



# wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 12:15 AM GMT

PDB ID : 2WNL  
Title : CRYSTAL STRUCTURE OF APLYSIA ACHBP IN COMPLEX WITH AN-  
ABASEINE  
Authors : Sulzenbacher, G.; Hibbs, R.; Shi, J.; Talley, T.; Conrod, S.; Kem, W.; Taylor,  
P.; Marchot, P.; Bourne, Y.  
Deposited on : 2009-07-09  
Resolution : 2.70 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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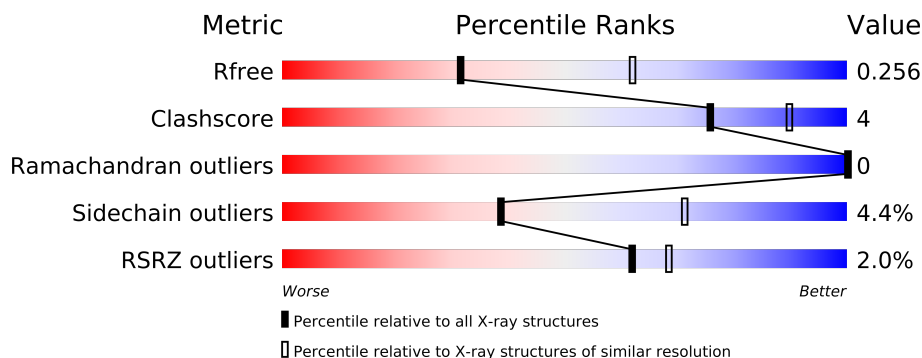
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
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 2.70 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))
$R_{free}$	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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.

Mol	Chain	Length	Quality of chain
1	A	227	
1	B	227	
1	C	227	
1	D	227	
1	E	227	
1	F	227	
1	G	227	
1	H	227	
1	I	227	
1	J	227	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	AN4	A	300	-	X
2	AN4	B	300	-	X
3	AN5	A	301	-	X
3	AN5	I	300	-	X
6	NAG	E	400	-	X
6	NAG	F	400	-	X

## 2 Entry composition

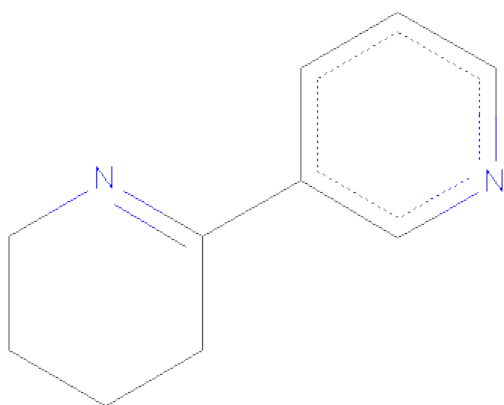
There are 7 unique types of molecules in this entry. The entry contains 17412 atoms, of which 0 are hydrogen and 0 are deuterium.

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 SOLUBLE ACETYLCHOLINE RECEPTOR.

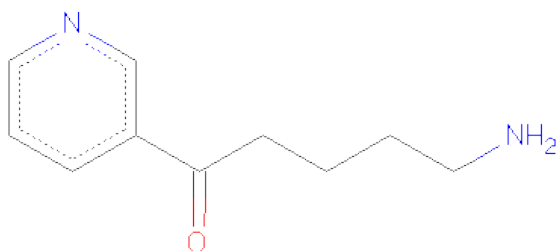
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	213	Total	C	N	O	S	0	2	0
			1713	1079	283	342	9			
1	B	211	Total	C	N	O	S	0	1	0
			1690	1065	281	336	8			
1	C	209	Total	C	N	O	S	0	1	0
			1677	1058	279	332	8			
1	D	212	Total	C	N	O	S	0	1	0
			1697	1071	282	335	9			
1	E	214	Total	C	N	O	S	0	0	0
			1708	1075	281	343	9			
1	F	211	Total	C	N	O	S	0	1	0
			1692	1068	281	334	9			
1	G	210	Total	C	N	O	S	0	0	0
			1677	1057	277	335	8			
1	H	212	Total	C	N	O	S	0	0	0
			1692	1067	279	337	9			
1	I	211	Total	C	N	O	S	0	1	0
			1692	1068	281	334	9			
1	J	212	Total	C	N	O	S	0	1	0
			1697	1071	282	335	9			

- Molecule 2 is 3,4,5,6-TETRAHYDRO-2,3'-BIPYRIDINE (three-letter code: AN4) (formula: C<sub>10</sub>H<sub>12</sub>N<sub>2</sub>).



