



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 10, 2020 – 09:38 AM BST

PDB ID : 6S9F
Title : Drosophila OTK, extracellular domains 3-5
Authors : Rozbesky, D.; Jones, E.Y.
Deposited on : 2019-07-12
Resolution : 1.97 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
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) : 2.13.1

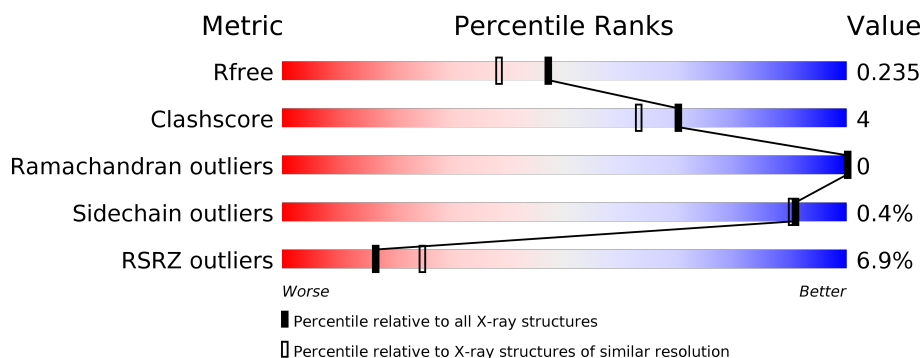
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.97 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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 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	569	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0;">%</div> <div style="position: absolute; top: 10px; left: 49%;"></div> <div style="position: absolute; top: 10px; left: 48%;"></div> </div> </div>
1	B	569	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0;">6%</div> <div style="position: absolute; top: 10px; left: 46%;"></div> <div style="position: absolute; top: 10px; left: 7%;"></div> <div style="position: absolute; top: 10px; left: 47%;"></div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5253 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.

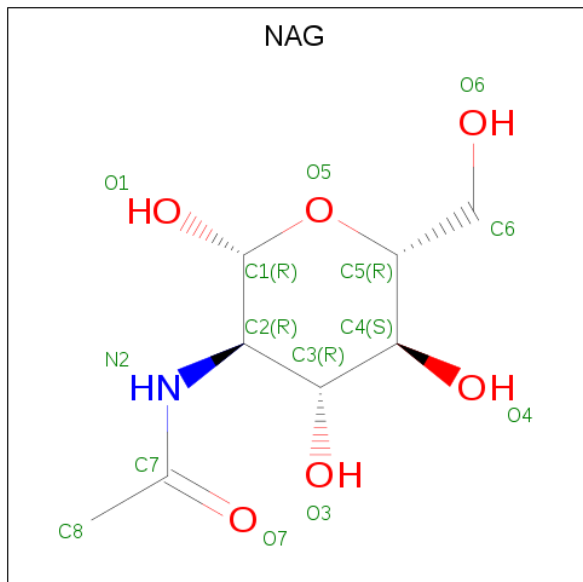
- Molecule 1 is a protein called Tyrosine-protein kinase-like otk.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	298	Total	C	N	O	S	0	0	0
			2302	1435	409	451	7			
1	B	300	Total	C	N	O	S	0	0	0
			2318	1444	413	454	7			

There are 24 discrepancies between the modelled and reference sequences:

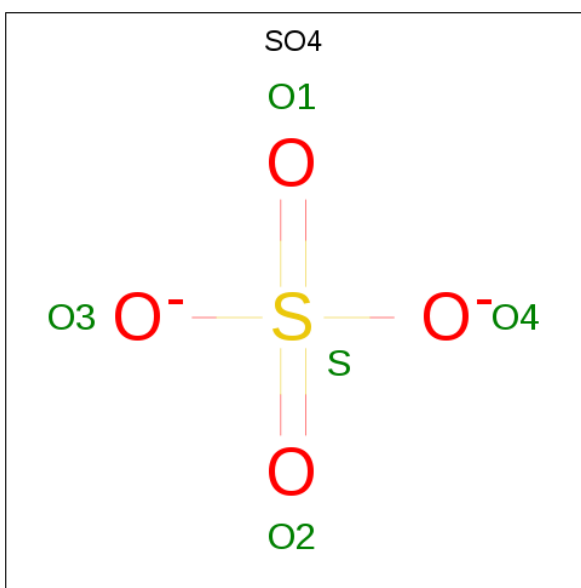
Chain	Residue	Modelled	Actual	Comment	Reference
A	21	GLU	-	expression tag	UNP Q6AWJ9
A	22	THR	-	expression tag	UNP Q6AWJ9
A	23	GLY	-	expression tag	UNP Q6AWJ9
A	581	GLY	-	expression tag	UNP Q6AWJ9
A	582	THR	-	expression tag	UNP Q6AWJ9
A	583	LYS	-	expression tag	UNP Q6AWJ9
A	584	HIS	-	expression tag	UNP Q6AWJ9
A	585	HIS	-	expression tag	UNP Q6AWJ9
A	586	HIS	-	expression tag	UNP Q6AWJ9
A	587	HIS	-	expression tag	UNP Q6AWJ9
A	588	HIS	-	expression tag	UNP Q6AWJ9
A	589	HIS	-	expression tag	UNP Q6AWJ9
B	21	GLU	-	expression tag	UNP Q6AWJ9
B	22	THR	-	expression tag	UNP Q6AWJ9
B	23	GLY	-	expression tag	UNP Q6AWJ9
B	581	GLY	-	expression tag	UNP Q6AWJ9
B	582	THR	-	expression tag	UNP Q6AWJ9
B	583	LYS	-	expression tag	UNP Q6AWJ9
B	584	HIS	-	expression tag	UNP Q6AWJ9
B	585	HIS	-	expression tag	UNP Q6AWJ9
B	586	HIS	-	expression tag	UNP Q6AWJ9
B	587	HIS	-	expression tag	UNP Q6AWJ9
B	588	HIS	-	expression tag	UNP Q6AWJ9
B	589	HIS	-	expression tag	UNP Q6AWJ9

