



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 01:47 PM UTC

PDB ID : 4NSB / pdb_00004nsb
Title : Crystal structure of the complex of signaling glycoprotein, SPB-40 and N-acetyl salicylic acid at 3.05 Å resolution
Authors : Yamini, S.; Chaudhary, A.; Sinha, M.; Kaur, P.; Sharma, S.; Singh, T.P.
Deposited on : 2013-11-28
Resolution : 3.05 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

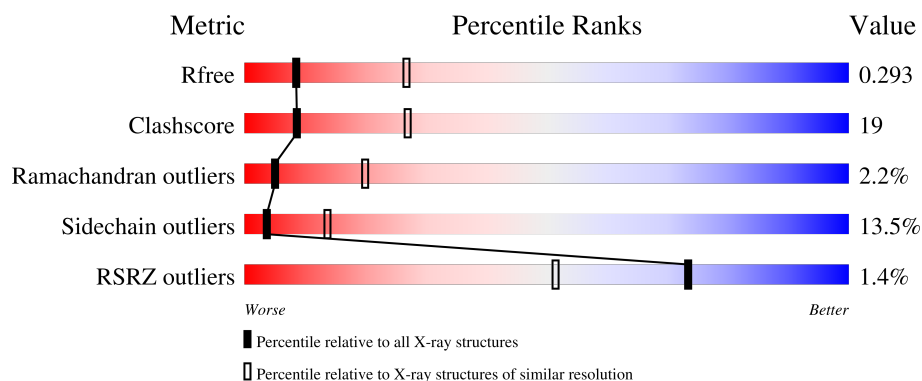
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 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}	180053	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

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 $\leq 5\%$. 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	361	56% 34% 8%

2 Entry composition [i](#)

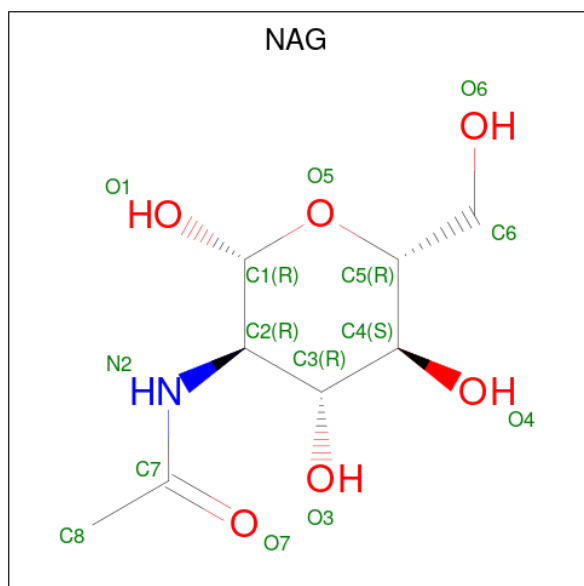
There are 4 unique types of molecules in this entry. The entry contains 3030 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Chitinase-3-like protein 1.

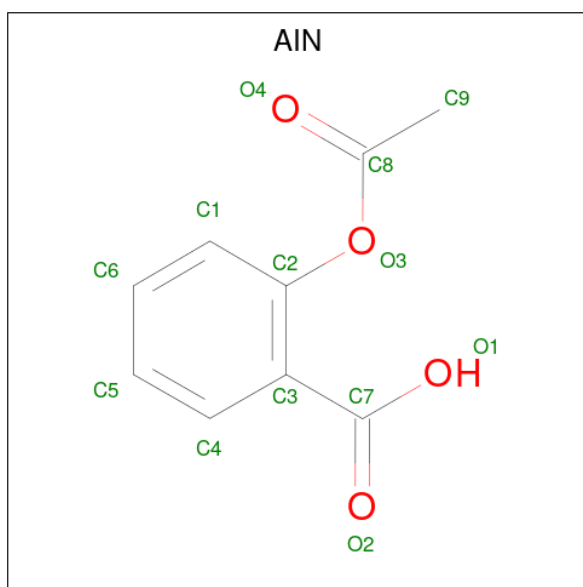
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	361	Total	C	N	O	S	0	0	0
			2893	1851	507	526	9			

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 3 is 2-(ACETYLOXY)BENZOIC ACID (CCD ID: AIN) (formula: $C_9H_8O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	9	4		

