



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:06 PM GMT

PDB ID : 1WHS
Title : STRUCTURE OF THE COMPLEX OF L-BENZYL SUCCINATE WITH
WHEAT SERINE CARBOXYPEPTIDASE II AT 2.0 ANGSTROMS RES-
OLUTION
Authors : Bullock, T.L.; Remington, S.J.
Deposited on : 1994-03-07
Resolution : 2.00 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

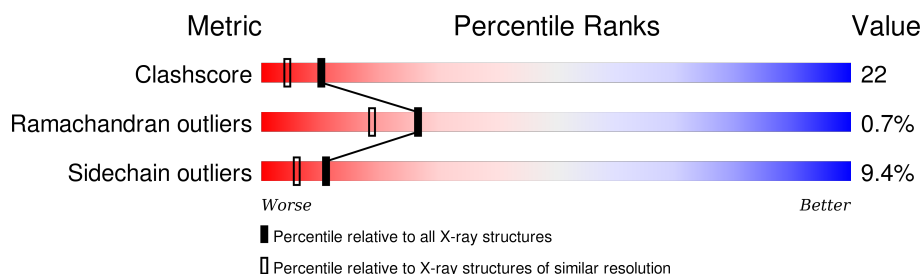
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	255	
2	B	153	

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	NAG	A	1131	X	-	-	-
4	NAG	A	1134	X	-	-	-
5	NAG	B	2911	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	NAG	B	2912	X	-	-	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 3683 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 SERINE CARBOXYPEPTIDASE II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	255	Total	C	N	O	S	0	0	0
			1999	1280	334	378	7			

- Molecule 2 is a protein called SERINE CARBOXYPEPTIDASE II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	153	Total	C	N	O	S	0	0	0
			1207	774	208	219	6			

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 4 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 5 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is ACETIC ACID (three-letter code: ACY) (formula: $C_2H_4O_2$).



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

- Molecule 8 is water.

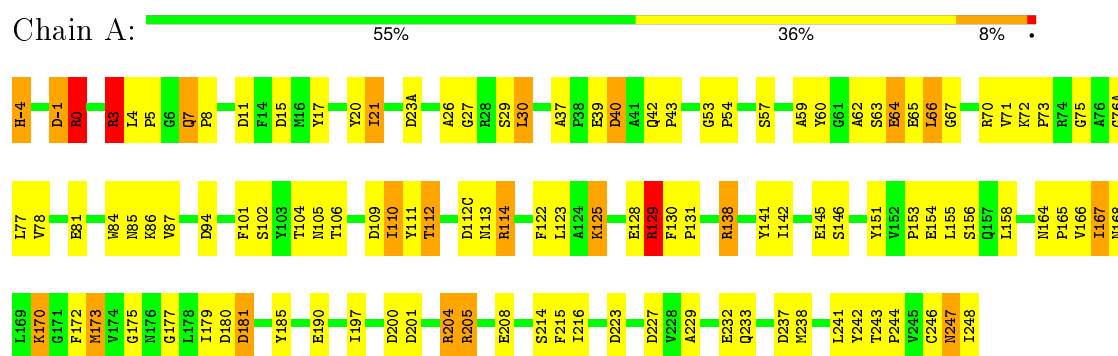
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	231	Total	O	0	0
			231	231		
8	B	152	Total	O	0	0
			152	152		

3 Residue-property plots

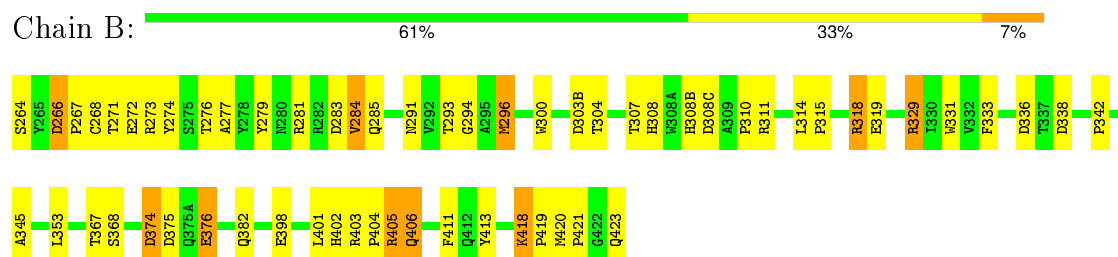
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

