



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 7, 2023 – 09:49 AM EDT

PDB ID : 3U8K
Title : Crystal structure of the acetylcholine binding protein (AChBP) from *Lymnaea stagnalis* in complex with NS3573 (1-(5-ethoxypyridin-3-yl)-1,4-diazepane)
Authors : Rohde, L.A.H.; Ahring, P.K.; Jensen, M.L.; Nielsen, E.O.; Peters, D.; Helgstrand, C.; Krintel, C.; Harpsoe, K.; Gajhede, M.; Kastrup, J.S.; Balle, T.
Deposited on : 2011-10-17
Resolution : 2.47 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : **FAILED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

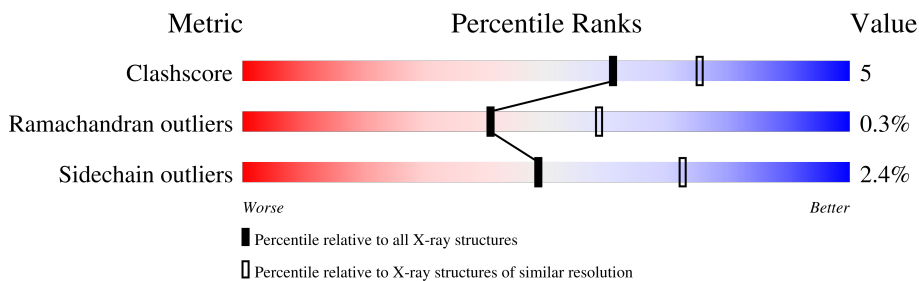
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.47 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	141614	6594 (2.50-2.46)
Ramachandran outliers	138981	6469 (2.50-2.46)
Sidechain outliers	138945	6471 (2.50-2.46)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	210	
1	B	210	
1	C	210	
1	D	210	
1	E	210	
1	F	210	
1	G	210	
1	H	210	

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Mol	Chain	Length	Quality of chain
1	I	210	 85% 9% 6%
1	J	210	 85% 11% .
1	K	210	 87% 9% .
1	L	210	 84% 10% . .
1	M	210	 90% 8% .
1	N	210	 85% 10% . .
1	O	210	 88% 7% 5%
1	P	210	 88% 7% . 5%
1	Q	210	 83% 11% 6%
1	R	210	 85% 10% .
1	S	210	 86% 8% 6%
1	T	210	 85% 11% . .

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 34188 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 Acetylcholine-binding protein.

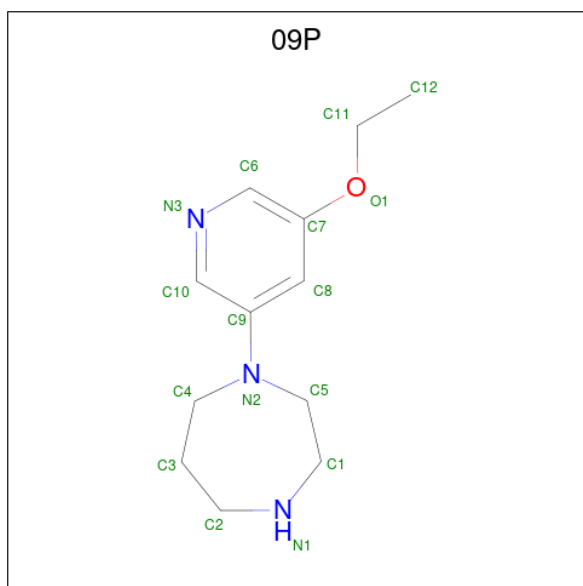
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	209	Total 1670	C 1043	N 287	O 335	S 5	0	0	0
1	B	200	Total 1598	C 1003	N 274	O 316	S 5	0	0	0
1	C	203	Total 1625	C 1018	N 277	O 324	S 6	0	1	0
1	D	203	Total 1630	C 1021	N 280	O 322	S 7	0	2	0
1	E	201	Total 1611	C 1010	N 275	O 320	S 6	0	1	0
1	F	203	Total 1624	C 1017	N 280	O 322	S 5	0	0	0
1	G	200	Total 1602	C 1005	N 274	O 318	S 5	0	0	0
1	H	208	Total 1662	C 1040	N 286	O 331	S 5	0	0	0
1	I	198	Total 1589	C 999	N 272	O 312	S 6	0	1	0
1	J	204	Total 1634	C 1023	N 278	O 326	S 7	0	2	0
1	K	203	Total 1629	C 1020	N 280	O 322	S 7	0	2	0
1	L	201	Total 1612	C 1011	N 275	O 320	S 6	0	1	0
1	M	207	Total 1661	C 1041	N 284	O 329	S 7	0	2	0
1	N	203	Total 1627	C 1021	N 280	O 320	S 6	0	1	0
1	O	199	Total 1590	C 999	N 273	O 313	S 5	0	0	0
1	P	200	Total 1604	C 1007	N 274	O 316	S 7	0	2	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	Q	198	Total 1585	C 997	N 269	O 312	S 7	0	2	0
1	R	201	Total 1612	C 1011	N 275	O 319	S 7	0	2	0
1	S	198	Total 1584	C 996	N 268	O 313	S 7	0	2	0
1	T	204	Total 1646	C 1030	N 284	O 325	S 7	0	3	0

- Molecule 2 is 1-(5-ethoxypyridin-3-yl)-1,4-diazepane (three-letter code: 09P) (formula: C₁₂H₁₉N₃O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	Total 16	C 12	N 3	O 1	0	0
2	B	1	Total 16	C 12	N 3	O 1	0	0
2	C	1	Total 16	C 12	N 3	O 1	0	0
2	D	1	Total 16	C 12	N 3	O 1	0	0
2	E	1	Total 16	C 12	N 3	O 1	0	0
2	F	1	Total 16	C 12	N 3	O 1	0	0
2	G	1	Total 16	C 12	N 3	O 1	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	H	1	Total	C	N	O	0	0
			16	12	3	1		
2	I	1	Total	C	N	O	0	0
			16	12	3	1		
2	J	1	Total	C	N	O	0	0
			16	12	3	1		
2	K	1	Total	C	N	O	0	0
			16	12	3	1		
2	L	1	Total	C	N	O	0	0
			16	12	3	1		
2	M	1	Total	C	N	O	0	0
			16	12	3	1		
2	N	1	Total	C	N	O	0	0
			16	12	3	1		
2	O	1	Total	C	N	O	0	0
			16	12	3	1		
2	P	1	Total	C	N	O	0	0
			16	12	3	1		
2	Q	1	Total	C	N	O	0	0
			16	12	3	1		
2	R	1	Total	C	N	O	0	0
			16	12	3	1		
2	S	1	Total	C	N	O	0	0
			16	12	3	1		
2	T	1	Total	C	N	O	0	0
			16	12	3	1		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 4 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	I	1	Total	O	S	0	0
			5	4	1		
4	K	1	Total	O	S	0	0
			5	4	1		
4	M	1	Total	O	S	0	0
			5	4	1		
4	N	1	Total	O	S	0	0
			5	4	1		
4	O	1	Total	O	S	0	0
			5	4	1		
4	P	1	Total	O	S	0	0
			5	4	1		
4	T	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	69	Total	O	0	0
			69	69		
5	B	69	Total	O	0	0
			69	69		
5	C	80	Total	O	0	0
			80	80		
5	D	80	Total	O	0	0
			80	80		
5	E	61	Total	O	0	0
			61	61		
5	F	81	Total	O	0	0
			81	81		
5	G	54	Total	O	0	0
			54	54		
5	H	50	Total	O	0	0
			50	50		
5	I	52	Total	O	0	0
			52	52		
5	J	62	Total	O	0	0
			62	62		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	K	62	Total O 62 62	0	0
5	L	63	Total O 63 63	0	0
5	M	83	Total O 83 83	0	0
5	N	73	Total O 73 73	0	0
5	O	59	Total O 59 59	0	0
5	P	73	Total O 73 73	0	0
5	Q	66	Total O 66 66	0	0
5	R	85	Total O 85 85	0	0
5	S	79	Total O 79 79	0	0
5	T	80	Total O 80 80	0	0

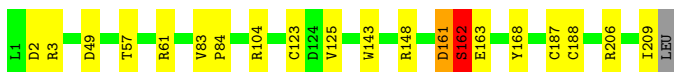
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

Note EDS failed to run properly.

