



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:28 AM GMT

PDB ID : 2HA6
Title : Crystal structure of mutant S203A of mouse acetylcholinesterase complexed with succinylcholine
Authors : Bourne, Y.; Radic, Z.; Sulzenbacher, G.; Kim, E.; Taylor, P.; Marchot, P.
Deposited on : 2006-06-12
Resolution : 2.25 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

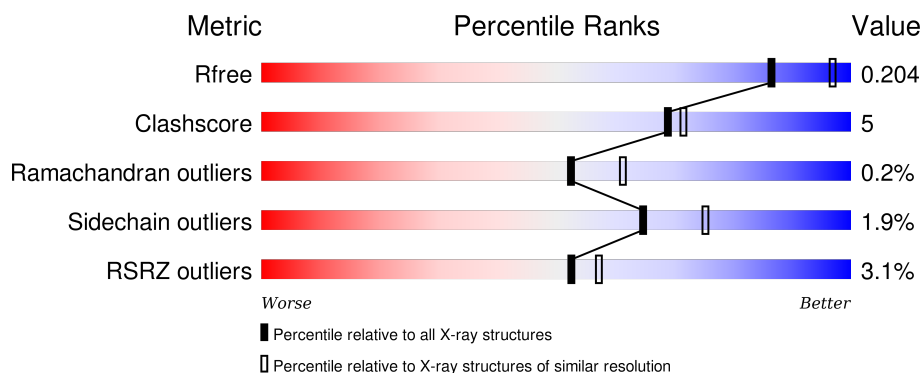
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1640 (2.28-2.24)
Clashscore	102246	1095 (2.26-2.26)
Ramachandran outliers	100387	1063 (2.26-2.26)
Sidechain outliers	100360	1063 (2.26-2.26)
RSRZ outliers	91569	1647 (2.28-2.24)

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

Mol	Chain	Length	Quality of chain
1	A	543	<div> <div>2%</div> <div>88%</div> <div>10% ..</div> </div>
1	B	543	<div> <div>4%</div> <div>88%</div> <div>9% ..</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SCK	A	901	-	-	-	X
2	SCK	B	951	-	-	-	X
2	SCK	B	952	-	-	-	X
4	ACY	A	903	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9075 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.

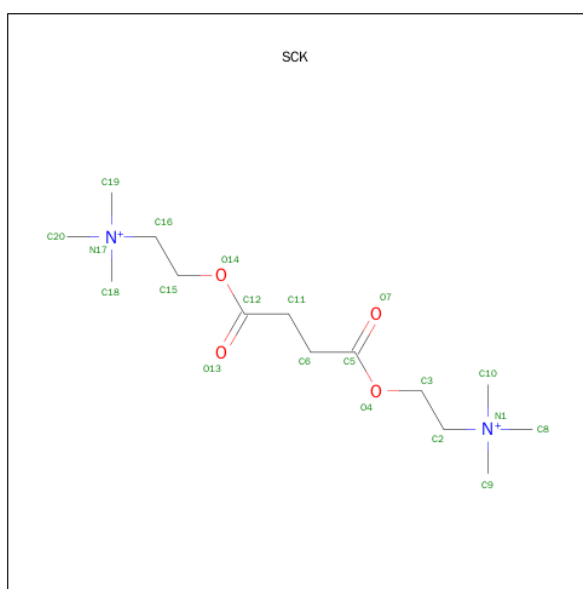
- Molecule 1 is a protein called Acetylcholinesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	536	Total	C	N	O	S	0	2	0
			4185	2685	725	761	14			
1	B	533	Total	C	N	O	S	0	1	0
			4163	2673	719	757	14			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	203	ALA	SER	ENGINEERED	UNP P21836
B	203	ALA	SER	ENGINEERED	UNP P21836

- Molecule 2 is 2,2'-[(1,4-DIOXOBUTANE-1,4-DIYL)BIS(OXY)]BIS(N,N,N-TRIMETHYLETHANAMINIUM) (three-letter code: SCK) (formula: C₁₄H₃₀N₂O₄).