• Molecule 1: SERINE CARBOXYPEPTIDASE II



• Molecule 2: SERINE CARBOXYPEPTIDASE II



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	95.60Å 95.60Å 208.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.175 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3683	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

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: GOL, ACY, NAG, FUC

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	0.97	9/2062 (0.4%)	1.38	37/2814 (1.3%)
2	B	0.90	4/1247 (0.3%)	1.33	15/1709 (0.9%)
All	All	0.95	13/3309 (0.4%)	1.36	52/4523 (1.1%)

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
2	B	1	0
4	A	2	0
5	B	3	0
All	All	6	0

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	81	GLU	CD-OE1	7.47	1.33	1.25
1	A	208	GLU	CD-OE1	7.34	1.33	1.25
2	B	376	GLU	CD-OE1	6.78	1.33	1.25
1	A	39	GLU	CD-OE2	6.64	1.32	1.25
1	A	128	GLU	CD-OE2	6.33	1.32	1.25
2	B	398	GLU	CD-OE2	6.33	1.32	1.25
1	A	154	GLU	CD-OE2	6.25	1.32	1.25
1	A	64	GLU	CD-OE1	5.71	1.31	1.25
1	A	232	GLU	CD-OE1	5.69	1.31	1.25
2	B	272	GLU	CD-OE1	5.62	1.31	1.25
1	A	208	GLU	CD-OE2	-5.16	1.20	1.25
2	B	319	GLU	CD-OE2	5.13	1.31	1.25
1	A	190	GLU	CD-OE1	5.07	1.31	1.25

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3	ARG	NE-CZ-NH1	9.12	124.86	120.30
1	A	151	TYR	CB-CG-CD1	8.80	126.28	121.00
2	B	405	ARG	NE-CZ-NH1	8.52	124.56	120.30
1	A	151	TYR	CB-CG-CD2	-8.38	115.97	121.00
1	A	23(A)	ASP	CB-CG-OD2	-7.73	111.35	118.30
1	A	200	ASP	CB-CG-OD1	7.68	125.21	118.30
1	A	114	ARG	NE-CZ-NH1	7.65	124.12	120.30
1	A	15	ASP	CB-CG-OD2	-7.61	111.45	118.30
1	A	0	ARG	NE-CZ-NH1	-7.31	116.65	120.30
2	B	336	ASP	CB-CG-OD1	-7.26	111.76	118.30
2	B	266	ASP	CB-CG-OD2	-7.13	111.88	118.30
1	A	11	ASP	CB-CG-OD2	-7.02	111.98	118.30
1	A	180	ASP	CB-CG-OD1	-6.84	112.14	118.30
2	B	283	ASP	CB-CG-OD1	-6.80	112.18	118.30
2	B	338	ASP	CB-CG-OD1	6.72	124.34	118.30
2	B	308(C)	ASP	CB-CG-OD2	-6.59	112.36	118.30
2	B	266	ASP	CB-CG-OD1	6.57	124.21	118.30
1	A	173	MET	CG-SD-CE	-6.55	89.72	100.20
1	A	242	TYR	CB-CG-CD1	-6.54	117.08	121.00
1	A	94	ASP	CB-CG-OD1	6.50	124.15	118.30
2	B	329	ARG	NE-CZ-NH1	6.50	123.55	120.30
1	A	200	ASP	CB-CG-OD2	-6.43	112.51	118.30
1	A	94	ASP	CB-CG-OD2	-6.38	112.56	118.30
1	A	227	ASP	CB-CG-OD2	6.35	124.02	118.30
1	A	181	ASP	CB-CG-OD1	6.28	123.95	118.30
1	A	181	ASP	CB-CG-OD2	-6.27	112.65	118.30
2	B	336	ASP	CB-CG-OD2	6.27	123.94	118.30
1	A	40	ASP	CB-CG-OD1	-6.23	112.69	118.30
1	A	201	ASP	CB-CG-OD2	-6.17	112.75	118.30
1	A	227	ASP	CB-CG-OD1	-6.17	112.75	118.30
1	A	60	TYR	CB-CG-CD1	-6.03	117.38	121.00
2	B	329	ARG	NE-CZ-NH2	-5.97	117.31	120.30
1	A	237	ASP	CB-CG-OD1	-5.97	112.93	118.30
1	A	15	ASP	CB-CG-OD1	5.85	123.57	118.30
1	A	11	ASP	CB-CG-OD1	5.84	123.56	118.30
1	A	242	TYR	CB-CG-CD2	5.80	124.48	121.00
1	A	129	ARG	NE-CZ-NH1	5.80	123.20	120.30
1	A	180	ASP	CB-CG-OD2	5.65	123.39	118.30
1	A	223	ASP	CB-CG-OD1	-5.61	113.25	118.30
2	B	308(C)	ASP	CB-CG-OD1	5.50	123.25	118.30
1	A	237	ASP	CB-CG-OD2	5.43	123.19	118.30
1	A	40	ASP	CB-CG-OD2	5.36	123.13	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	405	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	A	204	ARG	NE-CZ-NH2	-5.30	117.65	120.30
2	B	318	ARG	NE-CZ-NH1	5.23	122.91	120.30
1	A	-1	ASP	CB-CG-OD1	-5.22	113.61	118.30
2	B	376	GLU	CB-CA-C	-5.20	100.00	110.40
1	A	114	ARG	NE-CZ-NH2	-5.19	117.70	120.30
1	A	112(C)	ASP	CB-CG-OD1	-5.18	113.64	118.30
2	B	374	ASP	CB-CG-OD2	5.13	122.92	118.30
1	A	158	LEU	CB-CA-C	-5.09	100.53	110.20
1	A	138	ARG	NE-CZ-NH2	5.09	122.84	120.30

