



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 06:33 am GMT

PDB ID : 3Q7G
Title : Crystal Structure of E2 domain of Human Amyloid Precursor-Like Protein 1
in complex with SOS (sucrose octasulfate)
Authors : Xue, Y.; Ha, Y.
Deposited on : 2011-01-04
Resolution : 2.30 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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

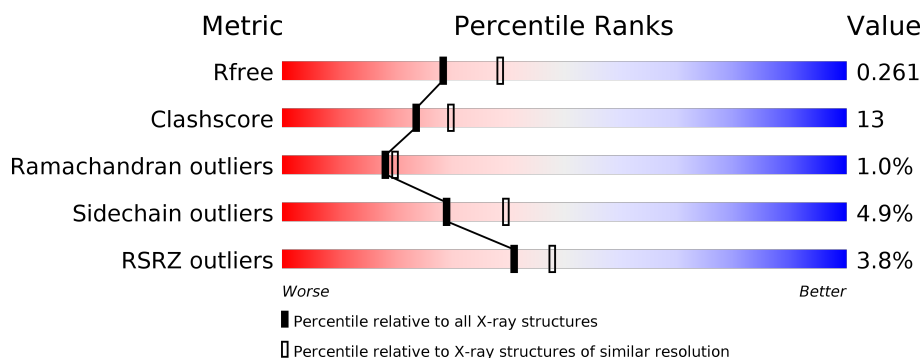
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	100719	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

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	214	
1	B	214	

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	SCR	B	2	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3349 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.

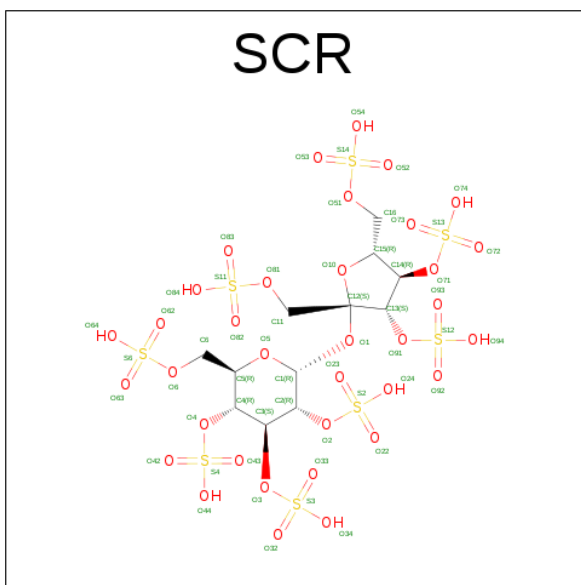
- Molecule 1 is a protein called Amyloid-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	203	Total	C	N	O	S	0	0	0
			1543	959	301	278	5			
1	B	195	Total	C	N	O	S	0	0	0
			1479	924	280	271	4			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	281	GLY	-	EXPRESSION TAG	UNP P51693
A	282	SER	-	EXPRESSION TAG	UNP P51693
A	283	HIS	-	EXPRESSION TAG	UNP P51693
A	284	MET	-	EXPRESSION TAG	UNP P51693
B	281	GLY	-	EXPRESSION TAG	UNP P51693
B	282	SER	-	EXPRESSION TAG	UNP P51693
B	283	HIS	-	EXPRESSION TAG	UNP P51693
B	284	MET	-	EXPRESSION TAG	UNP P51693

- Molecule 2 is SUGAR (SUCROSE OCTASULFATE) (three-letter code: SCR) (formula: $C_{12}H_{22}O_{35}S_8$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 55	C 12	O 35	S 8	0	0
2	A	1	Total 55	C 12	O 35	S 8	0	0
2	B	1	Total 55	C 12	O 35	S 8	0	0

- Molecule 3 is water.