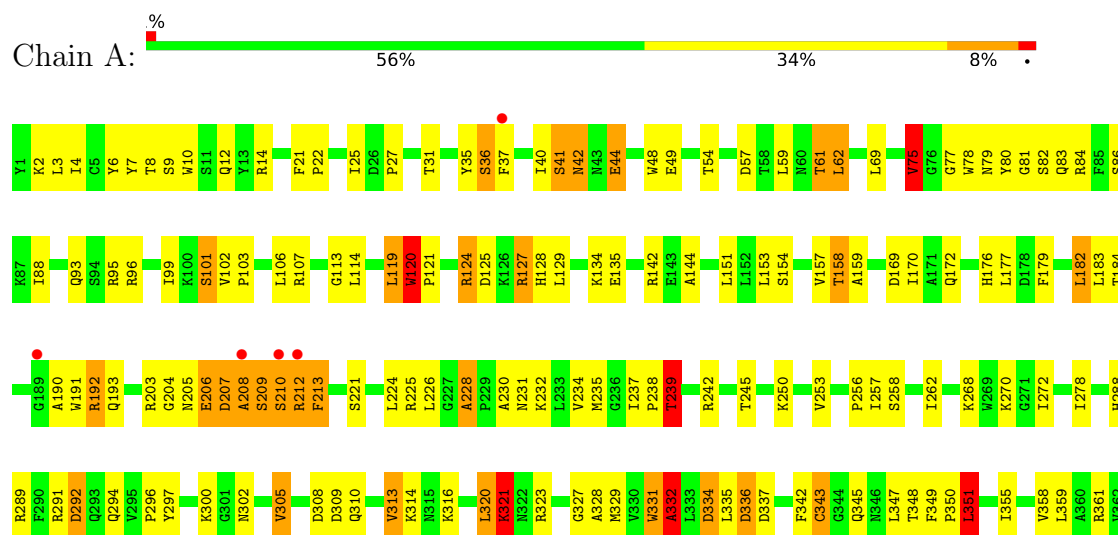
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	110	Total	O	0	0
			110	110		

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: Chitinase-3-like protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	60.74Å 66.92Å 106.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.71 – 3.05 41.71 – 3.05	Depositor EDS
% Data completeness (in resolution range)	97.2 (41.71-3.05) 97.3 (41.71-3.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.17 (at 3.06Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.231 , 0.254 0.230 , 0.293	Depositor DCC
R_{free} test set	398 reflections (4.58%)	wwPDB-VP
Wilson B-factor (Å ²)	42.6	Xtriage
Anisotropy	0.496	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 34.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3030	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.74% 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: NAG, AIN

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	0.64	3/2973 (0.1%)	1.27	37/4037 (0.9%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	332	ALA	CA-CB	7.35	1.65	1.53
1	A	332	ALA	CA-C	-7.01	1.43	1.52
1	A	120	TRP	N-CA	-5.09	1.39	1.46

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	120	TRP	CA-C-N	13.39	133.56	119.76
1	A	120	TRP	C-N-CA	13.39	133.56	119.76
1	A	331	TRP	CA-C-N	10.57	141.74	121.54
1	A	331	TRP	C-N-CA	10.57	141.74	121.54
1	A	332	ALA	N-CA-C	10.54	133.24	110.80
1	A	120	TRP	N-CA-C	10.19	132.33	109.81
1	A	119	LEU	CA-C-N	8.83	143.35	121.80
1	A	119	LEU	C-N-CA	8.83	143.35	121.80
1	A	336	ASP	N-CA-C	-8.53	98.22	110.59
1	A	206	GLU	N-CA-C	8.15	120.24	111.36
1	A	343	CYS	N-CA-C	7.70	121.27	112.57
1	A	332	ALA	CA-C-N	7.67	130.89	120.54
1	A	332	ALA	C-N-CA	7.67	130.89	120.54
1	A	170	ILE	N-CA-C	7.62	118.36	110.36
1	A	61	THR	N-CA-C	-6.93	104.71	113.72
1	A	119	LEU	O-C-N	6.93	131.53	122.38
1	A	332	ALA	O-C-N	6.87	131.72	122.59
1	A	42	ASN	N-CA-C	-6.68	103.69	112.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	31	THR	N-CA-C	-6.62	105.09	113.43
1	A	351	LEU	N-CA-C	6.33	118.99	111.33
1	A	321	LYS	N-CA-C	-6.21	104.43	111.14
1	A	62	LEU	N-CA-C	-6.19	104.99	112.54
1	A	239	THR	N-CA-C	-6.14	104.96	112.88
1	A	124	ARG	N-CA-C	-6.12	105.31	112.89
1	A	305	VAL	N-CA-C	5.90	117.25	108.46
1	A	75	VAL	N-CA-C	5.80	116.28	108.17
1	A	262	ILE	CA-C-N	5.78	125.71	119.76
1	A	262	ILE	C-N-CA	5.78	125.71	119.76
1	A	25	ILE	N-CA-C	5.63	116.53	108.93
1	A	82	SER	N-CA-C	-5.42	105.37	111.28
1	A	228	ALA	N-CA-C	-5.31	101.86	109.24
1	A	101	SER	N-CA-C	5.24	119.38	112.89
1	A	208	ALA	N-CA-C	-5.22	102.91	110.64
1	A	27	PRO	N-CA-C	5.16	120.37	114.03
1	A	144	ALA	N-CA-C	-5.11	105.89	111.82
1	A	291	ARG	N-CA-C	-5.07	105.65	111.07
1	A	119	LEU	CA-CB-CG	-5.05	98.62	116.30