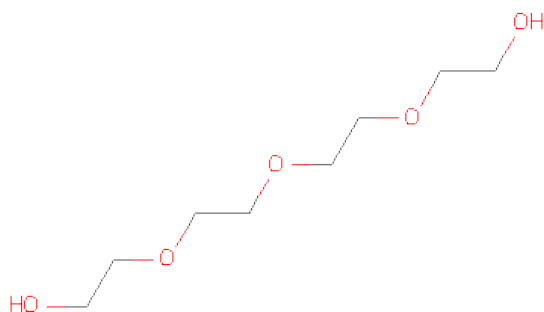
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			12	10	2		
2	B	1	Total	C	N	0	0
			12	10	2		
2	E	1	Total	C	N	0	0
			12	10	2		
2	G	1	Total	C	N	0	0
			12	10	2		
2	J	1	Total	C	N	0	0
			12	10	2		

- Molecule 3 is 5-AMINO-1-PYRIDIN-3-YLPENTAN-1-ONE (three-letter code: AN5) (formula: C<sub>10</sub>H<sub>14</sub>N<sub>2</sub>O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			13	10	2	1		
3	D	1	Total	C	N	O	0	0
			13	10	2	1		
3	F	1	Total	C	N	O	0	0
			13	10	2	1		
3	I	1	Total	C	N	O	0	0
			13	10	2	1		

- Molecule 4 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).

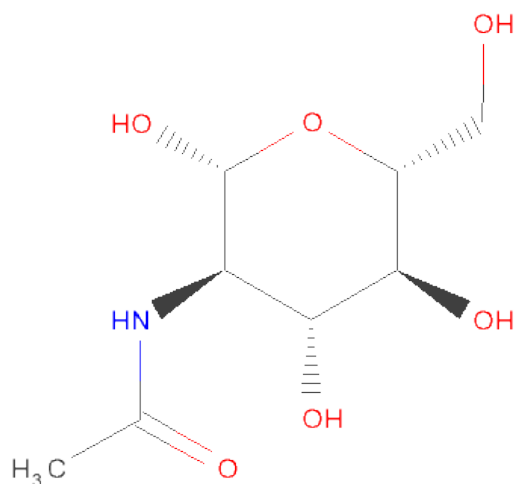


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			13	8	5		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	1	Total	Mg	0	0
			1	1		
5	C	1	Total	Mg	0	0
			1	1		
5	E	1	Total	Mg	0	0
			1	1		

- Molecule 6 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	E	1	Total	C	N	O	0	0
			14	8	1	5		
6	F	1	Total	C	N	O	0	0
			14	8	1	5		
6	H	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	47	Total 47	O 47	0	0
7	B	42	Total 42	O 42	0	0
7	C	32	Total 32	O 32	0	0
7	D	23	Total 23	O 23	0	0
7	E	23	Total 23	O 23	0	0
7	F	26	Total 26	O 26	0	0
7	G	27	Total 27	O 27	0	0
7	H	27	Total 27	O 27	0	0
7	I	29	Total 29	O 29	0	0
7	J	31	Total 31	O 31	0	0

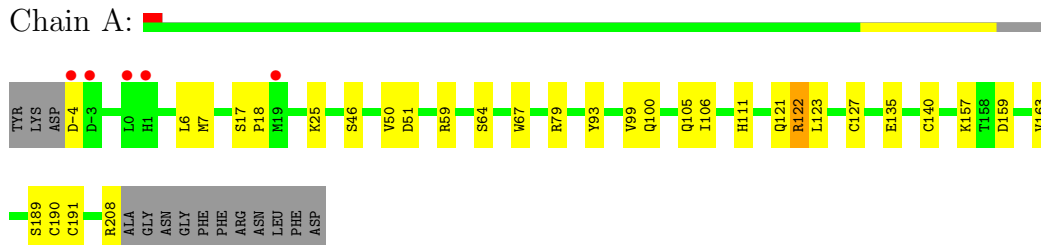


### 3 Residue-property plots

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.

