	2.44	0.48
1:B:30:ALA:HB2	1:B:313:VAL:HG13	1.95	0.48
1:B:188:ILE:HB	2:H:5[B]:GLY:HA2	1.95	0.48
1:A:332:ARG:HD2	1:A:332:ARG:N	2.29	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:74:ARG:NH1	7:B:535:HOH:O	2.41	0.48
1:B:387:ILE:HG23	1:B:399:MET:CE	2.44	0.47
1:A:57:ALA:HB1	1:A:74:ARG:NH2	2.30	0.47
1:A:100:ARG:HG2	1:A:125:GLU:HG3	1.97	0.47
2:H:13[B]:ARG:CG	2:H:13[B]:ARG:HH21	2.25	0.47
1:A:163:LYS:CG	2:H:10[B]:LYS:HB2	2.33	0.47
1:B:377:THR:CG2	1:B:387:ILE:HD11	2.45	0.47
1:A:151:HIS:HE1	7:A:544:HOH:O	1.98	0.47
1:B:142:MET:HG3	1:B:371:PHE:HB2	1.97	0.47
2:H:12[B]:ASP:OD1	2:H:12[B]:ASP:C	2.54	0.46
1:B:321:LEU:O	1:B:325:LEU:HD13	2.15	0.46
1:A:215:MET:HE1	1:A:225:ILE:HG21	1.97	0.46
1:A:158:VAL:HB	1:A:215:MET:HG2	1.97	0.46
2:H:12[A]:ASP:C	2:H:12[A]:ASP:OD1	2.52	0.46
1:A:163:LYS:HD2	1:A:163:LYS:N	2.31	0.46
1:B:148:ARG:NH1	1:B:182:GLU:OE1	2.38	0.46
7:B:641:HOH:O	2:H:22[A]:CYS:HA	2.16	0.46
1:A:1:GLU:O	1:A:2:ALA:C	2.54	0.46
1:A:3:LEU:HA	7:A:647:HOH:O	2.14	0.46
2:H:13[B]:ARG:O	2:H:15[B]:GLY:N	2.49	0.46
1:B:294:VAL:HG11	1:B:309:VAL:HG11	1.98	0.46
1:A:325:LEU:HD13	7:A:609:HOH:O	2.16	0.45
2:H:12[A]:ASP:C	2:H:14[A]:ILE:H	2.19	0.45
1:A:170:PHE:HE1	2:H:14[A]:ILE:HD13	1.81	0.45
1:A:35:LEU:O	1:A:38:VAL:HG22	2.17	0.45
1:B:113:GLY:C	1:B:115:LEU:HD13	2.37	0.45
2:H:12[B]:ASP:O	2:H:14[B]:ILE:N	2.50	0.45
2:H:12[A]:ASP:O	2:H:14[A]:ILE:N	2.50	0.45
1:B:261:ASP:HB3	1:B:263:HIS:H	1.82	0.45
1:A:28:ARG:HB3	1:A:29:PRO:HD3	1.98	0.45
2:H:8[A]:GLY:O	2:H:10[A]:LYS:HD2	2.16	0.45
1:A:3:LEU:HD23	7:A:647:HOH:O	2.16	0.45
1:A:370:ASP:OD1	1:A:391:PHE:HA	2.16	0.45
2:H:13[A]:ARG:O	2:H:15[A]:GLY:N	2.50	0.44
2:H:8[B]:GLY:O	2:H:10[B]:LYS:HD2	2.17	0.44
2:H:8[B]:GLY:O	2:H:9[B]:LEU:C	2.56	0.44
1:B:166:ARG:NH1	2:H:14[B]:ILE:CD1	2.78	0.44
1:A:188:ILE:HD12	1:A:188:ILE:N	2.32	0.44
1:B:163:LYS:NZ	2:H:10[A]:LYS:HG3	2.32	0.44
2:H:12[B]:ASP:C	2:H:14[B]:ILE:H	2.19	0.44
2:H:8[A]:GLY:O	2:H:9[A]:LEU:C	2.56	0.44
1:B:144:LEU:HD11	1:B:148:ARG:NH1	2.33	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:235:THR:O	1:B:236:SER:CB	2.65	0.44