- Molecule 1: Acetylcholine-binding protein

Chain A:  90% 9%




- Molecule 1: Acetylcholine-binding protein

Chain B:  86% 9% 5%




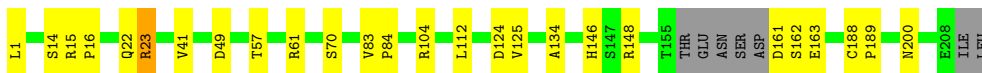
- Molecule 1: Acetylcholine-binding protein

Chain C:  85% 10% ..




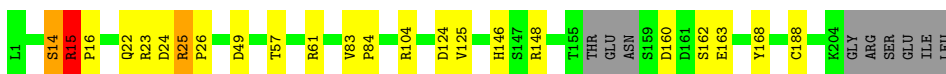
- Molecule 1: Acetylcholine-binding protein

Chain D:  84% 12% .




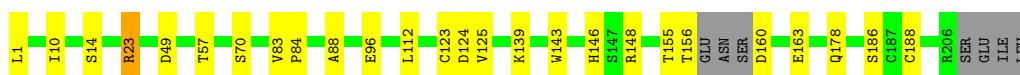
- Molecule 1: Acetylcholine-binding protein

Chain E:  85% 10% ..




- Molecule 1: Acetylcholine-binding protein

Chain F:  84% 12%




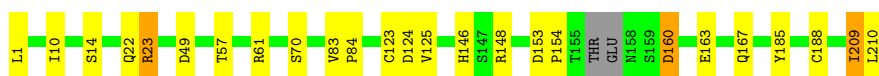
• Molecule 1: Acetylcholine-binding protein

Chain G:  87% 8% 5%




• Molecule 1: Acetylcholine-binding protein

Chain H:  87% 10%




• Molecule 1: Acetylcholine-binding protein

Chain I:  85% 9% 6%




• Molecule 1: Acetylcholine-binding protein

Chain J:  85% 11%




• Molecule 1: Acetylcholine-binding protein

Chain K:  87% 9%



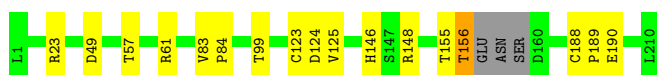
• Molecule 1: Acetylcholine-binding protein

Chain L:  84% 10%




• Molecule 1: Acetylcholine-binding protein

Chain M:  90% 8%




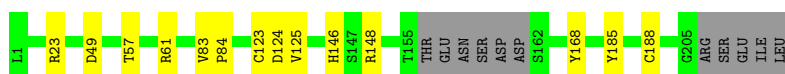
• Molecule 1: Acetylcholine-binding protein

Chain N:  85% 10%




• Molecule 1: Acetylcholine-binding protein

Chain O:  88% 7% 5%




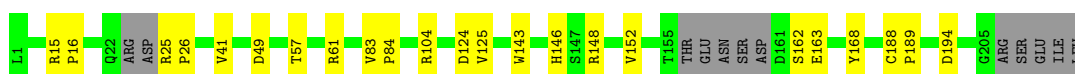
• Molecule 1: Acetylcholine-binding protein

Chain P:  88% 7% 5%




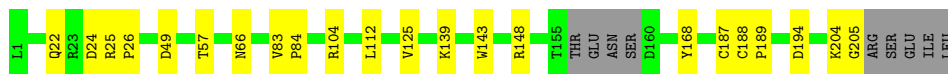
• Molecule 1: Acetylcholine-binding protein

Chain Q:  83% 11% 6%




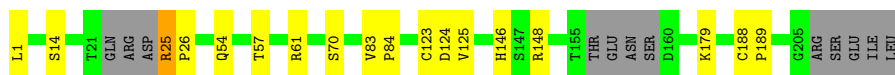
• Molecule 1: Acetylcholine-binding protein

Chain R:  85% 10%




• Molecule 1: Acetylcholine-binding protein

Chain S:  86% 8% 6%



• Molecule 1: Acetylcholine-binding protein

Chain T:  85% 11% ..



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	235.41Å 273.16Å 73.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	51.51 – 2.47	Depositor
% Data completeness (in resolution range)	98.9 (51.51-2.47)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.09 (at 2.48Å)	Xtrriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.196 , 0.236	Depositor
Wilson B-factor (Å ²)	28.4	Xtrriage
Anisotropy	0.413	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	34188	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.99% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, SO4, O9P

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	0.42	0/1706	0.53	0/2327
1	B	0.40	0/1633	0.52	0/2227
1	C	0.41	0/1663	0.52	0/2269
1	D	0.42	0/1671	0.52	0/2278
1	E	0.42	0/1649	0.53	0/2249
1	F	0.43	0/1659	0.52	0/2262
1	G	0.41	0/1637	0.55	0/2233
1	H	0.38	0/1697	0.53	0/2313
1	I	0.41	0/1627	0.53	0/2220
1	J	0.41	0/1675	0.54	0/2285
1	K	0.42	0/1670	0.55	0/2277
1	L	0.41	0/1650	0.54	0/2252
1	M	0.44	0/1702	0.55	0/2321
1	N	0.43	0/1665	0.54	0/2269
1	O	0.42	0/1625	0.53	0/2216
1	P	0.46	0/1645	0.56	0/2244
1	Q	0.45	0/1625	0.54	0/2216
1	R	0.46	0/1653	0.55	0/2255
1	S	0.44	0/1624	0.53	0/2215
1	T	0.44	0/1690	0.54	0/2303
All	All	0.42	0/33166	0.54	0/45231

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	E	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	22	GLN	Peptide