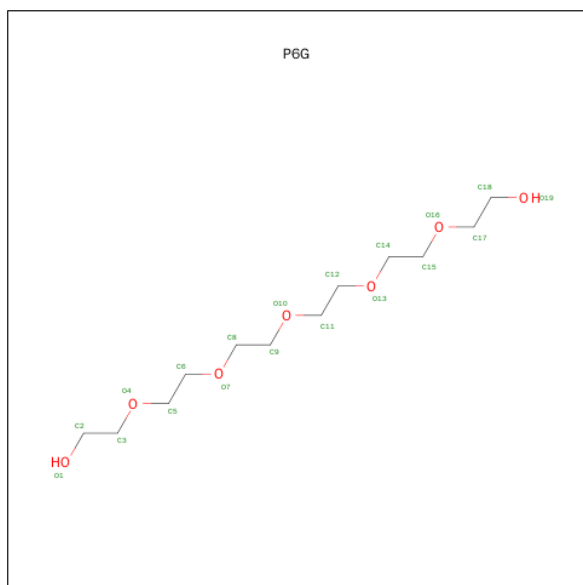
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			20	14	2	4		

Continued on next page...

Continued from previous page...

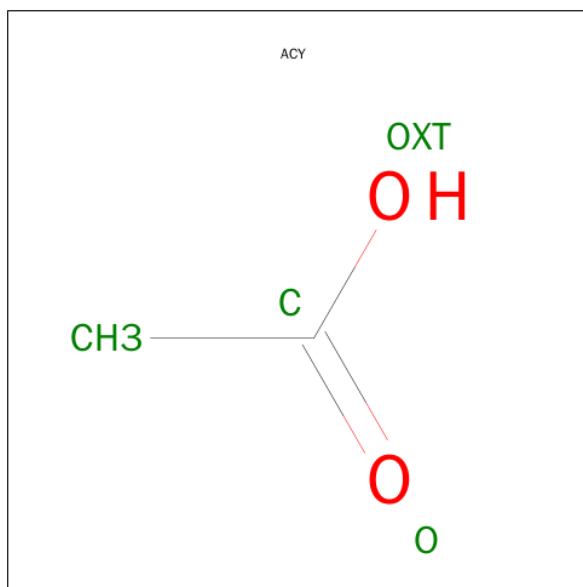
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			20	14	2	4		
2	B	1	Total	C	N	O	0	0
			20	14	2	4		
2	B	1	Total	C	N	O	0	0
			20	14	2	4		

- Molecule 3 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula: $C_{12}H_{26}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			19	12	7		

- Molecule 4 is ACETIC ACID (three-letter code: ACY) (formula: $C_2H_4O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		

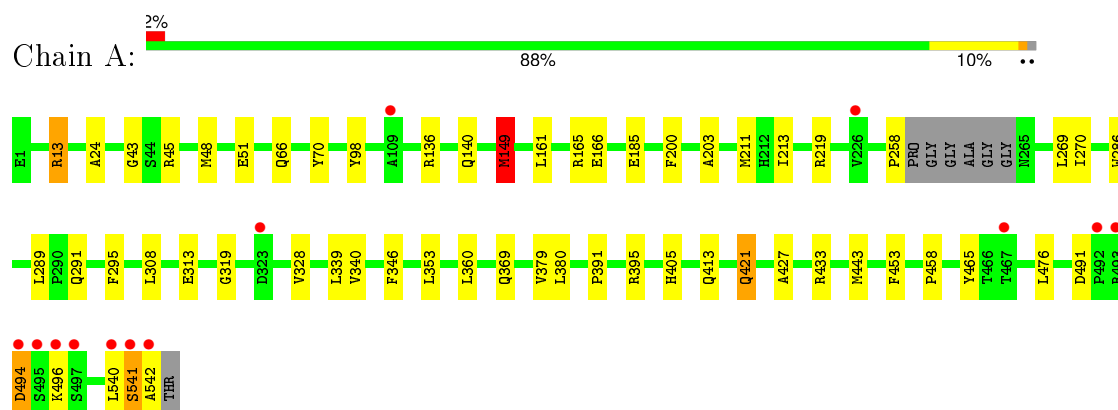
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	352	Total	O	0	0
			352	352		
5	B	272	Total	O	0	0
			272	272		