1:A:139:MET:HE2	1:A:244:ILE:HG21	1.99	0.44
1:A:79:ARG:NH1	1:B:78:ALA:O	2.51	0.44
1:B:194:THR:HG22	1:B:194:THR:O	2.18	0.44
1:A:330:VAL:HG13	1:A:335:TYR:HB2	2.00	0.44
1:B:393:LYS:HB3	7:B:667:HOH:O	2.18	0.44
2:H:13[A]:ARG:HG2	2:H:13[A]:ARG:NH2	2.24	0.43
1:A:298:VAL:CG1	1:A:303:LEU:HB2	2.47	0.43
1:A:72:VAL:HG11	1:B:105:TRP:CZ2	2.53	0.43
1:B:332:ARG:HH11	1:B:332:ARG:HG2	1.83	0.43
1:A:160:SER:HA	1:A:191:PHE:O	2.17	0.43
1:A:398:GLU:HG3	7:A:558:HOH:O	2.18	0.43
1:A:211:ARG:HD2	7:A:690:HOH:O	2.17	0.43
1:A:18:ASP:OD2	1:A:303:LEU:HD11	2.18	0.43
1:B:106:ASP:O	1:B:340:GLY:HA3	2.17	0.43
1:B:199:LEU:HB3	1:B:228:VAL:HG21	2.00	0.43
1:A:223:ARG:CZ	1:A:259:ARG:HG3	2.48	0.43
1:B:75:VAL:CG1	1:B:82:LYS:HD3	2.48	0.43
2:H:16[B]:SER:O	2:H:17[B]:MET:HB2	2.19	0.43
1:A:204:ARG:HA	1:A:207:GLN:HG2	2.00	0.43
1:A:31:ILE:HG23	1:A:320:ILE:HD12	2.00	0.43
1:B:227:LEU:HA	1:B:227:LEU:HD23	1.85	0.43
2:H:18[A]:SER:CB	7:H:269:HOH:O	2.66	0.43
1:B:396:ARG:NH1	1:B:398:GLU:OE1	2.44	0.43
1:B:130:THR:CG2	1:B:344:ILE:HD12	2.49	0.43
1:B:173:GLU:HB2	2:H:7[B]:PHE:CE1	2.54	0.43
1:A:181:GLU:HG3	7:A:586:HOH:O	2.17	0.43
2:H:10[B]:LYS:HG2	2:H:11[B]:LEU:N	2.33	0.43
1:B:200:GLU:HG3	1:B:204:ARG:CZ	2.48	0.43
2:H:18[B]:SER:CB	7:H:152:HOH:O	2.65	0.42
1:A:294:VAL:O	1:A:298:VAL:HG23	2.19	0.42
3:A:502:NDG:C8	3:A:502:NDG:H3	2.49	0.42
1:A:117:ALA:O	1:A:120:GLN:HB2	2.19	0.42
1:A:3:LEU:HB3	1:A:4:PRO:CD	2.46	0.42
1:B:332:ARG:C	1:B:334:GLY:H	2.22	0.42
1:B:342:LYS:HD3	7:B:619:HOH:O	2.18	0.42
2:H:16[A]:SER:O	2:H:17[A]:MET:HB2	2.18	0.42
2:H:13[B]:ARG:NH2	2:H:13[B]:ARG:HG2	2.25	0.42
1:B:327:LEU:C	1:B:330:VAL:HG12	2.39	0.42
1:A:100:ARG:NH1	2:H:16[B]:SER:CA	2.66	0.42
1:A:97:PRO:HG3	7:A:574:HOH:O	2.19	0.42
1:B:346:GLN:O	1:B:350:ARG:HD2	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:162:ASP:HB3	1:A:164:LEU:HB2	2.02	0.42
1:B:163:LYS:HZ3	2:H:10[A]:LYS:HG3	1.85	0.42
1:B:28:ARG:HG3	1:B:58:TYR:CE2	2.55	0.42
1:A:24:LEU:HD22	1:A:58:TYR:HB3	2.02	0.42
2:H:10[A]:LYS:HG2	2:H:11[A]:LEU:N	2.33	0.42
1:A:215:MET:HE3	1:A:225:ILE:HG21	2.02	0.42
1:A:396:ARG:NH2	1:A:398:GLU:OE1	2.53	0.42