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	2893	0	2818	108	0
2	A	14	0	13	3	0
3	A	13	0	7	2	0
4	A	110	0	0	6	0
All	All	3030	0	2838	108	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 19.

All (108) 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:212:ARG:O	1:A:213:PHE:CG	2.15	0.98
1:A:239:THR:HG21	1:A:332:ALA:O	1.66	0.95
1:A:212:ARG:O	1:A:213:PHE:CD1	2.26	0.88
1:A:205:ASN:ND2	1:A:292:ASP:HB3	1.97	0.80
1:A:36:SER:HB3	1:A:37:PHE:CD1	2.21	0.75
1:A:9:SER:OG	1:A:35:TYR:CZ	2.42	0.73
1:A:191:TRP:CH2	1:A:192:ARG:NH1	2.57	0.72
1:A:36:SER:HB3	1:A:37:PHE:CG	2.25	0.71
1:A:48:TRP:CZ2	2:A:401:NAG:H82	2.27	0.70
1:A:78:TRP:C	1:A:80:TYR:H	2.01	0.69
1:A:212:ARG:C	1:A:213:PHE:CG	2.69	0.67
1:A:238:PRO:HG2	1:A:308:ASP:OD1	1.95	0.67
1:A:292:ASP:OD2	1:A:292:ASP:N	2.28	0.67
1:A:212:ARG:O	1:A:213:PHE:CD2	2.49	0.66
1:A:48:TRP:CE2	2:A:401:NAG:H82	2.32	0.64
1:A:209:SER:O	1:A:210:SER:HB3	1.99	0.62
1:A:102:VAL:HB	1:A:103:PRO:HD3	1.82	0.61
1:A:320:LEU:HD23	1:A:321:LYS:N	2.14	0.61
1:A:124:ARG:HG3	4:A:556:HOH:O	2.01	0.60
1:A:119:LEU:HD22	1:A:120:TRP:CZ3	2.37	0.59
1:A:119:LEU:HD22	1:A:120:TRP:CE3	2.36	0.59
1:A:157:VAL:O	1:A:183:LEU:HG	2.03	0.59
1:A:78:TRP:O	1:A:80:TYR:N	2.30	0.58
1:A:210:SER:O	1:A:213:PHE:N	2.36	0.58
1:A:78:TRP:C	1:A:80:TYR:N	2.62	0.57
1:A:212:ARG:C	1:A:213:PHE:CD2	2.82	0.57
1:A:343:CYS:HB2	4:A:598:HOH:O	2.04	0.57
1:A:358:VAL:HA	1:A:361:ARG:HD2	1.87	0.56
1:A:75:VAL:CG2	1:A:114:LEU:HD11	2.37	0.54
1:A:289:ARG:NH2	1:A:309:ASP:OD2	2.40	0.54
1:A:225:ARG:C	1:A:225:ARG:HD3	2.32	0.53
1:A:182:LEU:HD13	1:A:184:THR:HG23	1.90	0.53
1:A:237:ILE:HG21	1:A:313:VAL:CG2	2.38	0.53
1:A:9:SER:OG	1:A:35:TYR:CE2	2.61	0.53
1:A:237:ILE:HG21	1:A:313:VAL:HG22	1.90	0.52
1:A:204:GLY:HA2	1:A:292:ASP:HB2	1.91	0.52
1:A:14:ARG:HH12	1:A:334:ASP:HB2	1.75	0.52
1:A:8:THR:HG1	1:A:334:ASP:CG	2.18	0.51
1:A:106:LEU:HD21	1:A:113:GLY:C	2.35	0.51
1:A:169:ASP:OD2	1:A:172:GLN:HG3	2.11	0.51
1:A:245:THR:HG23	1:A:302:ASN:ND2	2.26	0.51
1:A:86:SER:OG	1:A:125:ASP:OD1	2.28	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:ARG:HH21	3:A:402:AIN:C7	2.23	0.50
1:A:239:THR:CG2	1:A:335:LEU:HB2	2.41	0.50
1:A:206:GLU:O	1:A:207:ASP:HB3	2.11	0.50
1:A:320:LEU:HD23	1:A:320:LEU:C	2.37	0.49
1:A:230:ALA:C	1:A:232:LYS:H	2.21	0.49
1:A:239:THR:O	1:A:239:THR:HG23	2.14	0.48
1:A:190:ALA:HA	4:A:602:HOH:O	2.14	0.47
1:A:310:GLN:O	1:A:314:LYS:HG3	2.15	0.47
1:A:154:SER:HB3	1:A:179:PHE:CE1	2.50	0.47