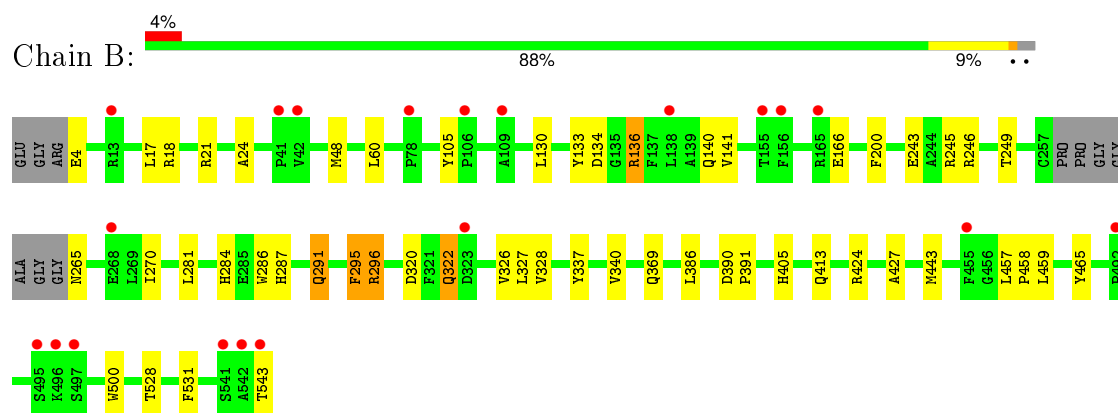
3 Residue-property plots

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: Acetylcholinesterase



• Molecule 1: Acetylcholinesterase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	78.98Å 109.83Å 227.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.25 29.05 – 2.20	Depositor EDS
% Data completeness (in resolution range)	94.9 (30.00-2.25) 83.4 (29.05-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.39 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.177 , 0.198 0.187 , 0.204	Depositor DCC
R_{free} test set	1813 reflections (2.27%)	DCC
Wilson B-factor (Å ²)	38.0	Xtriage
Anisotropy	0.744	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 51.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	1 of 93473 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9075	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.78% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACY, SCK, P6G

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	0.65	1/4316 (0.0%)	0.74	6/5898 (0.1%)
1	B	0.59	0/4290	0.70	0/5862
All	All	0.62	1/8606 (0.0%)	0.72	6/11760 (0.1%)

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	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	149	MET	CG-SD	-6.58	1.64	1.81

