Full wwPDB X-ray Structure Validation Report (i)

Jan 7, 2024 – 12:10 am GMT

PDB ID	:	6FFY
Title	:	Structure of the mouse SorCS2-NGF complex
Authors	:	Leloup, N.O.L.; Janssen, B.J.C.
Deposited on	:	2018-01-09
Resolution	:	3.90 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 (i) 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 (i)) were used in the production of this report:

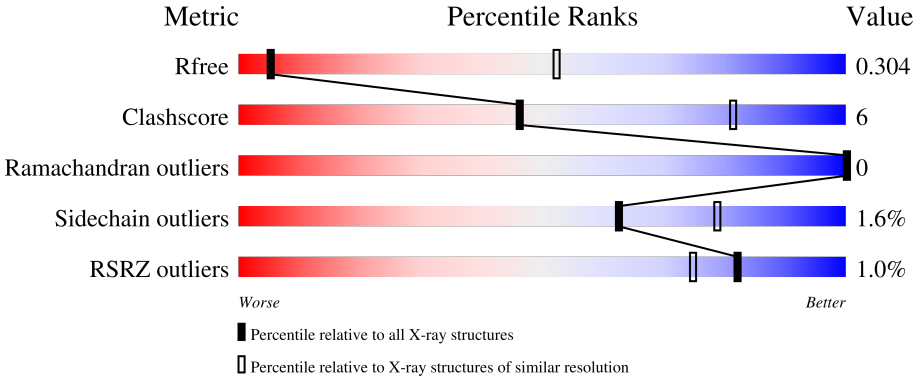
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.90 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}	130704	1002 (4.14-3.66)
Clashscore	141614	1004 (4.12-3.68)
Ramachandran outliers	138981	1021 (4.14-3.66)
Sidechain outliers	138945	1014 (4.14-3.66)
RSRZ outliers	127900	1275 (4.20-3.60)

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 <=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	972	% 77% 17% • 6%
2	B	129	% 81% • 15%
2	C	129	79% 7% 14%
3	D	3	67% 33%

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
3	BMA	D	3	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9111 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 VPS10 domain-containing receptor SorCS2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	918	7291	4632	1241	1391	27	0	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	115	GLY	-	expression tag	UNP Q9EPR5
A	252	THR	MET	conflict	UNP Q9EPR5
A	1078	ALA	-	expression tag	UNP Q9EPR5
A	1079	ALA	-	expression tag	UNP Q9EPR5
A	1080	ALA	-	expression tag	UNP Q9EPR5
A	1081	HIS	-	expression tag	UNP Q9EPR5
A	1082	HIS	-	expression tag	UNP Q9EPR5
A	1083	HIS	-	expression tag	UNP Q9EPR5
A	1084	HIS	-	expression tag	UNP Q9EPR5
A	1085	HIS	-	expression tag	UNP Q9EPR5
A	1086	HIS	-	expression tag	UNP Q9EPR5

- Molecule 2 is a protein called Beta-nerve growth factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	110	864	540	152	165	7	0	0	0
2	C	111	875	549	153	166	7	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

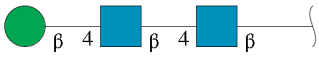
Chain	Residue	Modelled	Actual	Comment	Reference
B	239	ALA	-	expression tag	UNP P01139
B	240	ALA	-	expression tag	UNP P01139
B	241	GLY	-	expression tag	UNP P01139

Continued on next page...

Continued from previous page...