1:A:134:LYS:HG3	1:A:176:HIS:NE2	2.29	0.47
1:A:235:MET:CE	1:A:316:LYS:HB3	2.45	0.47
1:A:120:TRP:HA	1:A:121:PRO:HD3	1.35	0.46
1:A:41:SER:O	1:A:42:ASN:HB2	2.15	0.46
1:A:221:SER:OG	1:A:323:ARG:NH2	2.49	0.46
1:A:288:HIS:HB3	4:A:508:HOH:O	2.14	0.46
1:A:83:GLN:HG2	1:A:84:ARG:N	2.31	0.46
1:A:106:LEU:HD23	1:A:151:LEU:HD22	1.97	0.46
1:A:349:PHE:O	1:A:350:PRO:C	2.58	0.46
1:A:44:GLU:HB3	1:A:101:SER:CB	2.46	0.45
1:A:142:ARG:HB2	1:A:142:ARG:NH1	2.31	0.45
1:A:190:ALA:O	1:A:191:TRP:C	2.59	0.45
1:A:36:SER:HB3	1:A:37:PHE:CE1	2.50	0.45
1:A:212:ARG:O	1:A:212:ARG:HG3	2.18	0.44
1:A:95:ARG:O	1:A:99:ILE:HG13	2.17	0.44
1:A:212:ARG:O	1:A:213:PHE:CE1	2.68	0.44
1:A:10:TRP:C	1:A:12:GLN:N	2.73	0.44
1:A:134:LYS:HG3	1:A:176:HIS:CE1	2.52	0.44
1:A:242:ARG:NH1	4:A:601:HOH:O	2.51	0.44
1:A:75:VAL:HG22	1:A:114:LEU:HD11	1.98	0.44
1:A:207:ASP:O	1:A:208:ALA:C	2.60	0.44
1:A:297:TYR:HA	1:A:305:VAL:O	2.17	0.44
1:A:36:SER:HA	1:A:37:PHE:HA	1.55	0.43
1:A:48:TRP:CE2	2:A:401:NAG:C8	3.01	0.43
1:A:336:ASP:OD1	1:A:351:LEU:HB2	2.19	0.43
1:A:49:GLU:OE1	1:A:49:GLU:HA	2.18	0.43
1:A:153:LEU:HG	1:A:177:LEU:HD23	1.99	0.43
1:A:59:LEU:HD12	1:A:62:LEU:HD12	2.00	0.43
1:A:84:ARG:O	1:A:88:ILE:HD12	2.18	0.43
1:A:6:TYR:CD2	1:A:331:TRP:CZ3	3.06	0.43
1:A:35:TYR:CD2	1:A:35:TYR:C	2.97	0.43
1:A:14:ARG:NH2	3:A:402:AIN:O2	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:ARG:NE	1:A:135:GLU:OE1	2.46	0.42
1:A:256:PRO:HG2	4:A:555:HOH:O	2.20	0.42
1:A:234:VAL:CG1	1:A:328:ALA:C	2.92	0.42
1:A:234:VAL:HA	1:A:327:GLY:O	2.19	0.42
1:A:21:PHE:HB3	1:A:22:PRO:CD	2.49	0.42
1:A:142:ARG:HB2	1:A:142:ARG:HH11	1.84	0.42
1:A:191:TRP:O	1:A:192:ARG:C	2.62	0.42
1:A:40:ILE:HD12	1:A:80:TYR:OH	2.19	0.41
1:A:183:LEU:HD22	1:A:329:MET:HE1	2.01	0.41
1:A:37:PHE:CE2	1:A:77:GLY:HA3	2.54	0.41
1:A:80:TYR:CD2	1:A:80:TYR:C	2.98	0.41
1:A:337:ASP:HB3	1:A:350:PRO:CD	2.51	0.41
1:A:57:ASP:O	1:A:61:THR:HG23	2.20	0.41
1:A:230:ALA:C	1:A:232:LYS:N	2.78	0.41
1:A:7:TYR:CD2	1:A:7:TYR:C	2.99	0.41
1:A:2:LYS:HB3	1:A:4:ILE:HD11	2.02	0.41
1:A:6:TYR:CD2	1:A:331:TRP:HZ3	2.39	0.41
1:A:159:ALA:HB2	1:A:182:LEU:HD22	2.02	0.41
1:A:355:ILE:O	1:A:358:VAL:N	2.54	0.41
1:A:342:PHE:CD1	1:A:342:PHE:N	2.89	0.41
1:A:81:GLY:O	1:A:84:ARG:HB2	2.21	0.40
1:A:127:ARG:HG2	1:A:128:HIS:N	2.37	0.40
1:A:157:VAL:HG12	1:A:158:THR:O	2.21	0.40
1:A:224:LEU:HD23	1:A:228:ALA:O	2.22	0.40
1:A:36:SER:HB3	1:A:37:PHE:CD2	2.55	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	359/361 (99%)	324 (90%)	27 (8%)	8 (2%)	5 20