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	1670	0	1617	14	0
1	B	1598	0	1552	12	0
1	C	1625	0	1574	18	0
1	D	1630	0	1586	19	0
1	E	1611	0	1563	20	0
1	F	1624	0	1576	19	0
1	G	1602	0	1552	11	0
1	H	1662	0	1613	18	0
1	I	1589	0	1550	13	0
1	J	1634	0	1584	20	0
1	K	1629	0	1584	20	0
1	L	1612	0	1565	18	0
1	M	1661	0	1619	14	0
1	N	1627	0	1588	18	0
1	O	1590	0	1548	10	0
1	P	1604	0	1562	9	0
1	Q	1585	0	1544	13	0
1	R	1612	0	1564	14	0
1	S	1584	0	1540	13	0
1	T	1646	0	1603	19	0
2	A	16	0	19	0	0
2	B	16	0	19	2	0
2	C	16	0	19	2	0
2	D	16	0	19	1	0
2	E	16	0	19	1	0
2	F	16	0	19	3	0
2	G	16	0	19	1	0
2	H	16	0	19	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	I	16	0	19	4	0
2	J	16	0	19	2	0
2	K	16	0	19	1	0
2	L	16	0	19	1	0
2	M	16	0	19	0	0
2	N	16	0	19	2	0
2	O	16	0	19	1	0
2	P	16	0	19	2	0
2	Q	16	0	19	5	0
2	R	16	0	19	3	0
2	S	16	0	19	3	0
2	T	16	0	19	1	0
3	A	14	0	13	0	0
3	G	14	0	13	0	0
3	R	14	0	13	1	0
4	C	5	0	0	0	0
4	D	5	0	0	0	0
4	H	5	0	0	0	0
4	I	5	0	0	0	0
4	K	5	0	0	0	0
4	M	5	0	0	0	0
4	N	5	0	0	0	0
4	O	5	0	0	0	0
4	P	5	0	0	0	0
4	T	5	0	0	0	0
5	A	69	0	0	2	0
5	B	69	0	0	1	0
5	C	80	0	0	2	0
5	D	80	0	0	3	0
5	E	61	0	0	1	0
5	F	81	0	0	2	0
5	G	54	0	0	0	0
5	H	50	0	0	2	0
5	I	52	0	0	0	0
5	J	62	0	0	1	0
5	K	62	0	0	2	0
5	L	63	0	0	0	0
5	M	83	0	0	1	0
5	N	73	0	0	1	0
5	O	59	0	0	1	0
5	P	73	0	0	1	0
5	Q	66	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	R	85	0	0	1	0
5	S	79	0	0	3	0
5	T	80	0	0	2	0
All	All	34188	0	31903	292	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 (292) 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:T:49:ASP:OD1	1:T:120[B]:ARG:HG2	1.41	1.17
1:L:14:SER:HB3	1:L:16:PRO:HD3	1.48	0.96
1:K:206:ARG:HH11	1:K:206:ARG:CG	1.86	0.88
2:S:211:09P:H16	1:T:112:LEU:HD23	1.56	0.87
1:T:49:ASP:OD1	1:T:120[B]:ARG:CG	2.21	0.87
1:K:206:ARG:HH11	1:K:206:ARG:HG2	1.39	0.85
1:T:207:SER:O	1:T:208:GLU:HB2	1.76	0.85
1:E:14:SER:HB3	1:E:16:PRO:HD3	1.58	0.84
1:C:161:ASP:O	1:C:162:SER:HB3	1.80	0.81
1:H:160:ASP:HB2	1:H:163:GLU:HB2	1.62	0.81
1:A:123:CYS:HB2	5:A:233:HOH:O	1.81	0.78
1:M:155:THR:HG22	1:M:156:THR:N	1.98	0.78
1:K:205:GLY:O	1:K:206:ARG:HD3	1.85	0.77
1:A:161:ASP:O	1:A:163:GLU:N	2.16	0.76
1:T:14:SER:HA	5:T:215:HOH:O	1.85	0.75
1:D:14:SER:HA	5:D:237:HOH:O	1.90	0.71
1:J:188[B]:CYS:SG	1:J:189:PRO:HD2	2.31	0.71
2:I:211:09P:H20	1:J:104:ARG:HG2	1.72	0.71
1:R:188[B]:CYS:SG	1:R:189:PRO:HD2	2.32	0.70
1:H:210:LEU:HD23	1:H:210:LEU:H	1.57	0.70
1:C:146:HIS:CE1	1:C:148:ARG:HB2	2.27	0.69
1:T:188[B]:CYS:SG	1:T:189:PRO:HD2	2.32	0.69
1:E:14:SER:HA	5:E:233:HOH:O	1.93	0.68
1:A:188:CYS:HB3	5:A:234:HOH:O	1.93	0.68
2:S:211:09P:H16	1:T:112:LEU:CD2	2.23	0.67
1:L:155:THR:HG22	1:L:156:THR:N	2.10	0.67
1:H:22:GLN:C	1:H:23:ARG:HG2	2.17	0.65
1:F:160:ASP:HB3	1:F:163:GLU:HB2	1.79	0.65
1:K:206:ARG:HG2	1:K:206:ARG:NH1	2.12	0.64
1:R:22:GLN:O	1:R:25:ARG:HG2	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:ASP:CG	1:A:162:SER:N	2.51	0.63
1:A:161:ASP:C	1:A:163:GLU:H	2.01	0.63
1:Q:188[B]:CYS:SG	1:Q:189:PRO:HD2	2.38	0.63
1:L:155:THR:HG22	1:L:156:THR:H	1.62	0.63
1:N:205:GLY:O	1:N:208:GLU:HB2	1.99	0.63
1:B:148:ARG:HD3	1:M:190:GLU:OE2	2.00	0.61
1:F:23:ARG:NH1	1:F:23:ARG:HB3	2.16	0.61
1:E:15:ARG:N	1:E:16:PRO:HD3	2.15	0.61
1:N:15:ARG:N	1:N:16:PRO:HD3	2.16	0.59
1:F:146:HIS:CE1	1:F:148:ARG:HB2	2.38	0.59
1:D:188[B]:CYS:SG	1:D:189:PRO:HD2	2.42	0.58
1:T:146:HIS:CE1	1:T:148:ARG:HB2	2.38	0.58
2:P:211:09P:H19	1:Q:104:ARG:HG2	1.85	0.58
1:L:15:ARG:N	1:L:16:PRO:HD3	2.18	0.58
1:F:1:LEU:HB2	1:F:70:SER:OG	2.04	0.58
2:D:211:09P:H20	1:E:104:ARG:HG2	1.86	0.57
1:N:23:ARG:HH11	1:N:23:ARG:HB3	1.68	0.57
1:S:188[B]:CYS:SG	1:S:189:PRO:HD2	2.45	0.57
1:M:155:THR:CG2	1:M:156:THR:N	2.67	0.57
1:C:162:SER:HA	1:C:165:PHE:HB2	1.87	0.56
1:E:14:SER:O	1:E:15:ARG:HB2	2.03	0.56
1:C:146:HIS:HE1	1:C:148:ARG:HB2	1.69	0.56
1:L:188[B]:CYS:SG	1:L:189:PRO:HD2	2.45	0.56
1:K:205:GLY:O	1:K:206:ARG:HB2	2.05	0.56
1:F:23:ARG:HB3	1:F:23:ARG:HH11	1.70	0.56
1:Q:15:ARG:N	1:Q:16:PRO:HD3	2.21	0.56
1:I:1:LEU:HB2	1:I:70:SER:OG	2.07	0.55
2:Q:211:09P:H20	1:R:104:ARG:HG2	1.88	0.55
1:L:155:THR:O	1:L:156:THR:C	2.44	0.55
1:C:10:ILE:O	1:C:14:SER:HB2	2.07	0.54
1:D:15:ARG:N	1:D:16:PRO:HD3	2.23	0.54
1:E:146:HIS:CE1	1:E:148:ARG:HB2	2.43	0.54
1:F:112:LEU:HD23	2:J:211:09P:H20	1.89	0.53
1:G:146:HIS:CE1	1:G:148:ARG:HB2	2.43	0.53
1:D:146:HIS:CE1	1:D:148:ARG:HB2	2.44	0.53
1:D:22:GLN:C	1:D:23:ARG:HG2	2.29	0.53
1:L:161:ASP:O	1:L:162:SER:HB2	2.09	0.53
2:S:211:09P:C11	1:T:112:LEU:HD23	2.36	0.52
2:C:211:09P:H20	1:D:104:ARG:HG2	1.91	0.52
1:O:125:VAL:HG12	1:O:125:VAL:O	2.10	0.52
1:K:124:ASP:HB2	1:L:168:TYR:CE1	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:211:09P:H16	1:D:112:LEU:HD23	1.92	0.51
1:N:22:GLN:C	1:N:23:ARG:HG2	2.30	0.51
1:M:155:THR:O	1:M:156:THR:HB	2.11	0.51
1:R:143:TRP:CZ3	2:R:211:09P:H1	2.45	0.51
1:N:146:HIS:CE1	1:N:148:ARG:HB2	2.45	0.51
1:M:155:THR:HG22	1:M:156:THR:H	1.76	0.50
1:S:1:LEU:HB2	1:S:70:SER:OG	2.11	0.50
1:S:124:ASP:HB2	1:T:168:TYR:CE1	2.45	0.50
1:F:124:ASP:HB2	1:G:168:TYR:CE1	2.47	0.50
2:F:211:09P:H19	1:G:104:ARG:HG2	1.93	0.50
1:S:54:GLN:NE2	5:S:965:HOH:O	2.44	0.50