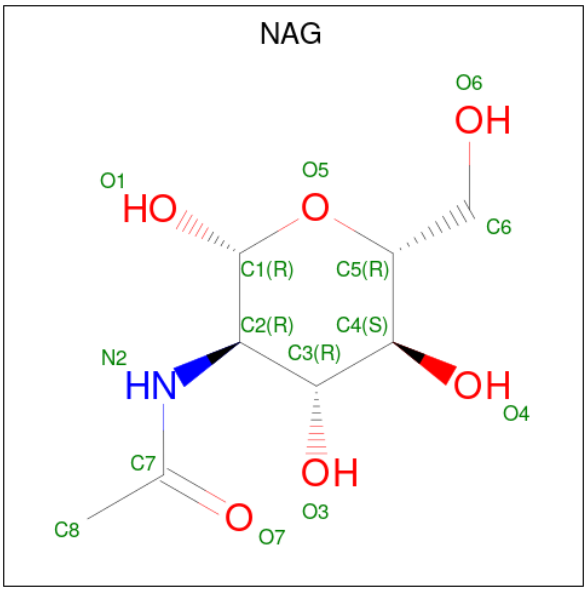
Chain	Residue	Modelled	Actual	Comment	Reference
B	242	ALA	-	expression tag	UNP P01139
B	243	ALA	-	expression tag	UNP P01139
B	244	ALA	-	expression tag	UNP P01139
B	245	HIS	-	expression tag	UNP P01139
B	246	HIS	-	expression tag	UNP P01139
B	247	HIS	-	expression tag	UNP P01139
B	248	HIS	-	expression tag	UNP P01139
B	249	HIS	-	expression tag	UNP P01139
B	250	HIS	-	expression tag	UNP P01139
C	239	ALA	-	expression tag	UNP P01139
C	240	ALA	-	expression tag	UNP P01139
C	241	GLY	-	expression tag	UNP P01139
C	242	ALA	-	expression tag	UNP P01139
C	243	ALA	-	expression tag	UNP P01139
C	244	ALA	-	expression tag	UNP P01139
C	245	HIS	-	expression tag	UNP P01139
C	246	HIS	-	expression tag	UNP P01139
C	247	HIS	-	expression tag	UNP P01139
C	248	HIS	-	expression tag	UNP P01139
C	249	HIS	-	expression tag	UNP P01139
C	250	HIS	-	expression tag	UNP P01139

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	D	3	39	22	2	15	0	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



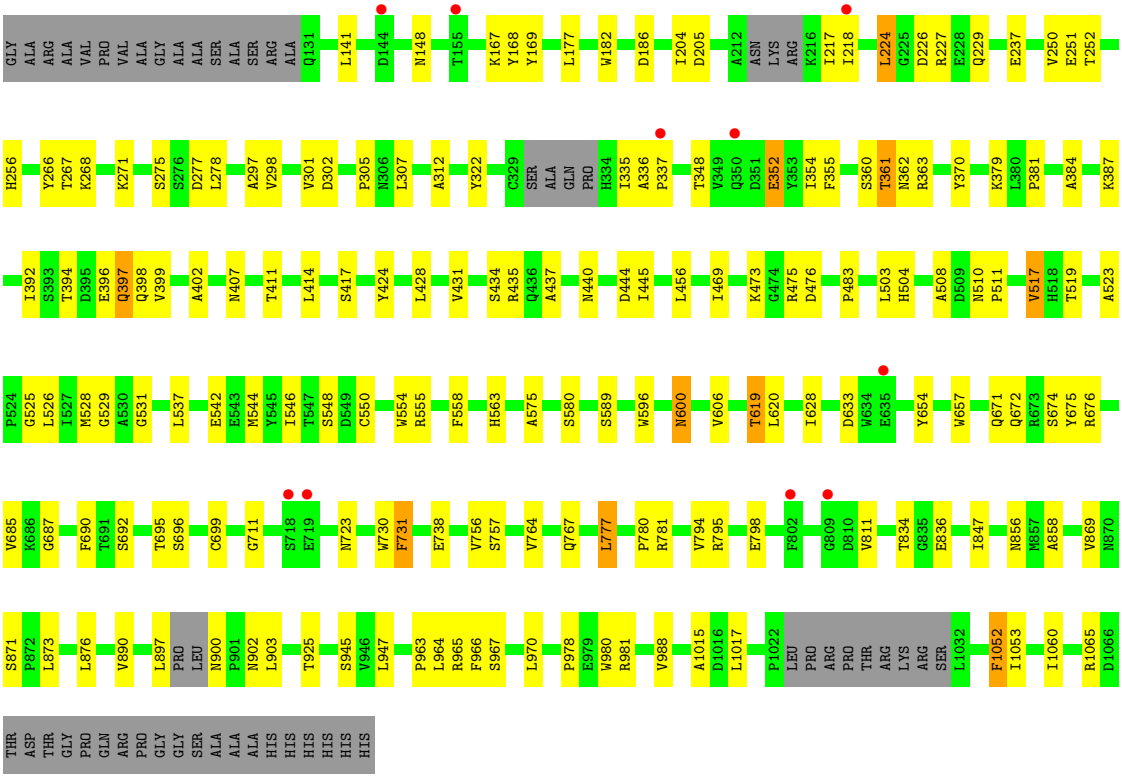
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	14	8	1	5	0	0
			Total	C	N	O		
4	A	1	14	8	1	5	0	0
			Total	C	N	O		
4	A	1	14	8	1	5	0	0

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 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.