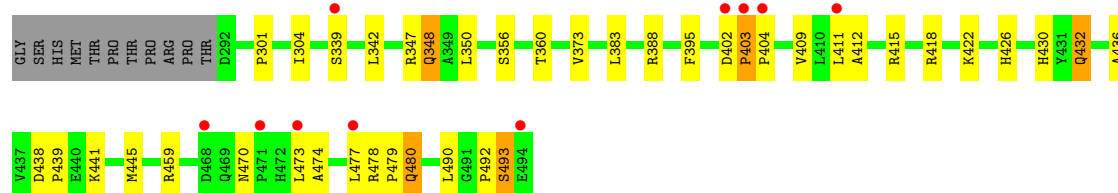
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	75	Total O 75 75	0	0
3	B	87	Total O 87 87	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

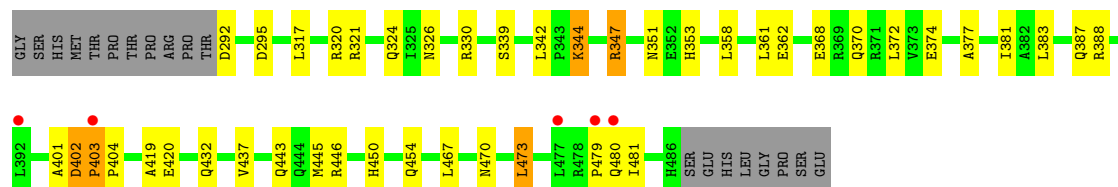
• Molecule 1: Amyloid-like protein 1

Chain A: 



• Molecule 1: Amyloid-like protein 1

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	73.55Å 82.24Å 89.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.39 – 2.30 28.47 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.0 (37.39-2.30) 96.8 (28.47-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.72 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.217 , 0.261 0.222 , 0.261	Depositor DCC
R_{free} test set	2366 reflections (10.92%)	DCC
Wilson B-factor (Å ²)	41.9	Xtriage
Anisotropy	0.111	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 41.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3349	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.15% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SCR

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	0/1569	0.54	0/2129
1	B	0.44	0/1503	0.57	0/2042
All	All	0.42	0/3072	0.55	0/4171

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1543	0	1454	26	0
1	B	1479	0	1395	40	0
2	A	110	0	44	15	0
2	B	55	0	22	2	0
3	A	75	0	0	5	0
3	B	87	0	0	6	0
All	All	3349	0	2915	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 13.