All (6) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	1134	NAG	C2,C1
2	B	423	GLN	CA
5	B	2912	NAG	C2,C5,C1

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	1999	0	1854	88	0
2	B	1207	0	1142	53	0
3	A	14	0	13	3	0
4	A	38	0	34	10	0
5	B	28	0	24	8	0
6	A	6	0	8	0	0
7	A	4	0	3	0	0
7	B	4	0	3	1	0
8	A	231	0	0	11	0
8	B	152	0	0	6	0
All	All	3683	0	3081	139	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 22.

All (139) 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)
4:A:1132:FUC:H3	4:A:1134:NAG:H61	1.22	1.15
1:A:5:PRO:HG2	2:B:284:VAL:HG12	1.35	1.03
1:A:27:GLY:HA3	1:A:105:ASN:HB2	1.53	0.88
2:B:418:LYS:HE3	2:B:419:PRO:HD2	1.59	0.84
4:A:1132:FUC:H3	4:A:1134:NAG:C6	2.07	0.83
4:A:1132:FUC:H5	4:A:1134:NAG:C1	2.10	0.82
1:A:30:LEU:HD12	1:A:102:SER:HB3	1.65	0.78
2:B:374:ASP:HB3	8:B:3064:HOH:O	1.83	0.78
2:B:403:ARG:HB3	2:B:406:GLN:HG2	1.67	0.76
1:A:72:LYS:HD3	1:A:76(A):GLY:CA	2.15	0.76
5:B:2911:NAG:H61	5:B:2912:NAG:N2	2.01	0.76
1:A:104:THR:HG21	1:A:109:ASP:HB2	1.69	0.74
1:A:214:SER:HB2	8:A:1224:HOH:O	1.88	0.74
2:B:300:TRP:HB2	5:B:2911:NAG:H81	1.69	0.73
2:B:296:MET:O	5:B:2911:NAG:H3	1.88	0.72
2:B:281:ARG:O	2:B:285:GLN:HG3	1.89	0.72
2:B:285:GLN:HE22	5:B:2911:NAG:H83	1.55	0.72
1:A:0:ARG:HG3	1:A:17:TYR:CE2	2.24	0.71
2:B:291:ASN:HD21	2:B:294:GLY:HA2	1.54	0.70
1:A:164:ASN:OD1	1:A:166:VAL:HG22	1.92	0.70
1:A:4:LEU:H	1:A:7:GLN:NE2	1.90	0.69
1:A:110:ILE:HG22	1:A:111:TYR:CD1	2.27	0.68
1:A:167:ILE:HA	8:A:1197:HOH:O	1.91	0.68
2:B:329:ARG:HD3	8:B:3013:HOH:O	1.94	0.67
1:A:229:ALA:O	1:A:233:GLN:HG3	1.95	0.67
2:B:318:ARG:HD3	8:B:3008:HOH:O	1.94	0.66
1:A:70:ARG:HB2	1:A:78:VAL:HG23	1.77	0.66
8:A:1306:HOH:O	2:B:273:ARG:HG3	1.94	0.66
1:A:72:LYS:HB3	1:A:73:PRO:HD2	1.76	0.65
1:A:7:GLN:HB2	1:A:77:LEU:HD12	1.79	0.64
1:A:20:TYR:HB3	1:A:29:SER:OG	1.97	0.64
5:B:2911:NAG:C6	5:B:2912:NAG:H2	2.28	0.64
1:A:247:ASN:ND2	8:A:1254:HOH:O	2.30	0.63
1:A:5:PRO:HG2	2:B:284:VAL:CG1	2.20	0.62
2:B:367:THR:O	2:B:382:GLN:HG3	1.99	0.62
1:A:72:LYS:HD3	1:A:76(A):GLY:HA3	1.81	0.62
1:A:155:LEU:O	1:A:155:LEU:HD12	1.99	0.62
1:A:243:THR:HB	1:A:244:PRO:HD2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:374:ASP:OD2	2:B:405:ARG:HD2	2.01	0.61
2:B:374:ASP:OD2	2:B:405:ARG:NH1	2.28	0.61