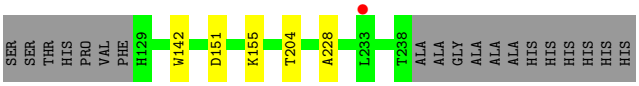
• Molecule 1: VPS10 domain-containing receptor SorCS2

Chain A:



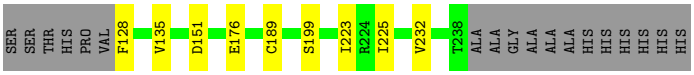
• Molecule 2: Beta-nerve growth factor

Chain B:



• Molecule 2: Beta-nerve growth factor

Chain C:



• Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	229.75Å 117.71Å 90.00Å 90.00° 111.87° 90.00°	Depositor
Resolution (Å)	60.84 – 3.90 60.84 – 3.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (60.84-3.90) 99.9 (60.84-3.90)	Depositor EDS
R_{merge}	0.34	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.57 (at 3.88Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.258 , 0.305 0.258 , 0.304	Depositor DCC
R_{free} test set	1045 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å^2)	115.1	Xtriage
Anisotropy	0.273	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.26 , 60.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.24$	Xtriage
Estimated twinning fraction	0.068 for -h-2*l,-k,l	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	9111	wwPDB-VP
Average B, all atoms (Å^2)	134.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.61% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: BMA, NAG

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	0.25	0/7455	0.47	0/10143
2	B	0.25	0/881	0.44	0/1193
2	C	0.25	0/893	0.47	0/1209
All	All	0.25	0/9229	0.47	0/12545

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 (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	7291	0	7164	107	0
2	B	864	0	837	3	0
2	C	875	0	846	4	0
3	D	39	0	34	1	0
4	A	42	0	39	0	0
All	All	9111	0	8920	113	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 6.