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:A:402:ASP:O	1:A:404:PRO:HD3	1.71	0.89
2:A:3:SCR:O73	1:B:437:VAL:HG12	1.76	0.84
1:B:321:ARG:HH11	1:B:324:GLN:HE22	1.27	0.81
1:B:339:SER:HB2	1:B:342:LEU:HD12	1.63	0.81
1:A:402:ASP:HB3	1:A:403:PRO:CD	2.12	0.80
1:B:470:ASN:CG	1:B:473:LEU:HB2	2.02	0.80
2:A:3:SCR:H15	2:A:3:SCR:O72	1.82	0.80
1:B:470:ASN:OD1	1:B:473:LEU:HB2	1.85	0.76
1:B:321:ARG:HH11	1:B:324:GLN:NE2	1.86	0.73
2:A:3:SCR:C15	2:A:3:SCR:O72	2.37	0.71
1:A:422:LYS:HG3	2:A:1:SCR:O24	1.89	0.71
1:A:402:ASP:HB3	1:A:403:PRO:HD3	1.72	0.70
1:A:430:HIS:HA	2:A:3:SCR:O64	1.91	0.70
1:B:317:LEU:HD13	1:B:368:GLU:HG2	1.75	0.68
1:B:321:ARG:NH1	1:B:324:GLN:HE22	1.93	0.66
1:B:344:LYS:HA	1:B:347:ARG:NH1	2.10	0.66
1:A:383:LEU:HD21	2:A:1:SCR:O53	1.97	0.65
1:B:467:LEU:CD2	1:B:481:ILE:HD11	2.26	0.64
1:A:477:LEU:HA	1:A:480:GLN:NE2	2.17	0.59
1:A:388:ARG:HD3	3:A:12:HOH:O	2.01	0.59
2:A:1:SCR:H61	3:A:37:HOH:O	2.03	0.59
2:A:1:SCR:O72	2:A:1:SCR:H162	2.03	0.58
1:A:492:PRO:O	1:A:493:SER:CB	2.50	0.58
1:B:358:LEU:O	1:B:362:GLU:HG3	2.03	0.58
1:B:450:HIS:CE1	1:B:454:GLN:HE21	2.21	0.57
2:A:3:SCR:H34	2:A:3:SCR:H44	1.51	0.56
1:A:474:ALA:O	1:A:478:ARG:N	2.38	0.56
1:B:470:ASN:ND2	1:B:473:LEU:HD12	2.21	0.56
1:B:402:ASP:CB	1:B:403:PRO:CD	2.84	0.55
1:A:479:PRO:HG2	1:A:480:GLN:H	1.73	0.54
1:B:443:GLN:HG3	1:B:446:ARG:NH2	2.24	0.53
1:B:401:ALA:O	1:B:402:ASP:C	2.48	0.53
2:A:1:SCR:O92	2:A:1:SCR:H112	2.09	0.52
1:B:450:HIS:NE2	1:B:454:GLN:NE2	2.57	0.52
1:B:324:GLN:OE1	1:B:361:LEU:HD11	2.09	0.52
1:B:402:ASP:CB	1:B:403:PRO:HD3	2.40	0.51
1:A:373:VAL:HG21	2:A:3:SCR:O74	2.10	0.51
1:A:301:PRO:HD2	1:A:304:ILE:HD12	1.91	0.51
1:B:450:HIS:CE1	1:B:454:GLN:NE2	2.78	0.51
2:A:1:SCR:O72	2:A:1:SCR:C16	2.59	0.51
2:B:2:SCR:O92	2:B:2:SCR:H111	2.11	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:3:SCR:O72	2:A:3:SCR:C16	2.60	0.50
1:A:342:LEU:H	1:A:347:ARG:NH2	2.09	0.50
1:A:360:THR:HG22	3:A:17:HOH:O	2.12	0.49
1:A:415:ARG:HD2	3:A:108:HOH:O	2.13	0.49
2:A:3:SCR:O73	1:B:437:VAL:CG1	2.55	0.48
2:A:3:SCR:O72	2:A:3:SCR:H162	2.14	0.48
1:B:320:ARG:HG2	1:B:324:GLN:HE21	1.79	0.48
1:B:419:ALA:HB1	3:B:88:HOH:O	2.14	0.47
1:B:321:ARG:HH11	1:B:324:GLN:CD	2.17	0.47
1:B:383:LEU:O	1:B:387:GLN:HG3	2.14	0.47
1:B:388:ARG:HD3	3:B:9:HOH:O	2.15	0.47
1:A:470:ASN:OD1	1:A:473:LEU:HB2	2.15	0.47
1:B:344:LYS:CA	1:B:347:ARG:NH1	2.78	0.46
1:B:353:HIS:HE1	3:B:495:HOH:O	1.99	0.46
1:A:441:LYS:O	1:A:445:MET:HG3	2.15	0.46
1:A:402:ASP:CB	1:A:403:PRO:CD	2.88	0.45
1:B:370:GLN:O	1:B:374:GLU:HB2	2.17	0.45
1:A:418:ARG:NH1	1:A:490:LEU:O	2.41	0.45
1:B:445:MET:HB2	3:B:45:HOH:O	2.18	0.44
1:B:317:LEU:HD22	1:B:368:GLU:CD	2.38	0.44
1:B:420:GLU:OE2	1:B:420:GLU:HA	2.18	0.44
1:A:432:GLN:HB3	1:A:432:GLN:HE21	1.65	0.43
1:B:377:ALA:O	1:B:381:ILE:HG12	2.17	0.43
1:A:395:PHE:HA	1:A:412:ALA:HB1	2.01	0.43
1:B:480:GLN:HG3	3:B:42:HOH:O	2.18	0.43
1:A:409:VAL:HG21	1:A:473:LEU:HD21	2.00	0.42
2:B:2:SCR:H112	2:B:2:SCR:O2	2.19	0.42
1:B:339:SER:CB	1:B:342:LEU:HD12	2.42	0.42
1:A:436:ALA:HB2	3:A:94:HOH:O	2.19	0.41
1:B:479:PRO:HG2	3:B:42:HOH:O	2.20	0.41
1:A:348:GLN:HB2	1:A:348:GLN:HE21	1.66	0.41
1:B:402:ASP:O	1:B:404:PRO:HD3	2.21	0.41
1:B:292:ASP:O	1:B:295:ASP:N	2.54	0.40
1:A:438:ASP:HA	1:A:439:PRO:HD2	1.88	0.40
1:B:317:LEU:HD12	1:B:372:LEU:HD22	2.02	0.40
1:B:326:ASN:O	1:B:330:ARG:HG3	2.22	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	201/214 (94%)	189 (94%)	10 (5%)	2 (1%)	18	20
1	B	193/214 (90%)	184 (95%)	7 (4%)	2 (1%)	18	20
All	All	394/428 (92%)	373 (95%)	17 (4%)	4 (1%)	18	20