1:F:83:VAL:HG13	1:F:84:PRO:HD2	1.94	0.49
1:N:22:GLN:NE2	1:N:61:ARG:HG3	2.27	0.49
1:B:83:VAL:HG13	1:B:84:PRO:HD2	1.94	0.49
1:F:10:ILE:O	1:F:14:SER:HB3	2.11	0.49
1:N:125:VAL:HG12	1:N:125:VAL:O	2.12	0.49
1:R:66:ASN:ND2	3:R:214:NAG:C7	2.72	0.49
1:K:188[B]:CYS:SG	1:K:189:PRO:HD2	2.53	0.49
1:Q:25:ARG:HG3	1:Q:26:PRO:HD2	1.94	0.49
1:S:125:VAL:HG12	1:S:125:VAL:O	2.12	0.49
1:D:161:ASP:OD2	1:D:161:ASP:N	2.44	0.49
1:E:23:ARG:O	1:E:24:ASP:HB2	2.12	0.49
1:A:104:ARG:HG2	2:E:211:09P:H19	1.94	0.49
1:H:125:VAL:HG12	1:H:125:VAL:O	2.13	0.49
1:L:125:VAL:HG12	1:L:125:VAL:O	2.13	0.49
1:N:3:ARG:HG3	1:N:71:PRO:HG2	1.95	0.49
1:B:146:HIS:CE1	1:B:148:ARG:HB2	2.47	0.49
1:M:125:VAL:HG12	1:M:125:VAL:O	2.12	0.49
1:T:83:VAL:HG13	1:T:84:PRO:HD2	1.95	0.49
1:I:143:TRP:CE3	2:I:211:09P:H1	2.48	0.48
1:K:22:GLN:NE2	1:K:61:ARG:HG3	2.28	0.48
1:Q:146:HIS:CE1	1:Q:148:ARG:HB2	2.47	0.48
1:I:188[B]:CYS:SG	1:I:189:PRO:HD2	2.53	0.48
1:H:210:LEU:HD23	1:H:210:LEU:N	2.27	0.48
1:J:156:THR:O	1:J:157:GLU:HG3	2.14	0.48
1:F:146:HIS:HE1	1:F:148:ARG:HB2	1.79	0.48
1:J:157:GLU:HB3	1:J:159:SER:N	2.28	0.48
1:R:143:TRP:CE3	2:R:211:09P:H1	2.49	0.48
1:S:146:HIS:CE1	1:S:148:ARG:HB2	2.48	0.48
1:M:188[B]:CYS:SG	1:M:189:PRO:HD2	2.53	0.48
1:G:125:VAL:HG12	1:G:125:VAL:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:146:HIS:CE1	1:O:148:ARG:HB2	2.49	0.48
1:T:146:HIS:HE1	1:T:148:ARG:HB2	1.78	0.48
1:D:61:ARG:HD2	5:D:232:HOH:O	2.14	0.48
1:H:1:LEU:HB2	1:H:70:SER:OG	2.14	0.48
1:C:155:THR:HG22	1:C:157:GLU:H	1.79	0.47
1:I:143:TRP:CZ3	2:I:211:09P:H1	2.49	0.47
1:B:134:ALA:O	1:B:200:ASN:HA	2.15	0.47
1:C:123:CYS:HB2	5:C:345:HOH:O	2.14	0.47
1:K:205:GLY:O	1:K:206:ARG:CB	2.63	0.47
1:L:155:THR:HG22	1:L:156:THR:HG23	1.97	0.47
1:M:123:CYS:HB2	5:M:279:HOH:O	2.14	0.47
1:D:125:VAL:HG12	1:D:125:VAL:O	2.14	0.47
1:P:125:VAL:HG12	1:P:125:VAL:O	2.14	0.47
1:D:83:VAL:HG13	1:D:84:PRO:HD2	1.96	0.47
1:E:146:HIS:HE1	1:E:148:ARG:HB2	1.80	0.47
1:C:188[B]:CYS:SG	1:C:189:PRO:HD2	2.55	0.47
1:K:143:TRP:CE2	2:K:211:09P:H11	2.48	0.47
1:S:83:VAL:HG13	1:S:84:PRO:HD2	1.96	0.47
1:E:125:VAL:HG12	1:E:125:VAL:O	2.14	0.47
2:G:211:09P:H16	2:G:211:09P:H14	1.74	0.47
1:N:124:ASP:HB2	1:O:168:TYR:CE1	2.50	0.47
1:B:124:ASP:HB2	1:C:168:TYR:CE1	2.49	0.47
1:F:155:THR:HG22	1:F:156:THR:N	2.30	0.47
1:C:41:VAL:HG13	1:C:125:VAL:HG11	1.97	0.47
1:J:120:ARG:NH1	5:J:747:HOH:O	2.48	0.47
1:P:15:ARG:N	1:P:16:PRO:HD3	2.30	0.47
1:P:83:VAL:HG13	1:P:84:PRO:HD2	1.96	0.47
1:R:125:VAL:HG12	1:R:125:VAL:O	2.15	0.46
2:I:211:09P:H16	1:J:112:LEU:HD23	1.96	0.46
1:J:156:THR:O	1:J:157:GLU:CG	2.64	0.46
1:T:125:VAL:HG12	1:T:125:VAL:O	2.15	0.46
5:B:511:HOH:O	1:M:189:PRO:HA	2.16	0.46
1:H:123:CYS:HB2	5:H:322:HOH:O	2.15	0.46
1:M:83:VAL:HG13	1:M:84:PRO:HD2	1.97	0.46
1:A:2:ASP:HB2	1:E:23:ARG:NH2	2.31	0.46
1:O:123:CYS:HB2	5:O:277:HOH:O	2.15	0.46
1:L:22:GLN:C	1:L:23:ARG:HG2	2.35	0.46
1:L:143:TRP:CE3	2:L:211:09P:H1	2.50	0.46
1:B:35:PHE:H	1:B:161:ASP:N	2.13	0.46
1:G:41:VAL:HG13	1:G:125:VAL:HG11	1.98	0.46
1:I:15:ARG:N	1:I:16:PRO:HD3	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:22:GLN:C	1:C:23:ARG:HG2	2.36	0.45
1:D:161:ASP:O	1:D:163:GLU:N	2.43	0.45
1:N:41:VAL:HG13	1:N:125:VAL:HG11	1.97	0.45
1:Q:125:VAL:HG12	1:Q:125:VAL:O	2.16	0.45
2:B:211:09P:H19	1:C:104:ARG:HG2	1.98	0.45
1:E:25:ARG:HH11	1:E:25:ARG:HB2	1.81	0.45
1:I:125:VAL:HG12	1:I:125:VAL:O	2.14	0.45
1:R:83:VAL:HG13	1:R:84:PRO:HD2	1.98	0.45
1:C:161:ASP:O	1:C:162:SER:CB	2.54	0.45
1:F:124:ASP:HB2	1:G:168:TYR:CZ	2.51	0.45
1:J:41:VAL:HG13	1:J:125:VAL:HG11	1.98	0.45
1:T:134:ALA:O	1:T:200:ASN:HA	2.16	0.45
1:A:125:VAL:HG12	1:A:125:VAL:O	2.17	0.45
1:F:125:VAL:HG12	1:F:125:VAL:O	2.17	0.45
1:H:167:GLN:HG2	5:H:1590:HOH:O	2.16	0.45
1:B:125:VAL:O	1:B:125:VAL:HG12	2.17	0.45
1:H:124:ASP:HB2	1:I:168:TYR:CE1	2.51	0.45
1:A:83:VAL:HG13	1:A:84:PRO:HD2	1.99	0.45
1:F:123:CYS:HB2	5:F:216:HOH:O	2.16	0.45
1:J:10:ILE:O	1:J:14:SER:HB3	2.17	0.45
1:K:61:ARG:NE	5:K:213:HOH:O	2.49	0.45
1:T:1:LEU:HB2	1:T:70:SER:OG	2.16	0.45
1:H:160:ASP:OD1	1:H:160:ASP:N	2.50	0.44
1:J:157:GLU:HG2	1:J:159:SER:N	2.32	0.44
1:C:125:VAL:HG12	1:C:125:VAL:O	2.16	0.44
1:E:83:VAL:HG13	1:E:84:PRO:HD2	1.98	0.44
1:N:83:VAL:HG13	1:N:84:PRO:HD2	1.98	0.44
1:Q:83:VAL:HG13	1:Q:84:PRO:HD2	1.98	0.44
1:Q:124:ASP:HB2	1:R:168:TYR:CE1	2.52	0.44
1:S:146:HIS:HE1	1:S:148:ARG:HB2	1.82	0.44
1:L:154:PRO:HB3	1:L:178:GLN:OE1	2.17	0.44
1:M:146:HIS:CE1	1:M:148:ARG:HB2	2.52	0.44
1:P:152:VAL:HG21	1:P:194:ASP:HA	1.99	0.44
1:J:83:VAL:HG13	1:J:84:PRO:HD2	2.00	0.44
1:K:41:VAL:HG13	1:K:125:VAL:HG11	1.99	0.44
1:K:83:VAL:HG13	1:K:84:PRO:HD2	1.99	0.44
1:G:146:HIS:HE1	1:G:148:ARG:HB2	1.81	0.44
1:D:146:HIS:HE1	1:D:148:ARG:HB2	1.82	0.44
1:G:83:VAL:HG13	1:G:84:PRO:HD2	1.99	0.44
1:L:155:THR:CG2	1:L:156:THR:N	2.80	0.44
1:P:124:ASP:HB2	1:Q:168:TYR:CE1	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:146:HIS:CE1	1:P:148:ARG:HB2	2.52	0.44
1:T:143:TRP:CE3	2:T:211:09P:H1	2.53	0.44
1:D:1:LEU:HB2	1:D:70:SER:OG	2.18	0.44
1:D:124:ASP:HB2	1:E:168:TYR:CE1	2.52	0.44
1:H:22:GLN:O	1:H:23:ARG:HG2	2.18	0.44