1:B:317:HIS:ND1	1:B:355:ILE:HG13	2.35	0.42
1:B:259:ARG:HB2	1:B:261:ASP:HB2	2.02	0.42
1:A:201:ASP:O	1:A:205:ASN:ND2	2.52	0.41
2:H:11[A]:LEU:CD2	2:H:11[A]:LEU:O	2.68	0.41
1:A:172:LEU:HA	1:A:172:LEU:HD12	1.71	0.41
1:A:286:GLU:N	1:A:286:GLU:OE2	2.39	0.41
1:A:59:GLU:HG2	1:A:70:SER:HB3	2.02	0.41
1:B:163:LYS:HB3	2:H:11[A]:LEU:H	1.85	0.41
1:A:10:VAL:HG22	1:A:56:VAL:HA	2.02	0.41
1:A:47:LEU:HD13	1:A:325:LEU:HD12	2.03	0.41
2:H:5[B]:GLY:C	2:H:7[B]:PHE:H	2.24	0.41
1:B:144:LEU:O	1:B:148:ARG:HG2	2.20	0.41
1:B:57:ALA:HB1	1:B:74:ARG:NH2	2.35	0.41
2:H:16[A]:SER:O	2:H:17[A]:MET:CG	2.68	0.41
1:B:329:GLU:H	1:B:329:GLU:HG2	1.45	0.41
2:H:18[B]:SER:O	2:H:19[B]:GLY:C	2.57	0.41
1:B:317:HIS:CE1	1:B:355:ILE:HG13	2.55	0.41
2:H:12[A]:ASP:OD1	2:H:12[A]:ASP:O	2.38	0.41
2:H:5[A]:GLY:C	2:H:7[A]:PHE:H	2.24	0.41
1:A:297:SER:O	1:A:301:GLN:HB2	2.21	0.41
1:B:93:TYR:CD1	2:H:15[B]:GLY:HA2	2.56	0.41
1:B:158:VAL:O	1:B:215:MET:HA	2.21	0.41
2:H:18[A]:SER:O	2:H:19[A]:GLY:C	2.57	0.41
7:A:585:HOH:O	2:H:22[B]:CYS:HA	2.19	0.41
1:B:228:VAL:O	1:B:232:HIS:HD2	2.04	0.41
1:A:308:TYR:O	1:A:309:VAL:C	2.58	0.41
1:B:194:THR:CG2	1:B:194:THR:O	2.68	0.41
1:A:295:LYS:HE3	1:A:299:GLU:CD	2.41	0.41
2:H:13[A]:ARG:NH2	2:H:13[A]:ARG:CG	2.82	0.40
1:A:252:TYR:C	1:A:254:ASP:N	2.75	0.40
2:H:6[B]:CYS:SG	2:H:22[B]:CYS:OXT	2.80	0.40
2:H:11[B]:LEU:CD2	2:H:11[B]:LEU:O	2.69	0.40
2:H:16[B]:SER:O	2:H:17[B]:MET:CG	2.68	0.40
1:B:10:VAL:HB	1:B:56:VAL:HG22	2.02	0.40
1:A:281:ARG:HH12	1:A:310:ASN:HA	1.85	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:150:HIS:O	1:B:151:HIS:HB2	2.21	0.40
1:B:100:ARG:NH1	2:H:17[A]:MET:N	2.68	0.40
1:B:38:VAL:CG1	1:B:39:GLU:N	2.85	0.40
1:B:8:ILE:HG23	1:B:84:ASP:HB2	2.03	0.40
1:A:348:TRP:CE2	1:A:365:GLY:HA3	2.56	0.40
1:A:166:ARG:HA	7:A:524:HOH:O	2.20	0.40
1:A:203:VAL:CG1	1:A:234:MET:SD	3.10	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	392/441 (89%)	377 (96%)	13 (3%)	2 (0%)	38	29
1	B	391/441 (89%)	373 (95%)	17 (4%)	1 (0%)	50	44
2	H	32/22 (146%)	10 (31%)	12 (38%)	10 (31%)	0	0
All	All	815/904 (90%)	760 (93%)	42 (5%)	13 (2%)	22	5