1:A:5:PRO:CG	2:B:284:VAL:HG12	2.21	0.60
4:A:1134:NAG:H81	2:B:293:THR:HG21	1.83	0.60
1:A:205:ARG:NH1	8:A:1205:HOH:O	2.29	0.59
2:B:314:LEU:HD22	2:B:353:LEU:HG	1.85	0.59
5:B:2911:NAG:H61	5:B:2912:NAG:H2	1.84	0.59
1:A:105:ASN:HD21	4:A:1133:NAG:C1	2.16	0.59
2:B:413:TYR:HB3	2:B:418:LYS:O	2.02	0.59
1:A:112:THR:HB	1:A:114:ARG:NH2	2.18	0.59
2:B:311:ARG:NH1	8:B:3038:HOH:O	2.35	0.58
1:A:129:ARG:HG2	1:A:130:PHE:CD1	2.39	0.58
1:A:114:ARG:HD2	8:A:1167:HOH:O	2.04	0.58
1:A:138:ARG:NH2	8:A:1275:HOH:O	2.35	0.57
1:A:42:GLN:HB3	1:A:43:PRO:HA	1.87	0.56
1:A:105:ASN:HD21	4:A:1133:NAG:C2	2.19	0.56
1:A:66:LEU:H	1:A:66:LEU:HD23	1.69	0.56
1:A:62:ALA:O	1:A:67:GLY:HA3	2.06	0.56
1:A:125:LYS:NZ	8:A:1191:HOH:O	2.39	0.55
2:B:276:THR:HA	2:B:300:TRP:CZ3	2.43	0.54
5:B:2911:NAG:H61	5:B:2912:NAG:C2	2.37	0.54
1:A:105:ASN:HD21	4:A:1133:NAG:H2	1.73	0.54
2:B:291:ASN:ND2	2:B:294:GLY:HA2	2.21	0.54
1:A:3:ARG:HD3	1:A:7:GLN:O	2.09	0.53
2:B:423:GLN:HA	8:B:3062:HOH:O	2.09	0.53
1:A:27:GLY:CA	1:A:105:ASN:HB2	2.32	0.53
1:A:64:GLU:O	2:B:401:LEU:HB2	2.09	0.52
1:A:76(A):GLY:O	1:A:77:LEU:HD23	2.09	0.52
2:B:303(B):ASP:O	2:B:307:THR:HG23	2.09	0.52
1:A:-4:HIS:HB3	1:A:129:ARG:HG3	1.91	0.52
4:A:1132:FUC:C3	4:A:1134:NAG:H61	2.16	0.52
2:B:342:PRO:O	2:B:345:ALA:HB3	2.09	0.52
1:A:3:ARG:NH1	1:A:7:GLN:O	2.28	0.51
2:B:274:TYR:N	2:B:274:TYR:CD1	2.75	0.51
1:A:110:ILE:HG22	1:A:111:TYR:CE1	2.46	0.51
1:A:-4:HIS:HB3	1:A:129:ARG:O	2.11	0.50
1:A:141:TYR:CE2	1:A:170:LYS:HB2	2.47	0.50
2:B:405:ARG:NH1	2:B:406:GLN:HE22	2.09	0.50
1:A:0:ARG:HD3	8:A:1143:HOH:O	2.12	0.50
1:A:164:ASN:OD1	1:A:165:PRO:HD2	2.13	0.48
1:A:105:ASN:ND2	4:A:1133:NAG:C1	2.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:413:TYR:CZ	2:B:421:PRO:HG3	2.49	0.48
1:A:75:GLY:HA3	2:B:277:ALA:HB3	1.94	0.48
1:A:65:GLU:OE2	1:A:145:GLU:OE1	2.32	0.48
1:A:112:THR:CB	1:A:114:ARG:HH22	2.27	0.47
1:A:173:MET:HA	2:B:331:TRP:O	2.14	0.47
1:A:177:GLY:O	1:A:179:ILE:HG13	2.14	0.47
2:B:268:CYS:O	2:B:273:ARG:HB2	2.15	0.47
1:A:142:ILE:O	1:A:172:PHE:HA	2.15	0.47
1:A:21:ILE:HB	1:A:122:PHE:CD1	2.50	0.47
1:A:59:ALA:O	1:A:63:SER:HB2	2.15	0.47
2:B:281:ARG:HD2	2:B:284:VAL:HG13	1.97	0.47
2:B:276:THR:HA	2:B:300:TRP:HZ3	1.79	0.47