1:L:146:HIS:CE1	1:L:148:ARG:HB2	2.53	0.44
1:B:143:TRP:CE2	2:B:211:09P:H11	2.53	0.43
1:F:186:SER:HB2	1:G:164:TYR:OH	2.18	0.43
1:H:185:TYR:CE1	2:H:211:09P:H5	2.53	0.43
1:K:168:TYR:CE1	1:O:124:ASP:HB2	2.52	0.43
1:Q:143:TRP:CE3	2:Q:211:09P:H1	2.53	0.43
1:A:61:ARG:HA	1:A:61:ARG:HD3	1.85	0.43
1:R:26:PRO:HD2	5:R:1558:HOH:O	2.17	0.43
1:R:204:LYS:O	1:R:205:GLY:C	2.56	0.43
2:F:211:09P:H20	1:G:112:LEU:HD23	2.00	0.43
1:H:83:VAL:HG13	1:H:84:PRO:HD2	2.00	0.43
1:J:22:GLN:HB2	1:J:25:ARG:HD2	2.00	0.43
1:K:160:ASP:HB3	1:K:163:GLU:HB2	2.01	0.43
1:D:134:ALA:O	1:D:200:ASN:HA	2.18	0.43
1:J:125:VAL:HG12	1:J:125:VAL:O	2.17	0.43
1:E:15:ARG:N	1:E:16:PRO:CD	2.81	0.43
1:H:61:ARG:HA	1:H:61:ARG:HD3	1.86	0.43
1:K:123:CYS:HB2	5:K:344:HOH:O	2.19	0.43
1:N:146:HIS:HE1	1:N:148:ARG:HB2	1.83	0.43
1:P:167:GLN:HG2	5:P:234:HOH:O	2.19	0.43
1:H:209:ILE:H	1:H:209:ILE:HG12	1.66	0.43
2:H:211:09P:H14	2:H:211:09P:H16	1.84	0.43
1:B:41:VAL:HG13	1:B:125:VAL:HG11	2.01	0.43
1:R:143:TRP:CE2	2:R:211:09P:H11	2.53	0.43
1:N:61:ARG:HA	1:N:61:ARG:HD3	1.85	0.43
1:E:23:ARG:C	1:E:25:ARG:H	2.23	0.42
1:E:61:ARG:HA	1:E:61:ARG:HD3	1.80	0.42
1:S:61:ARG:HA	1:S:61:ARG:HD3	1.90	0.42
1:O:185:TYR:CE1	2:O:211:09P:H5	2.54	0.42
1:T:41:VAL:HG13	1:T:125:VAL:HG11	1.99	0.42
1:N:143:TRP:CE2	2:N:211:09P:H11	2.55	0.42
1:H:146:HIS:CE1	1:H:148:ARG:HB2	2.54	0.42
1:I:61:ARG:HA	1:I:61:ARG:HD3	1.85	0.42
1:A:161:ASP:C	1:A:163:GLU:N	2.67	0.42
1:D:14:SER:CA	5:D:237:HOH:O	2.60	0.42
1:J:89:TYR:OH	2:J:211:09P:N1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:125:VAL:HG12	1:K:125:VAL:O	2.20	0.42
1:N:123:CYS:HB2	5:N:580:HOH:O	2.19	0.42
2:Q:211:09P:H14	2:Q:211:09P:H17	1.76	0.42
1:O:83:VAL:HG13	1:O:84:PRO:HD2	2.01	0.42
1:Q:61:ARG:HA	1:Q:61:ARG:HD3	1.83	0.42
1:S:123:CYS:HB2	5:S:360:HOH:O	2.18	0.42
1:A:143:TRP:CE2	1:B:99:THR:HG21	2.54	0.42
1:F:88:ALA:HA	1:F:139:LYS:O	2.20	0.42
1:I:83:VAL:HG13	1:I:84:PRO:HD2	2.02	0.42
1:A:168:TYR:CE1	1:E:124:ASP:HB2	2.54	0.42
1:I:124:ASP:HB2	1:J:168:TYR:CE1	2.54	0.42
1:Q:41:VAL:HG13	1:Q:125:VAL:HG11	2.02	0.42
1:S:25:ARG:HA	1:S:26:PRO:HD3	1.94	0.42
1:N:14:SER:HB3	1:N:15:ARG:H	1.64	0.41
2:N:211:09P:H14	2:N:211:09P:H16	1.79	0.41
1:K:206:ARG:HH11	1:K:206:ARG:HG3	1.75	0.41
1:N:134:ALA:O	1:N:200:ASN:HA	2.20	0.41
1:S:14:SER:HB3	5:S:224:HOH:O	2.20	0.41
1:T:123:CYS:HB2	5:T:844:HOH:O	2.19	0.41
1:C:167:GLN:HG2	5:C:1101:HOH:O	2.19	0.41
1:F:178:GLN:NE2	5:F:1146:HOH:O	2.52	0.41
1:O:146:HIS:HE1	1:O:148:ARG:HB2	1.85	0.41
1:P:23:ARG:HD2	1:P:23:ARG:N	2.35	0.41
1:C:155:THR:HG21	1:C:157:GLU:HG2	2.02	0.41
1:D:41:VAL:HG13	1:D:125:VAL:HG11	2.02	0.41
1:C:83:VAL:HG13	1:C:84:PRO:HD2	2.03	0.41
1:I:143:TRP:CE2	1:J:99:THR:HG21	2.55	0.41
1:O:61:ARG:HA	1:O:61:ARG:HD3	1.83	0.41
1:Q:152:VAL:HG21	1:Q:194:ASP:HA	2.02	0.41
1:J:160:ASP:HB3	1:J:163:GLU:HB2	2.03	0.41
1:J:179:LYS:HG3	1:S:179:LYS:HG3	2.03	0.41
1:I:143:TRP:CZ2	1:J:99:THR:HG21	2.55	0.41
1:K:164:TYR:HE1	1:O:185:TYR:HD2	1.67	0.41
1:L:83:VAL:HG13	1:L:84:PRO:HD2	2.01	0.41
1:M:124:ASP:HB2	1:N:168:TYR:CE1	2.56	0.41
2:Q:211:09P:H16	1:R:112:LEU:HD23	2.03	0.41
1:R:139:LYS:HE3	1:R:194:ASP:OD2	2.21	0.41
1:T:205:GLY:O	1:T:208:GLU:N	2.54	0.41
1:A:3:ARG:HH11	1:E:23:ARG:NH1	2.19	0.41
1:H:153:ASP:HA	1:H:154:PRO:HD3	1.92	0.41
1:K:206:ARG:CG	1:K:206:ARG:NH1	2.57	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:143:TRP:CZ2	1:M:99:THR:HG21	2.55	0.41
2:Q:211:09P:H15	2:Q:211:09P:H11	1.81	0.41
1:E:25:ARG:HA	1:E:26:PRO:HD3	1.92	0.40
1:L:61:ARG:HD3	1:L:61:ARG:HA	1.86	0.40
1:B:146:HIS:HE1	1:B:148:ARG:HB2	1.85	0.40
1:D:23:ARG:HB3	1:D:23:ARG:HH11	1.86	0.40
1:E:160:ASP:HB3	1:E:163:GLU:HB2	2.03	0.40
1:G:61:ARG:HA	1:G:61:ARG:HD3	1.85	0.40
1:I:41:VAL:HG13	1:I:125:VAL:HG11	2.02	0.40
1:M:61:ARG:HD3	1:M:61:ARG:HA	1.91	0.40
1:B:15:ARG:HD2	1:B:15:ARG:HA	1.84	0.40
1:F:96:GLU:HG3	1:J:94:LYS:HD2	2.02	0.40
1:C:153:ASP:HA	1:C:154:PRO:HD3	1.91	0.40
1:F:143:TRP:CE2	2:F:211:09P:H11	2.55	0.40
1:H:10:ILE:O	1:H:14:SER:HB3	2.22	0.40
1:P:143:TRP:CZ3	2:P:211:09P:H1	2.57	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	207/210 (99%)	204 (99%)	2 (1%)	1 (0%)	29	46
1	B	196/210 (93%)	195 (100%)	1 (0%)	0	100	100
1	C	200/210 (95%)	193 (96%)	5 (2%)	2 (1%)	15	26
1	D	201/210 (96%)	196 (98%)	4 (2%)	1 (0%)	29	46
1	E	198/210 (94%)	193 (98%)	3 (2%)	2 (1%)	15	26
1	F	199/210 (95%)	196 (98%)	3 (2%)	0	100	100
1	G	196/210 (93%)	191 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	204/210 (97%)	201 (98%)	3 (2%)	0	100	100
1	I	195/210 (93%)	193 (99%)	1 (0%)	1 (0%)	29	46
1	J	202/210 (96%)	198 (98%)	4 (2%)	0	100	100
1	K	201/210 (96%)	196 (98%)	5 (2%)	0	100	100
1	L	198/210 (94%)	194 (98%)	2 (1%)	2 (1%)	15	26
1	M	205/210 (98%)	202 (98%)	3 (2%)	0	100	100
1	N	200/210 (95%)	196 (98%)	3 (2%)	1 (0%)	29	46
1	O	195/210 (93%)	191 (98%)	4 (2%)	0	100	100
1	P	198/210 (94%)	194 (98%)	3 (2%)	1 (0%)	29	46
1	Q	194/210 (92%)	188 (97%)	5 (3%)	1 (0%)	29	46
1	R	199/210 (95%)	195 (98%)	4 (2%)	0	100	100
1	S	194/210 (92%)	192 (99%)	2 (1%)	0	100	100
1	T	203/210 (97%)	200 (98%)	3 (2%)	0	100	100
All	All	3985/4200 (95%)	3908 (98%)	65 (2%)	12 (0%)	41	59