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	433	ARG	NE-CZ-NH2	-8.14	116.23	120.30
1	A	258	PRO	N-CA-CB	6.96	111.65	103.30
1	A	433	ARG	NE-CZ-NH1	6.04	123.32	120.30
1	A	149	MET	CA-CB-CG	-5.99	103.12	113.30
1	A	395	ARG	NE-CZ-NH1	5.51	123.06	120.30
1	A	136	ARG	NE-CZ-NH2	5.37	122.98	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	494	ASP	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4185	0	4063	42	0
1	B	4163	0	4051	32	0
2	A	40	0	60	5	0
2	B	40	0	60	3	0
3	A	19	0	26	1	0
4	A	4	0	3	1	0
5	A	352	0	0	4	0
5	B	272	0	0	2	0
All	All	9075	0	8263	77	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 (77) 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:B:48:MET:HE1	1:B:166:GLU:HA	1.60	0.84
1:A:149:MET:HG2	1:A:149:MET:O	1.87	0.73
1:B:286:TRP:CE2	2:B:951:SCK:H81	2.25	0.71
1:A:48:MET:HE1	1:A:165:ARG:O	1.93	0.69
1:B:245:ARG:O	1:B:249:THR:HG23	1.96	0.66
1:A:161:LEU:HD11	1:A:269:LEU:HD22	1.78	0.66
1:A:286:TRP:CZ2	2:A:901:SCK:H92	2.34	0.63
1:A:203:ALA:HB1	4:A:903:ACY:C	2.32	0.60
1:A:369[A]:GLN:HE22	1:A:405:HIS:CE1	2.19	0.59
1:B:340:VAL:HG11	1:B:443:MET:CE	2.34	0.57
1:A:540:LEU:O	1:A:542:ALA:N	2.38	0.57
1:A:149:MET:CG	1:A:149:MET:O	2.54	0.56
1:A:340:VAL:HG11	1:A:443:MET:HE1	1.89	0.55
1:A:286:TRP:CE2	2:A:901:SCK:H92	2.42	0.54
1:A:541:SER:O	1:A:542:ALA:CB	2.55	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:GLY:O	1:A:421:GLN:HG2	2.08	0.54
1:A:66:GLN:HG2	1:A:98:TYR:CG	2.42	0.54
1:A:211:MET:HG2	1:A:308:LEU:HD21	1.89	0.53
1:B:328:VAL:O	1:B:427:ALA:HA	2.08	0.53
1:A:458:PRO:HA	1:A:465:TYR:CD2	2.44	0.52
1:A:291:GLN:OE1	1:A:369[B]:GLN:NE2	2.42	0.52
1:A:165:ARG:NH1	1:A:166:GLU:HG3	2.25	0.52
1:B:17:LEU:HD23	1:B:60:LEU:HB3	1.92	0.51
1:A:48:MET:HE1	1:A:166:GLU:HA	1.93	0.51
1:A:13:ARG:HG3	1:A:185:GLU:CD	2.32	0.50
1:A:166:GLU:HB2	1:A:270:ILE:HD13	1.94	0.49
1:A:465:TYR:OH	2:A:902:SCK:H203	2.13	0.49
1:B:166:GLU:HG2	1:B:270:ILE:HD13	1.95	0.48
1:B:458:PRO:HA	1:B:465:TYR:CD2	2.48	0.48
1:B:243:GLU:OE1	1:B:246:ARG:NH1	2.46	0.48
1:A:328:VAL:O	1:A:427:ALA:HA	2.14	0.48
1:A:541:SER:O	1:A:542:ALA:HB3	2.14	0.48
1:B:284:HIS:ND1	1:B:287:HIS:HD2	2.12	0.48
1:A:45:ARG:CZ	1:A:51:GLU:OE1	2.63	0.47
1:B:295:PHE:O	1:B:296:ARG:HD3	2.15	0.47
1:B:21:ARG:HD3	1:B:105:TYR:CE1	2.50	0.46
1:B:48:MET:CE	1:B:166:GLU:HA	2.37	0.46
1:B:543:THR:HG22	5:B:1217:HOH:O	2.15	0.46
1:A:453:PHE:HB3	1:A:476:LEU:HD12	1.98	0.45
1:B:326:VAL:HG12	1:B:328:VAL:HG13	1.98	0.45
1:B:340:VAL:HG11	1:B:443:MET:HE2	1.99	0.45
1:A:45:ARG:HG2	5:A:1077:HOH:O	2.16	0.44
1:A:413:GLN:NE2	5:A:1059:HOH:O	2.50	0.44
1:A:313:GLU:HG3	5:A:1147:HOH:O	2.17	0.44
1:A:66:GLN:CG	1:A:98:TYR:CD2	3.00	0.44
1:A:213:ILE:HA	1:A:219:ARG:HD3	2.00	0.44
1:A:289:LEU:HD12	5:A:1244:HOH:O	2.17	0.43
1:B:465:TYR:OH	2:B:952:SCK:H91	2.19	0.43
1:B:4:GLU:OE1	1:B:18:ARG:HD3	2.18	0.43
1:A:353:LEU:HB3	1:A:391:PRO:HB2	1.99	0.43
1:A:380:LEU:C	3:A:961:P6G:H152	2.39	0.43
2:A:902:SCK:O14	2:A:902:SCK:H192	2.18	0.43
1:B:528:THR:O	1:B:531:PHE:HB3	2.19	0.43
1:A:339:LEU:HD13	1:A:346:PHE:CE1	2.53	0.43
1:A:165:ARG:HH11	1:A:166:GLU:HG3	1.83	0.42
1:A:66:GLN:HG3	1:A:98:TYR:CD2	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:491:ASP:HB3	1:A:494:ASP:HB3	2.00	0.42
2:A:901:SCK:H32	2:A:901:SCK:H93	1.83	0.42
1:A:66:GLN:HG2	1:A:98:TYR:CD1	2.54	0.42
1:A:43:GLY:C	1:A:45:ARG:H	2.22	0.42
1:B:24:ALA:HB3	1:B:140:GLN:HG3	2.02	0.42
1:A:360:LEU:HD22	1:A:379:VAL:HG11	2.02	0.42
2:B:952:SCK:H203	2:B:952:SCK:H151	1.84	0.41
1:B:296:ARG:HH22	1:B:405:HIS:HE1	1.68	0.41
1:B:134:ASP:OD1	1:B:136:ARG:HD2	2.20	0.41
1:B:327:LEU:HD11	1:B:500:TRP:CH2	2.54	0.41
1:B:291:GLN:HE21	1:B:291:GLN:HB2	1.66	0.41
1:B:340:VAL:CG1	1:B:443:MET:HE2	2.50	0.41
1:B:141:VAL:HG21	1:B:459:LEU:CD2	2.50	0.41
1:B:130:LEU:HD12	1:B:133:TYR:CE2	2.56	0.41
1:B:369:GLN:HB2	5:B:964:HOH:O	2.20	0.41
1:A:24:ALA:HB3	1:A:140:GLN:HG3	2.03	0.41
1:B:390:ASP:HA	1:B:391:PRO:HD3	1.96	0.40
1:B:457:LEU:N	1:B:458:PRO:CD	2.84	0.40
1:B:337:TYR:O	1:B:340:VAL:HG22	2.22	0.40
1:A:66:GLN:HG2	1:A:98:TYR:CD2	2.56	0.40
1:B:320:ASP:OD1	1:B:322:GLN:HG3	2.22	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	534/543 (98%)	516 (97%)	16 (3%)	2 (0%)	39	43
1	B	530/543 (98%)	511 (96%)	19 (4%)	0	100	100
All	All	1064/1086 (98%)	1027 (96%)	35 (3%)	2 (0%)	52	61