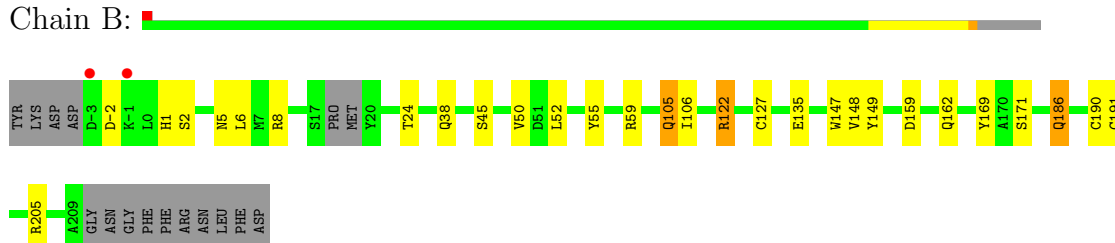
- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

Chain A:



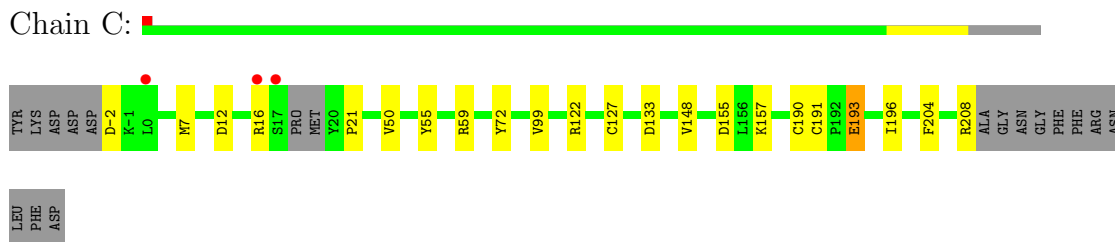
- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

Chain B:



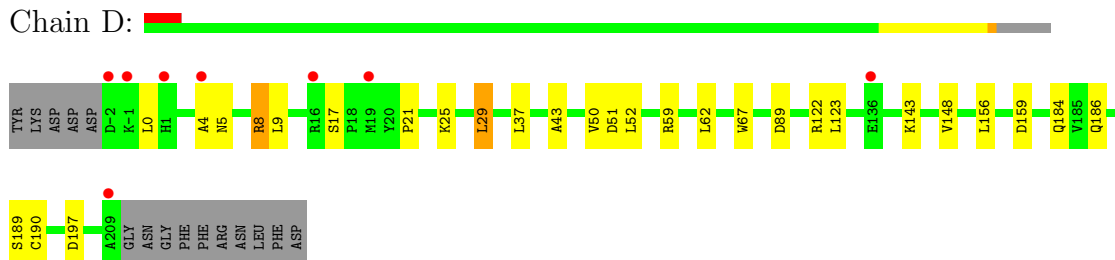
- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

Chain C:



- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

Chain D:



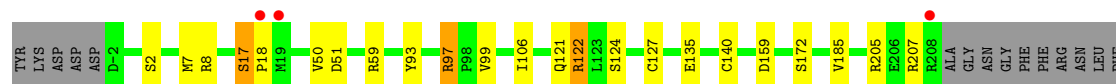
- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

Chain E:



• Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

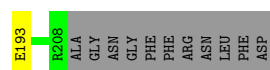
Chain F:



ASP

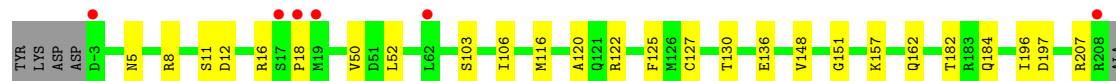
• Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