All (113) 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:204:ILE:HG21	1:A:224:LEU:HB3	1.43	1.01
1:A:674:SER:HB3	1:A:695:THR:HB	1.69	0.74
1:A:508:ALA:HB2	1:A:517:VAL:HB	1.72	0.71
1:A:217:ILE:HG21	1:A:237:GLU:HG2	1.73	0.71
1:A:876:LEU:HD22	1:A:947:LEU:HB3	1.71	0.71
1:A:967:SER:HB3	1:A:1060:ILE:HG23	1.73	0.70
1:A:777:LEU:HD21	1:A:858:ALA:HB2	1.74	0.70
1:A:606:VAL:HG22	1:A:628:ILE:HG22	1.75	0.68
1:A:437:ALA:HB3	1:A:440:ASN:HB2	1.76	0.68
1:A:414:LEU:HB3	1:A:428:LEU:HB3	1.77	0.67
1:A:510:ASN:HD21	1:A:542:GLU:CD	2.00	0.65
1:A:218:ILE:HG21	1:A:278:LEU:HD11	1.79	0.63
1:A:267:THR:HB	1:A:271:LYS:HB2	1.81	0.62
1:A:204:ILE:CG2	1:A:224:LEU:HB3	2.26	0.62
1:A:226:ASP:OD1	1:A:227:ARG:N	2.33	0.62
1:A:510:ASN:ND2	1:A:542:GLU:OE2	2.33	0.60
1:A:963:PRO:HB2	1:A:1065:ARG:HB3	1.84	0.60
1:A:544:MET:HB2	1:A:558:PHE:HB2	1.84	0.59
1:A:394:THR:HG22	1:A:399:VAL:HG22	1.84	0.59
1:A:475:ARG:HH21	1:A:723:ASN:HB2	1.67	0.59
1:A:360:SER:HB2	1:A:363:ARG:O	2.03	0.59
1:A:780:PRO:O	1:A:781:ARG:NH1	2.36	0.58
1:A:362:ASN:ND2	3:D:1:NAG:O7	2.37	0.57
1:A:348:THR:HG22	1:A:354:ILE:HG23	1.87	0.57
1:A:397:GLN:HG3	1:A:757:SER:HB3	1.86	0.56
1:A:847:ILE:HD11	1:A:903:LEU:HD13	1.88	0.55
1:A:475:ARG:NH1	1:A:476:ASP:OD2	2.39	0.55
1:A:177:LEU:HD12	1:A:204:ILE:HG22	1.89	0.55
1:A:297:ALA:HB2	1:A:307:LEU:HB2	1.87	0.55
1:A:256:HIS:NE2	1:A:305:PRO:O	2.32	0.54
1:A:381:PRO:HB2	1:A:384:ALA:HB3	1.87	0.54
1:A:392:ILE:HD13	1:A:445:ILE:HG21	1.89	0.54
2:C:151:ASP:HA	2:C:223:ILE:HA	1.91	0.53
1:A:523:ALA:HB3	1:A:526:LEU:HB2	1.89	0.53
1:A:417:SER:HB3	1:A:424:TYR:CE2	2.44	0.53
1:A:434:SER:OG	1:A:435:ARG:N	2.41	0.53
1:A:690:PHE:CE2	1:A:692:SER:HB3	2.44	0.52
1:A:519:THR:HG22	1:A:529:GLY:HA3	1.91	0.52
1:A:795:ARG:HB3	1:A:871:SER:HB2	1.90	0.52
1:A:780:PRO:HD3	1:A:856:ASN:HD22	1.75	0.51
1:A:456:LEU:HG	1:A:469:ILE:HG13	1.91	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:897:LEU:O	1:A:900:ASN:N	2.44	0.51
1:A:398:GLN:HE21	1:A:473:LYS:HE2	1.75	0.51
1:A:970:LEU:HD11	1:A:980:TRP:CH2	2.46	0.50
2:B:204:THR:OG1	2:B:228:ALA:N	2.44	0.49
1:A:167:LYS:HZ2	1:A:205:ASP:HA	1.77	0.49
1:A:169:TYR:HA	1:A:177:LEU:HD23	1.95	0.48
1:A:411:THR:HA	1:A:431:VAL:O	2.14	0.47
1:A:890:VAL:O	1:A:925:THR:HA	2.14	0.47
1:A:964:LEU:HD11	1:A:1017:LEU:HB2	1.96	0.47
1:A:528:MET:HB2	1:A:546:ILE:HG13	1.97	0.46
1:A:657:TRP:CE3	1:A:675:TYR:HB2	2.51	0.46
1:A:978:PRO:HA	1:A:981:ARG:HE	1.80	0.46
1:A:475:ARG:NH2	1:A:723:ASN:HB2	2.30	0.46
1:A:964:LEU:HB2	1:A:1015:ALA:HB3	1.98	0.46
1:A:387:LYS:HD3	1:A:407:ASN:HD21	1.81	0.46
1:A:355:PHE:CE1	1:A:394:THR:HG21	2.51	0.46
1:A:580:SER:HG	2:B:142:TRP:HE1	1.64	0.45