1:A:113:ASN:ND2	3:A:1131:NAG:N2	2.62	0.47
1:A:72:LYS:HD3	1:A:76(A):GLY:C	2.35	0.47
1:A:-1:ASP:OD2	1:A:129:ARG:NH1	2.41	0.47
2:B:308(B):HIS:HB3	8:B:3000:HOH:O	2.15	0.47
1:A:71:VAL:CG1	1:A:75:GLY:HA2	2.45	0.46
1:A:53:GLY:HA3	1:A:54:PRO:C	2.35	0.46
2:B:291:ASN:ND2	2:B:291:ASN:O	2.49	0.46
1:A:113:ASN:ND2	3:A:1131:NAG:C1	2.79	0.45
2:B:291:ASN:ND2	5:B:2911:NAG:C1	2.79	0.45
1:A:233:GLN:NE2	1:A:238:MET:SD	2.90	0.45
1:A:125:LYS:HD2	1:A:125:LYS:N	2.32	0.44
2:B:314:LEU:N	2:B:315:PRO:CD	2.81	0.44
1:A:105:ASN:ND2	4:A:1133:NAG:H83	2.32	0.44
1:A:3:ARG:HD2	8:A:1158:HOH:O	2.18	0.44
1:A:72:LYS:CB	1:A:73:PRO:HD2	2.45	0.44
2:B:314:LEU:N	2:B:315:PRO:HD2	2.32	0.44
1:A:175:GLY:HA3	2:B:333:PHE:CZ	2.53	0.44
1:A:129:ARG:C	1:A:131:PRO:HD3	2.38	0.43
1:A:138:ARG:O	1:A:168:ASN:HB3	2.17	0.43
1:A:0:ARG:CG	1:A:17:TYR:CE2	2.97	0.43
1:A:153:PRO:HA	1:A:156:SER:HB2	2.00	0.43
2:B:304:THR:HG23	2:B:308:HIS:CD2	2.52	0.43
1:A:181:ASP:OD2	2:B:311:ARG:HD3	2.17	0.43
1:A:112:THR:HB	1:A:114:ARG:HH22	1.83	0.42
3:A:1131:NAG:C8	3:A:1131:NAG:C1	2.97	0.42
1:A:27:GLY:HA3	1:A:105:ASN:CB	2.38	0.42
2:B:403:ARG:N	2:B:404:PRO:HD3	2.34	0.42
2:B:266:ASP:O	2:B:271:THR:HG23	2.20	0.42
1:A:241:LEU:HD23	1:A:241:LEU:HA	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:376:GLU:HA	7:B:461:ACY:H1	2.02	0.42
1:A:84:TRP:HB3	2:B:411:PHE:CE2	2.55	0.42
1:A:20:TYR:HE2	1:A:101:PHE:O	2.03	0.42
2:B:402:HIS:C	2:B:404:PRO:HD3	2.41	0.42
1:A:37:ALA:HA	1:A:85:ASN:O	2.20	0.42
1:A:123:LEU:HD23	1:A:123:LEU:HA	1.64	0.42
1:A:7:GLN:HG2	1:A:8:PRO:O	2.21	0.41
1:A:247:ASN:HD22	1:A:247:ASN:H	1.69	0.41
1:A:145:GLU:HA	1:A:175:GLY:O	2.19	0.41
1:A:0:ARG:HD2	1:A:0:ARG:HH11	1.69	0.41
1:A:247:ASN:HD22	1:A:247:ASN:N	2.19	0.41
2:B:279:TYR:HB2	2:B:300:TRP:CE3	2.55	0.41
1:A:181:ASP:OD2	2:B:311:ARG:HA	2.20	0.41
2:B:420:MET:HA	2:B:421:PRO:HD3	1.76	0.41
1:A:246:CYS:HA	2:B:267:PRO:HG2	2.03	0.41
1:A:26:ALA:O	1:A:105:ASN:HB2	2.21	0.41
1:A:106:THR:O	1:A:109:ASP:HB2	2.21	0.40
2:B:304:THR:O	2:B:308:HIS:CD2	2.74	0.40
1:A:238:MET:HG3	8:A:1328:HOH:O	2.20	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	253/255 (99%)	240 (95%)	13 (5%)	0	100	100
2	B	151/153 (99%)	142 (94%)	6 (4%)	3 (2%)	9	3
All	All	404/408 (99%)	382 (95%)	19 (5%)	3 (1%)	26	19