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	SER
1	E	14	SER
1	L	14	SER
1	L	162	SER
1	N	14	SER
1	C	161	ASP
1	Q	163	GLU
1	D	162	SER
1	I	14	SER
1	C	162	SER
1	P	24	ASP
1	E	15	ARG

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	195/196 (100%)	187 (96%)	8 (4%)	30	53
1	B	186/196 (95%)	180 (97%)	6 (3%)	39	63
1	C	190/196 (97%)	187 (98%)	3 (2%)	62	82
1	D	191/196 (97%)	188 (98%)	3 (2%)	62	82
1	E	189/196 (96%)	183 (97%)	6 (3%)	39	63
1	F	189/196 (96%)	185 (98%)	4 (2%)	53	76
1	G	187/196 (95%)	181 (97%)	6 (3%)	39	63
1	H	194/196 (99%)	188 (97%)	6 (3%)	40	64
1	I	186/196 (95%)	182 (98%)	4 (2%)	52	75
1	J	192/196 (98%)	189 (98%)	3 (2%)	62	82
1	K	191/196 (97%)	187 (98%)	4 (2%)	53	76
1	L	189/196 (96%)	184 (97%)	5 (3%)	46	70
1	M	195/196 (100%)	191 (98%)	4 (2%)	53	76
1	N	190/196 (97%)	184 (97%)	6 (3%)	39	63
1	O	185/196 (94%)	181 (98%)	4 (2%)	52	75
1	P	188/196 (96%)	184 (98%)	4 (2%)	53	76
1	Q	186/196 (95%)	183 (98%)	3 (2%)	62	82
1	R	189/196 (96%)	183 (97%)	6 (3%)	39	63
1	S	186/196 (95%)	184 (99%)	2 (1%)	73	88
1	T	193/196 (98%)	188 (97%)	5 (3%)	46	70
All	All	3791/3920 (97%)	3699 (98%)	92 (2%)	49	72