1:A:654:TYR:HB3	1:A:676:ARG:HB3	1.97	0.45
2:B:151:ASP:OD1	2:B:155:LYS:N	2.48	0.45
1:A:398:GLN:NE2	1:A:473:LYS:HE2	2.31	0.45
1:A:392:ILE:HD12	1:A:414:LEU:HD13	1.98	0.45
1:A:965:ARG:HG3	1:A:1065:ARG:HA	1.97	0.45
2:C:176:GLU:HG2	2:C:225:ILE:HG23	1.99	0.45
1:A:970:LEU:HD11	1:A:980:TRP:HH2	1.82	0.45
1:A:510:ASN:HA	1:A:511:PRO:HD3	1.78	0.45
1:A:730:TRP:CD1	1:A:731:PHE:HB3	2.52	0.45
1:A:794:VAL:HB	1:A:869:VAL:HG22	1.98	0.44
2:C:135:VAL:HG12	2:C:189:CYS:HB3	1.98	0.44
1:A:275:SER:OG	1:A:277:ASP:OD1	2.34	0.44
1:A:218:ILE:HG21	1:A:278:LEU:HD21	1.99	0.44
1:A:795:ARG:HG3	1:A:798:GLU:HB2	2.00	0.44
1:A:379:LYS:NZ	1:A:738:GLU:OE2	2.50	0.44
1:A:600:ASN:OD1	1:A:600:ASN:N	2.51	0.44
1:A:619:THR:HG22	1:A:620:LEU:H	1.83	0.44
1:A:711:GLY:HA3	1:A:731:PHE:CE2	2.52	0.44
1:A:756:VAL:O	1:A:757:SER:OG	2.31	0.43
1:A:252:THR:HG22	1:A:266:TYR:HB3	2.00	0.43
1:A:397:GLN:H	1:A:397:GLN:HG2	1.60	0.43
1:A:312:ALA:HB3	1:A:322:TYR:CE1	2.53	0.43
1:A:672:GLN:HG3	1:A:699:CYS:SG	2.58	0.43
1:A:229:GLN:HE22	1:A:250:VAL:H	1.65	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:ASP:OD1	1:A:186:ASP:N	2.50	0.43
1:A:685:VAL:HG12	1:A:687:GLY:H	1.84	0.43
1:A:483:PRO:HB3	1:A:555:ARG:HA	2.01	0.43
1:A:525:GLY:HA2	1:A:550:CYS:HB2	2.00	0.43
1:A:671:GLN:HE21	1:A:696:SER:HB2	1.83	0.43
1:A:148:ASN:HB2	1:A:168:TYR:HA	2.01	0.42
1:A:764:VAL:O	1:A:767:GLN:NE2	2.27	0.42
1:A:1052:PHE:HD2	1:A:1053:ILE:N	2.17	0.42
1:A:336:ALA:HB3	1:A:337:PRO:HD3	2.01	0.42
1:A:229:GLN:HE22	1:A:250:VAL:N	2.17	0.42
1:A:229:GLN:NE2	1:A:250:VAL:HG12	2.35	0.42
1:A:361:THR:HG23	1:A:362:ASN:H	1.83	0.42
1:A:141:LEU:HD22	1:A:182:TRP:CD2	2.54	0.42
1:A:301:VAL:O	1:A:302:ASP:HB2	2.19	0.42
1:A:834:THR:HG22	1:A:836:GLU:H	1.84	0.42
1:A:322:TYR:CD2	1:A:335:ILE:HG12	2.55	0.42
1:A:483:PRO:HB3	1:A:554:TRP:O	2.20	0.42
1:A:352:GLU:HG3	1:A:370:TYR:HE1	1.85	0.42
1:A:251:GLU:HB2	1:A:268:LYS:HA	2.01	0.41
1:A:503:LEU:HA	1:A:531:GLY:HA3	2.02	0.41
1:A:526:LEU:HD23	1:A:548:SER:HA	2.02	0.41
1:A:589:SER:HB2	1:A:596:TRP:CD2	2.55	0.41
1:A:504:HIS:CD2	1:A:537:LEU:HD22	2.56	0.41
1:A:563:HIS:O	1:A:575:ALA:HA	2.19	0.41
1:A:966:PHE:HZ	1:A:988:VAL:HG21	1.85	0.41
1:A:392:ILE:HD11	1:A:402:ALA:HB2	2.03	0.41
2:C:199:SER:HA	2:C:232:VAL:O	2.21	0.41
1:A:392:ILE:HG21	1:A:445:ILE:HD13	2.03	0.40
1:A:633:ASP:N	1:A:633:ASP:OD1	2.54	0.40
1:A:690:PHE:HE2	1:A:692:SER:HB3	1.85	0.40
1:A:873:LEU:HB2	1:A:945:SER:OG	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	908/972 (93%)	808 (89%)	100 (11%)	0	100	100
2	B	108/129 (84%)	95 (88%)	13 (12%)	0	100	100
2	C	109/129 (84%)	99 (91%)	10 (9%)	0	100	100
All	All	1125/1230 (92%)	1002 (89%)	123 (11%)	0	100	100