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	375	ASP
2	B	310	PRO
2	B	296	MET

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	205/208 (99%)	179 (87%)	26 (13%)	5	3
2	B	124/128 (97%)	119 (96%)	5 (4%)	38	33
All	All	329/336 (98%)	298 (91%)	31 (9%)	11	6

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-4	HIS
1	A	0	ARG
1	A	3	ARG
1	A	7	GLN
1	A	21	ILE
1	A	30	LEU
1	A	40	ASP
1	A	57	SER
1	A	66	LEU
1	A	86	LYS
1	A	87	VAL
1	A	110	ILE
1	A	112	THR
1	A	125	LYS
1	A	129	ARG
1	A	146	SER
1	A	167	ILE
1	A	170	LYS
1	A	185	TYR
1	A	197	ILE
1	A	204	ARG

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Mol	Chain	Res	Type
1	A	205	ARG
1	A	215	PHE
1	A	216	ILE
1	A	247	ASN
1	A	248	ILE
2	B	264	SER
2	B	284	VAL
2	B	368	SER
2	B	406	GLN
2	B	418	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-4	HIS
1	A	7	GLN
1	A	117	HIS
1	A	183	HIS
1	A	217	HIS
1	A	233	GLN
1	A	247	ASN
2	B	285	GLN
2	B	308	HIS
2	B	412	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](#)

5 carbohydrates 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	FUC	A	1132	4	10,10,11	2.71	3 (30%)	14,14,16	3.59	6 (42%)
4	NAG	A	1133	4	14,14,15	0.93	0	15,19,21	4.40	3 (20%)
4	NAG	A	1134	4	14,14,15	0.75	0	15,19,21	1.91	5 (33%)
5	NAG	B	2911	5	14,14,15	0.92	1 (7%)	15,19,21	1.87	4 (26%)
5	NAG	B	2912	5	14,14,15	1.60	2 (14%)	15,19,21	5.21	7 (46%)