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	496	LYS
1	A	541	SER

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	439/442 (99%)	433 (99%)	6 (1%)	74	84
1	B	438/442 (99%)	427 (98%)	11 (2%)	55	66
All	All	877/884 (99%)	860 (98%)	17 (2%)	65	75

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ARG
1	A	70	TYR
1	A	149	MET
1	A	200	PHE
1	A	295	PHE
1	A	421	GLN
1	B	136	ARG
1	B	200	PHE
1	B	265	ASN
1	B	281	LEU
1	B	291	GLN
1	B	295	PHE
1	B	296	ARG
1	B	322	GLN
1	B	386	LEU
1	B	413	GLN
1	B	424	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	GLN
1	A	265	ASN
1	A	508	GLN
1	B	265	ASN
1	B	287	HIS
1	B	291	GLN
1	B	405	HIS

5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

6 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	SCK	A	901	-	19,19,19	1.60	2 (10%)	26,26,26	1.32	4 (15%)
2	SCK	A	902	-	19,19,19	1.55	2 (10%)	26,26,26	1.10	2 (7%)
4	ACY	A	903	-	1,3,3	1.50	0	0,3,3	0.00	-
3	P6G	A	961	-	18,18,18	2.17	6 (33%)	17,17,17	1.33	2 (11%)
2	SCK	B	951	-	19,19,19	1.47	2 (10%)	26,26,26	1.16	3 (11%)
2	SCK	B	952	-	19,19,19	1.48	2 (10%)	26,26,26	1.00	1 (3%)

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	SCK	A	901	-	-	0/19/19/19	0/0/0/0
2	SCK	A	902	-	-	0/19/19/19	0/0/0/0
4	ACY	A	903	-	-	0/0/0/0	0/0/0/0
3	P6G	A	961	-	-	0/16/16/16	0/0/0/0
2	SCK	B	951	-	-	0/19/19/19	0/0/0/0
2	SCK	B	952	-	-	0/19/19/19	0/0/0/0