There are no Ramachandran outliers to report.

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	824/862 (96%)	809 (98%)	15 (2%)	59	77
2	B	97/110 (88%)	97 (100%)	0	100	100
2	C	98/110 (89%)	97 (99%)	1 (1%)	76	86
All	All	1019/1082 (94%)	1003 (98%)	16 (2%)	62	79

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	224	LEU
1	A	298	VAL
1	A	352	GLU
1	A	361	THR
1	A	396	GLU
1	A	397	GLN
1	A	444	ASP
1	A	517	VAL
1	A	600	ASN
1	A	619	THR
1	A	731	PHE
1	A	777	LEU
1	A	811	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	902	ASN
1	A	1052	PHE
2	C	128	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	472	ASN
1	A	510	ASN

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)

3 monosaccharides 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	$\#\|Z\| > 2$
3	NAG	D	1	3,1	14,14,15	1.20	1 (7%)	17,19,21	1.32	2 (11%)
3	NAG	D	2	3	14,14,15	0.19	0	17,19,21	0.64	0
3	BMA	D	3	3	11,11,12	0.73	0	15,15,17	0.87	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	D	1	3,1	-	1/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
3	BMA	D	3	3	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1	NAG	O5-C1	-4.05	1.37	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	1	NAG	C2-N2-C7	3.63	128.07	122.90
3	D	1	NAG	O4-C4-C5	-2.00	104.32	109.30

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	1	NAG	C1-C2-N2-C7
3	D	2	NAG	C1-C2-N2-C7
3	D	2	NAG	C3-C2-N2-C7

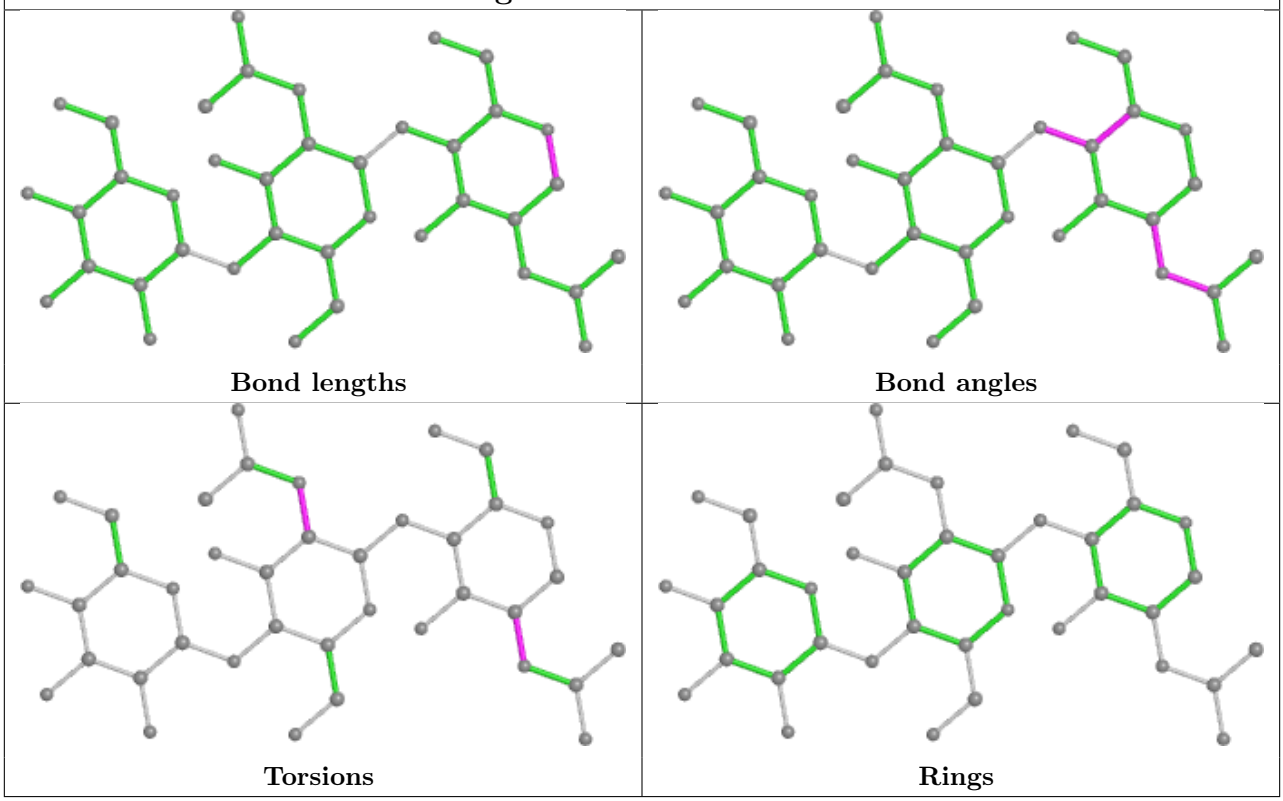
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	1	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