All (92) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	ASP
1	A	57	THR
1	A	148	ARG
1	A	161	ASP
1	A	162	SER
1	A	187	CYS
1	A	206	ARG
1	A	209	ILE
1	B	23	ARG

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Mol	Chain	Res	Type
1	B	49	ASP
1	B	57	THR
1	B	161	ASP
1	B	162	SER
1	B	188	CYS
1	C	23	ARG
1	C	49	ASP
1	C	57	THR
1	D	23	ARG
1	D	49	ASP
1	D	57	THR
1	E	15	ARG
1	E	25	ARG
1	E	49	ASP
1	E	57	THR
1	E	162	SER
1	E	188	CYS
1	F	23	ARG
1	F	49	ASP
1	F	57	THR
1	F	188	CYS
1	G	23	ARG
1	G	49	ASP
1	G	57	THR
1	G	161	ASP
1	G	162	SER
1	G	188	CYS
1	H	23	ARG
1	H	49	ASP
1	H	57	THR
1	H	160	ASP
1	H	188	CYS
1	H	209	ILE
1	I	24	ASP
1	I	49	ASP
1	I	57	THR
1	I	148	ARG
1	J	49	ASP
1	J	57	THR
1	J	156	THR
1	K	23	ARG
1	K	49	ASP

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Mol	Chain	Res	Type
1	K	57	THR
1	K	206	ARG
1	L	14	SER
1	L	23	ARG
1	L	49	ASP
1	L	57	THR
1	L	187	CYS
1	M	23	ARG
1	M	49	ASP
1	M	57	THR
1	M	156	THR
1	N	14	SER
1	N	23	ARG
1	N	49	ASP
1	N	57	THR
1	N	188	CYS
1	N	208	GLU
1	O	23	ARG
1	O	49	ASP
1	O	57	THR
1	O	188	CYS
1	P	23	ARG
1	P	24	ASP
1	P	49	ASP
1	P	57	THR
1	Q	49	ASP
1	Q	57	THR
1	Q	162	SER
1	R	24	ASP
1	R	49	ASP
1	R	57	THR
1	R	148	ARG
1	R	187[A]	CYS
1	R	187[B]	CYS
1	S	25	ARG
1	S	57	THR
1	T	23	ARG
1	T	49	ASP
1	T	57	THR
1	T	161	ASP
1	T	208	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10)

such sidechains are listed below:

Mol	Chain	Res	Type
1	B	22	GLN
1	C	22	GLN
1	C	167	GLN
1	K	22	GLN
1	K	167	GLN
1	N	22	GLN
1	P	22	GLN
1	Q	22	GLN
1	S	54	GLN
1	T	22	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

33 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	09P	J	211	-	15,17,17	1.08	0	17,21,21	1.26	1 (5%)
2	09P	K	211	-	15,17,17	1.16	1 (6%)	17,21,21	1.73	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	09P	C	211	-	15,17,17	1.31	2 (13%)	17,21,21	1.19	2 (11%)
2	09P	L	211	-	15,17,17	0.95	0	17,21,21	1.20	1 (5%)
2	09P	P	211	-	15,17,17	1.13	2 (13%)	17,21,21	1.48	2 (11%)
2	09P	T	211	-	15,17,17	1.09	1 (6%)	17,21,21	1.35	1 (5%)
4	SO4	M	212	-	4,4,4	0.11	0	6,6,6	0.11	0
3	NAG	A	212	1	14,14,15	0.50	0	17,19,21	1.31	1 (5%)
4	SO4	I	212	-	4,4,4	0.15	0	6,6,6	0.21	0
4	SO4	P	212	-	4,4,4	0.15	0	6,6,6	0.14	0
2	09P	S	211	-	15,17,17	1.17	1 (6%)	17,21,21	1.72	3 (17%)
2	09P	I	211	-	15,17,17	1.20	1 (6%)	17,21,21	1.42	1 (5%)
2	09P	H	211	-	15,17,17	1.12	1 (6%)	17,21,21	1.45	2 (11%)
2	09P	O	211	-	15,17,17	1.14	1 (6%)	17,21,21	1.67	2 (11%)
4	SO4	K	212	-	4,4,4	0.14	0	6,6,6	0.24	0
4	SO4	T	212	-	4,4,4	0.14	0	6,6,6	0.07	0
4	SO4	O	212	-	4,4,4	0.14	0	6,6,6	0.12	0
2	09P	F	211	-	15,17,17	1.12	1 (6%)	17,21,21	1.26	2 (11%)
4	SO4	D	212	-	4,4,4	0.15	0	6,6,6	0.11	0
4	SO4	N	212	-	4,4,4	0.12	0	6,6,6	0.16	0
4	SO4	H	212	-	4,4,4	0.14	0	6,6,6	0.14	0
2	09P	D	211	-	15,17,17	1.35	3 (20%)	17,21,21	1.16	2 (11%)
3	NAG	R	214	1	14,14,15	0.46	0	17,19,21	1.41	4 (23%)
2	09P	Q	211	-	15,17,17	1.03	0	17,21,21	1.60	1 (5%)
2	09P	N	211	-	15,17,17	1.23	1 (6%)	17,21,21	1.41	2 (11%)
2	09P	E	211	-	15,17,17	1.07	1 (6%)	17,21,21	0.96	1 (5%)
4	SO4	C	212	-	4,4,4	0.14	0	6,6,6	0.14	0
2	09P	G	211	-	15,17,17	1.23	2 (13%)	17,21,21	1.41	1 (5%)
3	NAG	G	213	1	14,14,15	0.49	0	17,19,21	1.28	3 (17%)
2	09P	B	211	-	15,17,17	1.29	3 (20%)	17,21,21	1.80	2 (11%)
2	09P	R	211	-	15,17,17	1.17	1 (6%)	17,21,21	1.92	4 (23%)
2	09P	M	211	-	15,17,17	1.17	1 (6%)	17,21,21	1.59	4 (23%)
2	09P	A	211	-	15,17,17	1.15	0	17,21,21	1.36	2 (11%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	09P	J	211	-	-	1/7/16/16	0/2/2/2
2	09P	K	211	-	-	1/7/16/16	0/2/2/2
2	09P	C	211	-	-	1/7/16/16	0/2/2/2
2	09P	L	211	-	-	1/7/16/16	0/2/2/2
2	09P	P	211	-	-	1/7/16/16	0/2/2/2
2	09P	T	211	-	-	0/7/16/16	0/2/2/2
3	NAG	A	212	1	-	0/6/23/26	0/1/1/1
2	09P	S	211	-	-	3/7/16/16	0/2/2/2
2	09P	I	211	-	-	2/7/16/16	0/2/2/2
2	09P	H	211	-	-	1/7/16/16	0/2/2/2
2	09P	O	211	-	-	0/7/16/16	0/2/2/2
2	09P	F	211	-	-	0/7/16/16	0/2/2/2
2	09P	D	211	-	-	1/7/16/16	0/2/2/2
3	NAG	R	214	1	-	0/6/23/26	0/1/1/1
2	09P	Q	211	-	-	1/7/16/16	0/2/2/2
2	09P	N	211	-	-	1/7/16/16	0/2/2/2
2	09P	E	211	-	-	0/7/16/16	0/2/2/2
2	09P	G	211	-	-	1/7/16/16	0/2/2/2
3	NAG	G	213	1	-	0/6/23/26	0/1/1/1
2	09P	B	211	-	-	0/7/16/16	0/2/2/2
2	09P	R	211	-	-	1/7/16/16	0/2/2/2
2	09P	M	211	-	-	3/7/16/16	0/2/2/2
2	09P	A	211	-	-	1/7/16/16	0/2/2/2