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	493	SER
1	B	402	ASP
1	B	403	PRO
1	A	403	PRO

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	145/186 (78%)	136 (94%)	9 (6%)	21	28
1	B	140/186 (75%)	135 (96%)	5 (4%)	40	55
All	All	285/372 (77%)	271 (95%)	14 (5%)	29	39

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	339	SER
1	A	348	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	350	LEU
1	A	356	SER
1	A	411	LEU
1	A	426	HIS
1	A	432	GLN
1	A	459	ARG
1	A	480	GLN
1	B	344	LYS
1	B	347	ARG
1	B	351	ASN
1	B	432	GLN
1	B	473	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	348	GLN
1	A	359	GLN
1	A	400	GLN
1	A	426	HIS
1	A	432	GLN
1	A	480	GLN
1	B	353	HIS
1	B	359	GLN
1	B	405	GLN
1	B	430	HIS
1	B	432	GLN
1	B	443	GLN
1	B	448	GLN
1	B	454	GLN

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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

3 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	SCR	A	1	-	55,56,56	1.98	8 (14%)	67,92,92	1.58	13 (19%)
2	SCR	A	3	-	55,56,56	2.01	8 (14%)	67,92,92	1.40	9 (13%)
2	SCR	B	2	-	55,56,56	2.00	8 (14%)	67,92,92	1.54	11 (16%)

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	SCR	A	1	-	-	0/49/88/88	0/2/2/2
2	SCR	A	3	-	-	0/49/88/88	0/2/2/2
2	SCR	B	2	-	-	0/49/88/88	0/2/2/2

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	SCR	O6-S6	-4.86	1.42	1.56
2	A	3	SCR	O6-S6	-4.83	1.43	1.56
2	B	2	SCR	O4-S4	-4.72	1.43	1.56
2	A	3	SCR	O91-S12	-4.71	1.43	1.56
2	B	2	SCR	O51-S14	-4.71	1.43	1.56
2	B	2	SCR	O91-S12	-4.70	1.43	1.56
2	A	3	SCR	O71-S13	-4.70	1.43	1.56
2	B	2	SCR	O71-S13	-4.69	1.43	1.56
2	A	3	SCR	O81-S11	-4.67	1.43	1.56

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	SCR	O51-S14	-4.66	1.43	1.56
2	A	1	SCR	O71-S13	-4.64	1.43	1.56
2	A	1	SCR	O6-S6	-4.64	1.43	1.56
2	A	3	SCR	O2-S2	-4.63	1.43	1.56
2	A	1	SCR	O81-S11	-4.63	1.43	1.56
2	B	2	SCR	O81-S11	-4.62	1.43	1.56
2	A	1	SCR	O3-S3	-4.57	1.43	1.56
2	B	2	SCR	O3-S3	-4.57	1.43	1.56
2	A	3	SCR	O4-S4	-4.56	1.43	1.56
2	A	1	SCR	O91-S12	-4.56	1.43	1.56
2	A	3	SCR	O51-S14	-4.55	1.43	1.56
2	A	3	SCR	O3-S3	-4.55	1.43	1.56
2	A	1	SCR	O4-S4	-4.52	1.43	1.56
2	A	1	SCR	O2-S2	-4.52	1.43	1.56
2	B	2	SCR	O2-S2	-4.45	1.44	1.56