Oligosaccharide Chain D



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	$\#\|Z\| > 2$
4	NAG	A	1104	1	14,14,15	0.19	0	17,19,21	0.60	0
4	NAG	A	1106	1	14,14,15	0.32	0	17,19,21	0.42	0
4	NAG	A	1105	1	14,14,15	0.23	0	17,19,21	0.39	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	1104	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1106	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1105	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1105	NAG	O5-C5-C6-O6
4	A	1105	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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	918/972 (94%)	-0.10	10 (1%) 80 73	71, 132, 174, 249	0
2	B	110/129 (85%)	-0.37	1 (0%) 84 77	92, 127, 171, 187	0
2	C	111/129 (86%)	-0.33	0 100 100	101, 134, 175, 199	0
All	All	1139/1230 (92%)	-0.15	11 (0%) 82 75	71, 131, 175, 249	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	718	SER	4.0
1	A	144	ASP	3.4
1	A	218	ILE	3.0
1	A	719	GLU	2.7
1	A	155	THR	2.6
1	A	635	GLU	2.6
1	A	337	PRO	2.5
1	A	802	PHE	2.2
1	A	809	GLY	2.2
1	A	350	GLN	2.1
2	B	233	LEU	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)

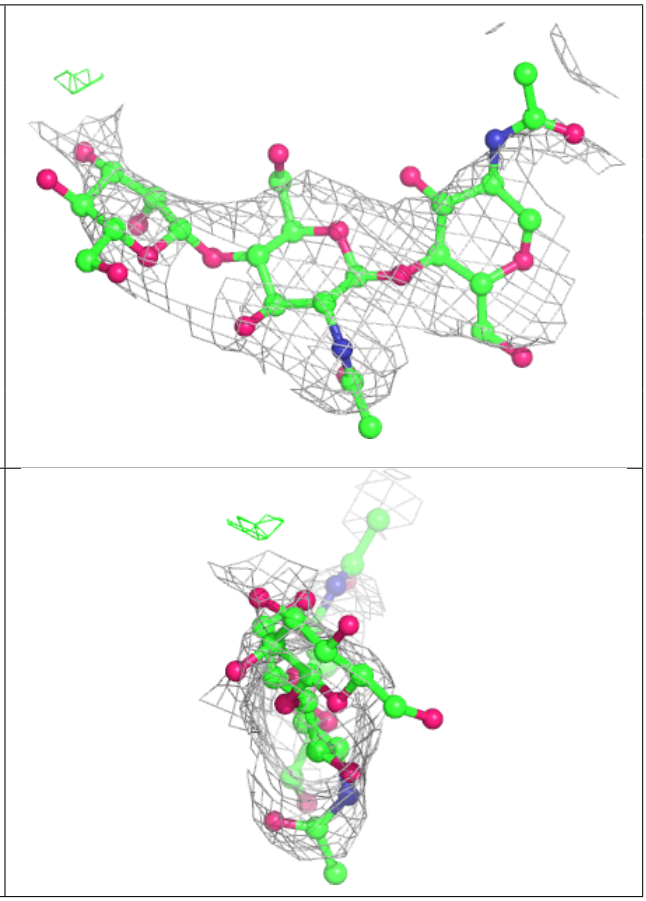
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	BMA	D	3	11/12	0.69	0.41	169,183,204,209	0
3	NAG	D	2	14/15	0.88	0.22	146,171,179,179	0
3	NAG	D	1	14/15	0.89	0.33	140,158,171,184	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain D:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)



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. 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	B-factors(Å^2)	Q<0.9
4	NAG	A	1106	14/15	0.73	0.35	136,188,208,208	0
4	NAG	A	1104	14/15	0.83	0.16	139,173,187,187	0
4	NAG	A	1105	14/15	0.84	0.17	160,173,188,191	0

6.5 Other polymers (i)

There are no such residues in this entry.