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	211	09P	C6-C7	2.64	1.42	1.38
2	E	211	09P	C6-C7	2.42	1.41	1.38
2	G	211	09P	C6-C7	2.39	1.41	1.38
2	B	211	09P	C6-C7	2.35	1.41	1.38
2	K	211	09P	C6-C7	2.31	1.41	1.38
2	D	211	09P	C10-C9	2.30	1.43	1.38
2	C	211	09P	C4-N2	2.27	1.49	1.46
2	N	211	09P	C6-C7	2.27	1.41	1.38
2	T	211	09P	C10-C9	2.25	1.43	1.38
2	D	211	09P	C8-C7	2.25	1.42	1.38
2	G	211	09P	C8-C7	2.23	1.42	1.38
2	R	211	09P	C8-C7	2.21	1.42	1.38
2	C	211	09P	C6-C7	2.21	1.41	1.38
2	O	211	09P	C6-C7	2.20	1.41	1.38
2	B	211	09P	C8-C7	2.11	1.42	1.38
2	B	211	09P	C10-C9	2.09	1.42	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	M	211	09P	C8-C7	2.08	1.42	1.38
2	I	211	09P	C8-C7	2.07	1.42	1.38
2	S	211	09P	C10-C9	2.06	1.42	1.38
2	P	211	09P	C10-C9	2.03	1.42	1.38
2	P	211	09P	C6-C7	2.03	1.41	1.38
2	F	211	09P	C5-N2	2.03	1.49	1.46
2	H	211	09P	C6-C7	2.01	1.41	1.38

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R	211	09P	C8-C9-C10	-5.47	115.14	119.48
2	B	211	09P	C8-C9-C10	-5.12	115.42	119.48
2	K	211	09P	C8-C9-C10	-5.05	115.48	119.48
2	S	211	09P	C8-C9-C10	-5.02	115.50	119.48
2	Q	211	09P	C8-C9-C10	-4.85	115.64	119.48
2	O	211	09P	C8-C9-C10	-4.64	115.81	119.48
2	T	211	09P	C8-C9-C10	-4.46	115.94	119.48
2	P	211	09P	C8-C9-C10	-4.38	116.01	119.48
2	G	211	09P	C8-C9-C10	-4.24	116.12	119.48
2	M	211	09P	C8-C9-C10	-3.95	116.35	119.48
2	H	211	09P	C8-C9-C10	-3.95	116.35	119.48
2	N	211	09P	C8-C9-C10	-3.81	116.46	119.48
2	I	211	09P	C8-C9-C10	-3.80	116.47	119.48
2	J	211	09P	C8-C9-C10	-3.53	116.68	119.48
2	L	211	09P	C8-C9-C10	-3.45	116.74	119.48
2	B	211	09P	C5-N2-C4	-3.41	111.39	117.47
2	F	211	09P	C8-C9-C10	-3.25	116.90	119.48
2	K	211	09P	C5-N2-C4	-3.25	111.67	117.47
2	A	211	09P	C8-C9-C10	-3.24	116.92	119.48
3	R	214	NAG	C1-O5-C5	-3.14	107.94	112.19
2	C	211	09P	C8-C9-C10	-3.04	117.07	119.48
3	A	212	NAG	C4-C3-C2	-3.04	106.57	111.02
3	G	213	NAG	C1-O5-C5	-2.94	108.21	112.19
2	R	211	09P	C1-C5-N2	2.92	118.46	113.12
2	O	211	09P	C5-N2-C4	-2.83	112.41	117.47
2	R	211	09P	C9-C10-N3	2.79	126.01	122.92
2	R	211	09P	C5-N2-C4	-2.75	112.56	117.47
2	S	211	09P	C5-N2-C4	-2.69	112.68	117.47
2	E	211	09P	C8-C9-N2	-2.63	118.50	121.33
2	D	211	09P	C8-C9-C10	-2.61	117.41	119.48
2	P	211	09P	C9-C10-N3	2.49	125.69	122.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	211	09P	C8-C9-N2	2.40	123.91	121.33
2	S	211	09P	C11-O1-C7	-2.39	111.88	117.99
2	N	211	09P	C5-N2-C4	-2.34	113.30	117.47
2	M	211	09P	C9-C10-N3	2.33	125.50	122.92
3	R	214	NAG	O5-C5-C6	2.30	110.81	107.20
3	R	214	NAG	C8-C7-N2	2.23	119.88	116.10
3	R	214	NAG	C4-C3-C2	-2.17	107.83	111.02
3	G	213	NAG	C8-C7-N2	2.17	119.77	116.10
2	D	211	09P	C8-C7-C6	-2.13	116.74	119.28
2	F	211	09P	C5-N2-C4	-2.12	113.68	117.47
2	A	211	09P	C8-C7-C6	-2.11	116.77	119.28
2	H	211	09P	C5-N2-C4	-2.09	113.73	117.47
3	G	213	NAG	O5-C5-C6	2.02	110.38	107.20
2	C	211	09P	C1-C5-N2	2.01	116.81	113.12
2	M	211	09P	C5-N2-C4	-2.01	113.88	117.47

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	211	09P	C12-C11-O1-C7
2	M	211	09P	C12-C11-O1-C7
2	H	211	09P	C12-C11-O1-C7
2	G	211	09P	C12-C11-O1-C7
2	Q	211	09P	C12-C11-O1-C7
2	C	211	09P	C12-C11-O1-C7
2	J	211	09P	C12-C11-O1-C7
2	K	211	09P	C12-C11-O1-C7
2	N	211	09P	C12-C11-O1-C7
2	S	211	09P	C8-C7-O1-C11
2	S	211	09P	C6-C7-O1-C11
2	R	211	09P	C12-C11-O1-C7
2	M	211	09P	C6-C7-O1-C11
2	I	211	09P	C8-C7-O1-C11
2	M	211	09P	C8-C7-O1-C11
2	L	211	09P	C12-C11-O1-C7
2	P	211	09P	C12-C11-O1-C7
2	I	211	09P	C6-C7-O1-C11
2	D	211	09P	C8-C7-O1-C11
2	S	211	09P	C12-C11-O1-C7

There are no ring outliers.

19 monomers are involved in 38 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	J	211	09P	2	0
2	K	211	09P	1	0
2	C	211	09P	2	0
2	L	211	09P	1	0
2	P	211	09P	2	0
2	T	211	09P	1	0
2	S	211	09P	3	0
2	I	211	09P	4	0
2	H	211	09P	2	0
2	O	211	09P	1	0
2	F	211	09P	3	0
2	D	211	09P	1	0
3	R	214	NAG	1	0
2	Q	211	09P	5	0
2	N	211	09P	2	0
2	E	211	09P	1	0
2	G	211	09P	1	0
2	B	211	09P	2	0
2	R	211	09P	3	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

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

6.4 Ligands

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers

EDS failed to run properly - this section is therefore empty.