Chain G:



• Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

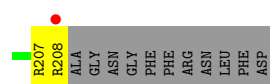
Chain H:



GLY  
ASN  
GLY  
PHE  
PHE  
ARG  
ASN  
LEU  
PHE  
ASP

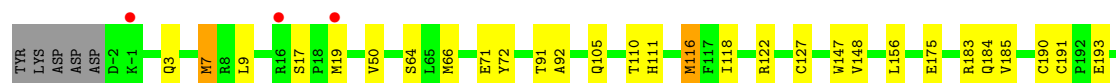
• Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

Chain I:



• Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

Chain J:



I196	D197	V198	N199	R205	A209	GLY	ASN	GLY	PHE	PHE	ARG	ASN	LEU	PHE	ASP
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## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	84.25Å 125.77Å 257.00Å 90.00° 95.40° 90.00°	Depositor
Resolution (Å)	258.20 – 2.70 69.78 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.5 (258.20-2.70) 99.5 (69.78-2.70)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.26 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.202 , 0.251 0.212 , 0.256	Depositor DCC
$R_{free}$ test set	2199 reflections (3.11%)	DCC
Wilson B-factor (Å <sup>2</sup> )	40.7	Xtriage
Anisotropy	0.588	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 15.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 72926 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	17412	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 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: AN4, AN5, MG, NAG, PG4

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	0.40	0/1760	0.61	1/2399 (0.0%)
1	B	0.40	0/1732	0.60	0/2359
1	C	0.38	0/1719	0.60	0/2341
1	D	0.38	0/1741	0.60	0/2373
1	E	0.37	0/1749	0.60	1/2384 (0.0%)
1	F	0.41	0/1736	0.62	1/2365 (0.0%)
1	G	0.38	0/1716	0.59	0/2337
1	H	0.40	0/1733	0.60	0/2362
1	I	0.40	0/1736	0.60	1/2366 (0.0%)
1	J	0.37	0/1741	0.59	0/2373
All	All	0.39	0/17363	0.60	4/23659 (0.0%)

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	C	0	1
1	D	0	1
All	All	0	2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	140	CYS	CA-CB-SG	-6.83	101.71	114.00
1	I	140	CYS	CA-CB-SG	-5.33	104.41	114.00
1	A	140	CYS	CA-CB-SG	-5.33	104.41	114.00
1	E	122	ARG	NE-CZ-NH2	-5.18	117.71	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	190	CYS	Peptide
1	D	190	CYS	Peptide

## 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	1713	0	1642	19	0
1	B	1690	0	1622	21	0
1	C	1677	0	1613	12	0
1	D	1697	0	1635	14	0
1	E	1708	0	1628	8	0
1	F	1692	0	1629	18	0
1	G	1677	0	1604	13	0
1	H	1692	0	1620	10	0
1	I	1692	0	1630	14	0
1	J	1697	0	1635	20	0
2	A	12	0	8	2	0
2	B	12	0	12	2	0
2	E	12	0	12	0	0
2	G	12	0	12	2	0
2	J	12	0	12	4	0
3	A	13	0	8	1	0
3	D	13	0	14	0	0
3	F	13	0	14	3	0
3	I	13	0	14	0	0
4	C	13	0	18	1	0
5	C	1	0	0	0	0
5	E	1	0	0	0	0
5	H	1	0	0	0	0
6	E	14	0	13	1	0
6	F	14	0	13	0	0
6	H	14	0	13	0	0
7	A	47	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	42	0	0	0	0
7	C	32	0	0	0	0
7	D	23	0	0	0	0
7	E	23	0	0	0	0
7	F	26	0	0	0	0
7	G	27	0	0	0	0
7	H	27	0	0	0	0
7	I	29	0	0	0	0
7	J	31	0	0	0	0
All	All	17412	0	16421	131	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 4.