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	13[A]	ARG
2	H	13[B]	ARG
2	H	17[A]	MET
2	H	17[B]	MET
1	A	2	ALA
1	A	309	VAL
1	B	302	GLY
2	H	8[A]	GLY
2	H	8[B]	GLY
2	H	21[A]	GLY
2	H	21[B]	GLY
2	H	14[A]	ILE

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Mol	Chain	Res	Type
2	H	14[B]	ILE

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	331/371 (89%)	312 (94%)	19 (6%)	29	21
1	B	330/371 (89%)	306 (93%)	24 (7%)	20	13
2	H	26/16 (162%)	14 (54%)	12 (46%)	0	0
All	All	687/758 (91%)	632 (92%)	55 (8%)	20	10

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LEU
1	A	35	LEU
1	A	71	LEU
1	A	79	ARG
1	A	85	LEU
1	A	87	LEU
1	A	115	LEU
1	A	142	MET
1	A	144	LEU
1	A	172	LEU
1	A	200	GLU
1	A	210	GLU
1	A	262	LYS
1	A	264	ASP
1	A	304	ASN
1	A	308	TYR
1	A	331	LEU
1	A	332	ARG
1	A	350	ARG
1	B	11	LEU
1	B	35	LEU
1	B	38	VAL

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Mol	Chain	Res	Type
1	B	71	LEU
1	B	79	ARG
1	B	85	LEU
1	B	87	LEU
1	B	115	LEU
1	B	130	THR
1	B	142	MET
1	B	144	LEU
1	B	210	GLU
1	B	261	ASP
1	B	274	LEU
1	B	304	ASN
1	B	305	MET
1	B	306	GLU
1	B	307	ASP
1	B	308	TYR
1	B	309	VAL
1	B	329	GLU
1	B	331	LEU
1	B	367	ARG
1	B	387	ILE
2	H	6[A]	CYS
2	H	6[B]	CYS
2	H	9[A]	LEU
2	H	9[B]	LEU
2	H	10[A]	LYS
2	H	10[B]	LYS
2	H	13[A]	ARG
2	H	13[B]	ARG
2	H	17[A]	MET
2	H	17[B]	MET
2	H	22[A]	CYS
2	H	22[B]	CYS

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

Mol	Chain	Res	Type
1	A	232	HIS
1	B	151	HIS
1	B	232	HIS
1	B	304	ASN
1	B	345	GLN

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Mol	Chain	Res	Type
1	B	346	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

2 carbohydrates 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	$\# Z > 2$
4	NAG	B	501	1,4	12,14,15	0.59	0	15,19,21	0.76	0
4	NAG	B	502	4	12,14,15	0.49	0	15,19,21	0.70	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
4	NAG	B	501	1,4	-	0/6/23/26	0/1/1/1
4	NAG	B	502	4	-	0/6/23/26	0/1/1/1

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.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	NDG	A	501	1	12,14,15	0.39	0	15,19,21	0.68	0
3	NDG	A	502	1	12,14,15	0.54	0	15,19,21	0.88	0
5	NAG	B	503	1	12,14,15	0.55	0	15,19,21	0.80	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
3	NDG	A	501	1	-	2/6/23/26	0/1/1/1
3	NDG	A	502	1	-	0/6/23/26	0/1/1/1
5	NAG	B	503	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	NDG	C8-C7-N2-C2
3	A	501	NDG	O7-C7-N2-C2
5	B	503	NAG	O7-C7-N2-C2

There are no ring outliers.

5.7 Other polymers ⓘ

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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.