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	FUC	A	1132	4	-	0/0/17/20	0/1/1/1
4	NAG	A	1133	4	-	0/6/23/26	0/1/1/1
4	NAG	A	1134	4	2/2/5/7	0/6/23/26	0/1/1/1
5	NAG	B	2911	5	-	0/6/23/26	0/1/1/1
5	NAG	B	2912	5	3/3/5/7	0/6/23/26	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1132	FUC	C2-C3	-2.24	1.49	1.52
5	B	2911	NAG	O5-C1	-2.20	1.40	1.43
5	B	2912	NAG	O4-C4	2.11	1.48	1.43
4	A	1132	FUC	C4-C3	2.54	1.59	1.52
5	B	2912	NAG	C1-C2	3.68	1.57	1.52
4	A	1132	FUC	O5-C1	7.21	1.55	1.43

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1132	FUC	C2-C3-C4	-6.48	100.03	111.04
4	A	1133	NAG	C4-C3-C2	-4.45	104.31	111.23
5	B	2912	NAG	O7-C7-C8	-2.37	117.72	122.06
4	A	1134	NAG	C4-C3-C2	-2.32	107.62	111.23
4	A	1134	NAG	C1-O5-C5	2.09	114.90	112.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	2911	NAG	C2-N2-C7	2.15	125.80	123.04
4	A	1134	NAG	C2-N2-C7	2.24	125.91	123.04
5	B	2912	NAG	C3-C2-N2	2.28	116.03	110.56
4	A	1132	FUC	O4-C4-C5	2.41	115.50	109.84
5	B	2912	NAG	O7-C7-N2	2.49	126.94	121.86
5	B	2912	NAG	C2-N2-C7	2.64	126.42	123.04
4	A	1132	FUC	C6-C5-C4	2.66	118.33	113.08
5	B	2912	NAG	C4-C3-C2	2.71	115.45	111.23
4	A	1132	FUC	O5-C5-C4	2.72	114.23	109.53
5	B	2911	NAG	O3-C3-C4	2.84	116.73	110.34
5	B	2911	NAG	O3-C3-C2	2.92	114.89	109.11
4	A	1132	FUC	O2-C2-C3	2.95	116.05	110.12
4	A	1134	NAG	C3-C2-N2	3.42	118.75	110.56
5	B	2911	NAG	C4-C3-C2	3.84	117.20	111.23
5	B	2912	NAG	C3-C4-C5	4.31	117.72	110.20
4	A	1134	NAG	O6-C6-C5	4.59	126.50	111.33
4	A	1133	NAG	C3-C4-C5	4.94	118.82	110.20
4	A	1132	FUC	O3-C3-C2	9.71	127.54	110.00
4	A	1133	NAG	O6-C6-C5	15.33	161.98	111.33
5	B	2912	NAG	O6-C6-C5	18.74	173.27	111.33

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	B	2912	NAG	C2
5	B	2912	NAG	C5
5	B	2912	NAG	C1
4	A	1134	NAG	C2
4	A	1134	NAG	C1

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1132	FUC	4	0
4	A	1133	NAG	5	0
4	A	1134	NAG	5	0
5	B	2911	NAG	8	0
5	B	2912	NAG	4	0

5.6 Ligand geometry

4 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$
3	NAG	A	1131	-	14,14,15	1.04	1 (7%)	15,19,21	1.74	4 (26%)
6	GOL	A	450	-	5,5,5	0.63	0	5,5,5	0.62	0
7	ACY	A	460	-	1,3,3	1.64	0	0,3,3	0.00	-
7	ACY	B	461	-	1,3,3	2.28	1 (100%)	0,3,3	0.00	-

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	A	1131	-	1/1/5/7	0/6/23/26	0/1/1/1
6	GOL	A	450	-	-	0/4/4/4	0/0/0/0
7	ACY	A	460	-	-	0/0/0/0	0/0/0/0
7	ACY	B	461	-	-	0/0/0/0	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	461	ACY	CH3-C	2.28	1.52	1.48
3	A	1131	NAG	C1-C2	2.41	1.55	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1131	NAG	O7-C7-C8	-3.38	115.87	122.06
3	A	1131	NAG	C8-C7-N2	2.71	121.30	116.11
3	A	1131	NAG	C1-O5-C5	2.77	115.76	112.25
3	A	1131	NAG	C2-N2-C7	3.46	127.48	123.04

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	1131	NAG	C2

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1131	NAG	3	0
7	B	461	ACY	1	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](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.