The worst 5 of 131 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:93:TYR:HB3	3:F:300:AN5:H14	1.45	0.97
1:A:93:TYR:HB3	3:A:301:AN5:H14	1.54	0.88
1:J:185:VAL:HG22	1:J:196:ILE:HD13	1.58	0.86
1:F:18:PRO:HG2	1:J:7:MET:SD	2.18	0.84
1:C:12:ASP:OD2	1:C:72:TYR:OH	1.96	0.81

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	213/227 (94%)	210 (99%)	3 (1%)	0	100	100
1	B	208/227 (92%)	201 (97%)	7 (3%)	0	100	100
1	C	206/227 (91%)	201 (98%)	5 (2%)	0	100	100
1	D	211/227 (93%)	207 (98%)	4 (2%)	0	100	100
1	E	212/227 (93%)	207 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	210/227 (92%)	204 (97%)	6 (3%)	0	100	100
1	G	206/227 (91%)	200 (97%)	6 (3%)	0	100	100
1	H	210/227 (92%)	208 (99%)	2 (1%)	0	100	100
1	I	210/227 (92%)	206 (98%)	4 (2%)	0	100	100
1	J	211/227 (93%)	206 (98%)	5 (2%)	0	100	100
All	All	2097/2270 (92%)	2050 (98%)	47 (2%)	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	196/205 (96%)	185 (94%)	11 (6%)	30	59
1	B	192/205 (94%)	185 (96%)	7 (4%)	47	79
1	C	191/205 (93%)	184 (96%)	7 (4%)	45	78
1	D	193/205 (94%)	186 (96%)	7 (4%)	47	79
1	E	195/205 (95%)	188 (96%)	7 (4%)	47	79
1	F	193/205 (94%)	187 (97%)	6 (3%)	52	83
1	G	191/205 (93%)	180 (94%)	11 (6%)	28	57
1	H	193/205 (94%)	184 (95%)	9 (5%)	36	69
1	I	193/205 (94%)	184 (95%)	9 (5%)	36	69
1	J	193/205 (94%)	182 (94%)	11 (6%)	29	58
All	All	1930/2050 (94%)	1845 (96%)	85 (4%)	39	71

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	208	ARG
1	G	59	ARG
1	J	66	MET
1	F	2	SER

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Mol	Chain	Res	Type
1	F	97	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	105	GLN
1	F	3	GLN
1	J	63	ASN
1	E	199	ASN
1	F	63	ASN

### 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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 16 ligands modelled in this entry, 3 are monoatomic - leaving 13 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
2	AN4	A	300	3	13,13,13	0.97	1 (7%)	16,16,16	3.04	4 (25%)
3	AN5	A	301	2	13,13,13	0.49	0	15,15,15	1.13	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	AN4	B	300	-	13,13,13	1.14	1 (7%)	16,16,16	2.90	5 (31%)
4	PG4	C	300	-	12,12,12	0.51	0	11,11,11	0.23	0
3	AN5	D	300	-	13,13,13	0.34	0	15,15,15	1.37	3 (20%)
2	AN4	E	300	-	13,13,13	0.95	1 (7%)	16,16,16	2.67	5 (31%)
6	NAG	E	400	1	12,14,15	0.52	0	15,19,21	1.88	2 (13%)
3	AN5	F	300	-	13,13,13	0.73	0	15,15,15	1.83	3 (20%)
6	NAG	F	400	1	12,14,15	0.60	0	15,19,21	1.73	2 (13%)
2	AN4	G	300	-	13,13,13	1.16	1 (7%)	16,16,16	3.22	4 (25%)
6	NAG	H	400	1	12,14,15	0.56	0	15,19,21	1.20	2 (13%)
3	AN5	I	300	-	13,13,13	0.75	0	15,15,15	0.78	1 (6%)
2	AN4	J	300	-	13,13,13	1.31	1 (7%)	16,16,16	3.15	6 (37%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	AN4	A	300	3	-	0/4/12/12	0/2/2/2
3	AN5	A	301	2	-	0/9/9/9	0/1/1/1
2	AN4	B	300	-	-	0/4/12/12	0/2/2/2
4	PG4	C	300	-	-	0/10/10/10	0/0/0/0
3	AN5	D	300	-	-	0/9/9/9	0/1/1/1
2	AN4	E	300	-	-	0/4/12/12	0/2/2/2
6	NAG	E	400	1	-	0/6/23/26	0/1/1/1
3	AN5	F	300	-	-	0/9/9/9	0/1/1/1
6	NAG	F	400	1	-	0/6/23/26	0/1/1/1
2	AN4	G	300	-	-	0/4/12/12	0/2/2/2
6	NAG	H	400	1	-	0/6/23/26	0/1/1/1
3	AN5	I	300	-	-	0/9/9/9	0/1/1/1
2	AN4	J	300	-	-	0/4/12/12	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	300	AN4	C1-N1	-4.40	1.25	1.28
2	B	300	AN4	C1-N1	-3.89	1.25	1.28
2	G	300	AN4	C1-N1	-3.86	1.26	1.28
2	A	300	AN4	C1-N1	-2.94	1.26	1.28
2	E	300	AN4	C1-N1	-2.80	1.26	1.28