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	SCR	C2-O2-S2	-5.00	109.35	118.97
2	A	3	SCR	C2-O2-S2	-4.95	109.45	118.97
2	A	1	SCR	C14-O71-S13	-4.61	110.10	118.97
2	B	2	SCR	C3-O3-S3	-4.59	110.14	118.97
2	A	1	SCR	C3-O3-S3	-4.55	110.22	118.97
2	B	2	SCR	C2-O2-S2	-4.52	110.28	118.97
2	B	2	SCR	C4-O4-S4	-4.38	110.54	118.97
2	A	3	SCR	C3-O3-S3	-4.37	110.57	118.97
2	B	2	SCR	C14-O71-S13	-4.24	110.81	118.97
2	A	1	SCR	C6-C5-C4	-3.56	104.45	113.30
2	A	3	SCR	C4-O4-S4	-3.45	112.32	118.97
2	A	1	SCR	O63-S6-O62	-3.16	98.62	112.25
2	A	1	SCR	C4-O4-S4	-3.07	113.07	118.97
2	B	2	SCR	C12-O1-C1	-3.02	109.55	117.62
2	A	3	SCR	O63-S6-O62	-2.96	99.48	112.25
2	B	2	SCR	O63-S6-O62	-2.84	99.97	112.25
2	B	2	SCR	O64-S6-O62	-2.80	98.86	108.79
2	A	1	SCR	O64-S6-O62	-2.55	99.77	108.79
2	A	3	SCR	O64-S6-O62	-2.53	99.82	108.79
2	A	3	SCR	C15-C14-C13	-2.50	96.41	103.28
2	A	1	SCR	C11-C12-C13	-2.45	109.94	115.33
2	A	1	SCR	O5-C5-C6	-2.27	102.11	106.64
2	B	2	SCR	C6-C5-C4	-2.19	107.87	113.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	SCR	O6-S6-O62	-2.03	100.54	106.78
2	A	3	SCR	O6-S6-O63	2.16	113.42	106.78
2	B	2	SCR	O6-S6-O63	2.18	113.50	106.78
2	B	2	SCR	O6-C6-C5	2.20	111.86	107.67
2	A	1	SCR	O5-C5-C4	2.34	114.54	109.75
2	A	1	SCR	O6-S6-O63	2.35	114.03	106.78
2	A	3	SCR	O64-S6-O63	2.49	117.61	108.79
2	A	3	SCR	O71-C14-C13	2.61	114.58	108.91
2	A	1	SCR	O64-S6-O63	2.89	119.01	108.79
2	B	2	SCR	O64-S6-O63	3.02	119.50	108.79

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	SCR	6	0
2	A	3	SCR	9	0
2	B	2	SCR	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	203/214 (94%)	0.37	10 (4%) 30 37	31, 52, 92, 132	0
1	B	195/214 (91%)	0.27	5 (2%) 56 63	27, 47, 80, 97	0
All	All	398/428 (92%)	0.32	15 (3%) 41 48	27, 49, 87, 132	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	494	GLU	6.0
1	B	477	LEU	3.9
1	B	403	PRO	3.8
1	A	402	ASP	3.7
1	B	479	PRO	3.1
1	A	473	LEU	2.8
1	A	403	PRO	2.8
1	A	477	LEU	2.7
1	A	339	SER	2.5
1	A	411	LEU	2.5
1	A	404	PRO	2.3
1	B	392	LEU	2.2
1	A	471	PRO	2.1
1	A	468	ASP	2.1
1	B	480	GLN	2.1

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	SCR	B	2	55/55	0.85	0.28	4.60	53,90,114,119	0
2	SCR	A	3	55/55	0.79	0.23	1.65	88,126,155,166	0
2	SCR	A	1	55/55	0.80	0.18	0.39	60,103,128,137	0

6.5 Other polymers [i](#)

There are no such residues in this entry.