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	120	TRP
1	A	207	ASP
1	A	210	SER
1	A	212	ARG
1	A	79	ASN
1	A	213	PHE
1	A	332	ALA
1	A	231	ASN

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	304/304 (100%)	263 (86%)	41 (14%)	4 14

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	36	SER
1	A	41	SER
1	A	44	GLU
1	A	54	THR
1	A	69	LEU
1	A	75	VAL
1	A	93	GLN
1	A	96	ARG
1	A	107	ARG
1	A	127	ARG
1	A	129	LEU
1	A	158	THR
1	A	182	LEU
1	A	192	ARG
1	A	193	GLN
1	A	203	ARG

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Mol	Chain	Res	Type
1	A	209	SER
1	A	226	LEU
1	A	239	THR
1	A	250	LYS
1	A	253	VAL
1	A	257	ILE
1	A	258	SER
1	A	268	LYS
1	A	270	LYS
1	A	272	ILE
1	A	278	ILE
1	A	292	ASP
1	A	294	GLN
1	A	296	PRO
1	A	300	LYS
1	A	313	VAL
1	A	320	LEU
1	A	321	LYS
1	A	334	ASP
1	A	345	GLN
1	A	347	LEU
1	A	348	THR
1	A	351	LEU
1	A	359	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
1	A	205	ASN
1	A	288	HIS
1	A	303	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	NAG	A	401	1	14,14,15	0.82	1 (7%)	17,19,21	1.47	2 (11%)
3	AIN	A	402	-	13,13,13	2.46	3 (23%)	17,17,17	1.55	2 (11%)

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	NAG	A	401	1	-	2/6/23/26	0/1/1/1
3	AIN	A	402	-	-	6/8/8/8	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	402	AIN	C3-C2	6.55	1.52	1.40
3	A	402	AIN	O3-C8	4.46	1.51	1.36
2	A	401	NAG	C1-C2	2.50	1.55	1.52
3	A	402	AIN	C1-C2	2.01	1.43	1.39

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	AIN	O3-C8-C9	4.12	119.89	110.97
2	A	401	NAG	O5-C1-C2	3.60	116.86	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	NAG	C1-O5-C5	3.37	116.70	112.19
3	A	402	AIN	O1-C7-C3	2.11	121.27	115.28

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	AIN	O4-C8-O3-C2
3	A	402	AIN	C9-C8-O3-C2
3	A	402	AIN	C2-C3-C7-O1
3	A	402	AIN	C2-C3-C7-O2
2	A	401	NAG	O5-C5-C6-O6
2	A	401	NAG	C4-C5-C6-O6
3	A	402	AIN	C4-C3-C7-O1
3	A	402	AIN	C4-C3-C7-O2

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	NAG	3	0
3	A	402	AIN	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	361/361 (100%)	0.02	5 (1%)	73 51	9, 26, 45, 69	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	212	ARG	3.1
1	A	208	ALA	2.6
1	A	210	SER	2.5
1	A	189	GLY	2.1
1	A	37	PHE	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 oligosaccharides 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. 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
2	NAG	A	401	14/15	0.79	0.17	25,28,29,30	0
3	AIN	A	402	13/13	0.83	0.24	41,48,53,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.