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	G	300	AN4	C5-N1-C1	9.46	130.87	116.98
2	B	300	AN4	C5-N1-C1	8.85	129.97	116.98
2	E	300	AN4	C5-N1-C1	8.44	129.37	116.98
2	A	300	AN4	C5-N1-C1	8.13	128.92	116.98
2	J	300	AN4	C2-C1-N1	-7.93	114.19	124.59

There are no chirality outliers.

There are no torsion outliers.

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 ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	213/227 (93%)	-0.15	5 (2%) 57 64	20, 32, 57, 81	0
1	B	211/227 (92%)	-0.07	2 (0%) 81 85	21, 35, 74, 100	0
1	C	209/227 (92%)	0.04	3 (1%) 72 77	24, 36, 70, 95	0
1	D	212/227 (93%)	0.22	8 (3%) 38 43	25, 41, 82, 111	0
1	E	214/227 (94%)	0.05	5 (2%) 57 64	25, 41, 69, 93	0
1	F	211/227 (92%)	-0.17	3 (1%) 72 77	20, 31, 54, 77	0
1	G	210/227 (92%)	0.02	3 (1%) 72 77	23, 38, 73, 101	0
1	H	212/227 (93%)	0.05	6 (2%) 50 56	26, 39, 67, 77	0
1	I	211/227 (92%)	-0.05	5 (2%) 56 62	23, 36, 74, 102	0
1	J	212/227 (93%)	-0.17	3 (1%) 72 77	22, 37, 62, 78	0
All	All	2115/2270 (93%)	-0.02	43 (2%) 62 68	20, 37, 70, 111	0

The worst 5 of 43 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	-4	ASP	4.3
1	C	0	LEU	4.0
1	H	19	MET	3.7
1	I	1	HIS	3.7
1	H	18	PRO	3.6

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

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

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

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, 95<sup>th</sup> 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
6	NAG	E	400	14/15	0.40	60.30	37,43,45,46	0
3	AN5	A	301	13/13	0.19	3.27	29,31,32,32	13
2	AN4	B	300	12/12	0.20	3.08	44,45,45,45	0
6	NAG	F	400	14/15	0.28	2.65	35,40,43,44	0
2	AN4	A	300	12/12	0.17	2.21	27,28,29,29	12
3	AN5	I	300	13/13	0.24	2.07	33,36,38,38	0
2	AN4	G	300	12/12	0.20	1.61	45,45,46,46	0
3	AN5	D	300	13/13	0.24	1.09	37,39,39,41	0
2	AN4	J	300	12/12	0.20	1.01	47,48,48,48	0
3	AN5	F	300	13/13	0.18	0.65	28,32,33,33	0
2	AN4	E	300	12/12	0.21	0.60	55,55,56,56	0
4	PG4	C	300	13/13	0.16	-0.26	67,69,70,70	0
6	NAG	H	400	14/15	0.14	-0.55	27,28,29,29	0
5	MG	C	1209	1/1	0.14	-2.04	34,34,34,34	0
5	MG	E	1209	1/1	0.10	-2.21	45,45,45,45	0
5	MG	H	1209	1/1	0.15	-2.38	60,60,60,60	0

### 6.5 Other polymers ⓘ

There are no such residues in this entry.