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	961	P6G	O7-C6	2.72	1.53	1.42
3	A	961	P6G	O19-C18	3.27	1.59	1.42
2	B	951	SCK	O4-C5	3.31	1.43	1.33
3	A	961	P6G	O16-C15	3.47	1.56	1.42
3	A	961	P6G	O4-C3	3.59	1.57	1.42
3	A	961	P6G	O13-C12	3.74	1.58	1.42
2	A	902	SCK	O4-C5	3.80	1.44	1.33
2	B	951	SCK	O14-C12	3.87	1.45	1.33
2	B	952	SCK	O14-C12	3.91	1.45	1.33
2	B	952	SCK	O4-C5	3.93	1.45	1.33
2	A	901	SCK	O4-C5	4.36	1.46	1.33
3	A	961	P6G	O10-C9	4.41	1.60	1.42
2	A	901	SCK	O14-C12	4.47	1.46	1.33
2	A	902	SCK	O14-C12	4.65	1.47	1.33

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	951	SCK	C15-C16-N17	-2.55	107.85	116.03
2	A	901	SCK	O14-C12-O13	-2.15	117.95	123.49
2	B	951	SCK	O14-C12-C11	2.00	118.00	111.90
3	A	961	P6G	O13-C12-C11	2.18	120.05	110.36
2	B	952	SCK	O4-C5-C6	2.40	119.21	111.90
2	B	951	SCK	C3-O4-C5	2.59	124.28	117.02
2	A	901	SCK	O4-C5-C6	2.88	120.67	111.90
2	A	901	SCK	C15-O14-C12	2.89	125.11	117.02
2	A	902	SCK	C15-O14-C12	2.95	125.29	117.02
2	A	901	SCK	O14-C12-C11	3.15	121.51	111.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	961	P6G	O1-C2-C3	3.16	131.56	112.03
2	A	902	SCK	C3-O4-C5	3.26	126.16	117.02

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	SCK	3	0
2	A	902	SCK	2	0
4	A	903	ACY	1	0
3	A	961	P6G	1	0
2	B	951	SCK	1	0
2	B	952	SCK	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	536/543 (98%)	-0.09	13 (2%) 62 66	42, 55, 75, 107	0
1	B	533/543 (98%)	-0.05	20 (3%) 44 48	44, 60, 79, 109	0
All	All	1069/1086 (98%)	-0.07	33 (3%) 52 57	42, 57, 78, 109	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	542	ALA	6.6
1	A	495	SER	6.2
1	B	543	THR	6.2
1	A	540	LEU	5.1
1	B	495	SER	4.7
1	A	542	ALA	4.3
1	B	323	ASP	4.2
1	A	541	SER	4.0
1	A	497	SER	3.4
1	A	493	ARG	3.3
1	A	494	ASP	3.3
1	B	42	VAL	3.3
1	B	268	GLU	3.0
1	B	109	ALA	2.8
1	B	165	ARG	2.7
1	B	41	PRO	2.5
1	B	156	PHE	2.4
1	A	109	ALA	2.4
1	B	496	LYS	2.4
1	B	455	PHE	2.4
1	A	496	LYS	2.3
1	B	155	THR	2.3
1	B	497	SER	2.2
1	A	492	PRO	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	541	SER	2.2
1	B	78	PRO	2.2
1	B	13	ARG	2.2
1	B	138	LEU	2.2
1	A	467	THR	2.1
1	B	492	PRO	2.1
1	A	323	ASP	2.1
1	A	226	VAL	2.0
1	B	106	PRO	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	SCK	B	952	20/20	0.94	0.28	5.34	80,84,87,87	0
4	ACY	A	903	4/4	0.98	0.20	3.46	70,71,71,72	0
2	SCK	A	901	20/20	0.89	0.19	3.16	64,71,78,79	0
2	SCK	B	951	20/20	0.89	0.18	2.97	79,83,84,86	0
3	P6G	A	961	19/19	0.90	0.15	0.41	60,71,74,75	0
2	SCK	A	902	20/20	0.91	0.18	0.32	67,73,79,79	0

6.5 Other polymers [i](#)

There are no such residues in this entry.