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: 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		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).

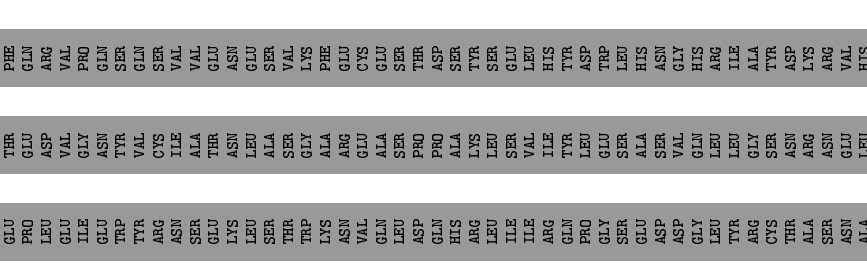


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

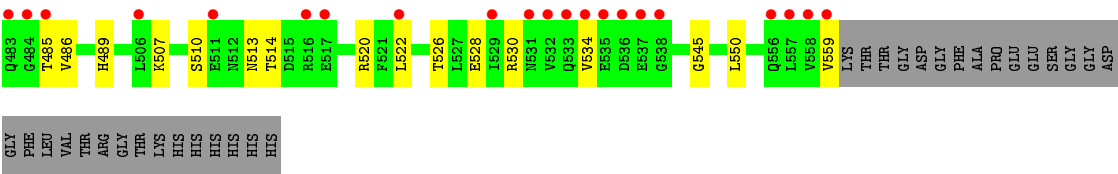
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	239	Total	O	0	0
			239	239		
4	B	191	Total	O	0	0
			191	191		

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.

- Chain A: 

Sequence: GLY THR GLY SER ARG PHE GLN ARG VAL PRO GLN SER GLN SER VAL VAL GLU THR LYS PHE GLU ASN CYS GLU SER VAL LYS ALA ARG GLU CYS GLU SER THR ASP SER TYR SER GLU LEU HIS TYR TRP LEU HIS ASN GLY HIS ARG LEU ILE GLY ALA TYR ASP LYS VAL GLN HIS CYS SER ASN HIS VAL GLN ILE GLY THR CYS VAL GLY THR TRP LYS ASN GLY LEU VAL GLN ASP PRO PRO ALA LYS LEU SER VAL ILE VAL ILE TYR GLN ARG LEU LEU LEU SER CYS ARG THR ALA SER LEU VAL VAL MET ARG MET GLU SER THR VAL ARG MET GLU SER TRP VAL GLN GLY THR VAL GLN SER PRO GLN VAL VAL VAL CYS LEU GLY LEU HIS SER PHE ASP SER GLY LYS ASP ALA LEU GLU LYS ARG MET GLU D327 L330 V380 P381 V394 E416 Q483 I500 E517 R518 Q583 V584 E585 D586 V589 R560 T561 THR GLY ASP GLY PHE PRO GLU CYS

- [illegible]



GLY
PHE
LEU
VAL
THR
ARG
GLY
THR
LYS
HIS
HIS
HIS
HIS
HIS
HIS

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	80.97Å 189.91Å 131.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.48 – 1.97 47.48 – 1.97	Depositor EDS
% Data completeness (in resolution range)	97.3 (47.48-1.97) 97.3 (47.48-1.97)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 1.97Å)	Xtriage
Refinement program	PHENIX dev_3488	Depositor
R, R_{free}	0.207 , 0.235 0.207 , 0.235	Depositor DCC
R_{free} test set	3536 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	32.2	Xtriage
Anisotropy	0.641	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 52.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5253	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.43% 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, SO4

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	0.28	0/2341	0.51	0/3183
1	B	0.27	0/2358	0.49	0/3207
All	All	0.27	0/4699	0.50	0/6390

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	2302	0	2285	12	0
1	B	2318	0	2296	23	0
2	A	84	0	78	0	0
2	B	84	0	78	1	0
3	A	20	0	0	0	0
3	B	15	0	0	1	0
4	A	239	0	0	2	0
4	B	191	0	0	0	0
All	All	5253	0	4737	34	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 4.

All (34) 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:483:GLN:O	4:A:701:HOH:O	2.12	0.68
1:B:507:LYS:HE3	1:B:513:ASN:HD22	1.57	0.67
1:B:534:VAL:HG12	1:B:559:VAL:HG11	1.76	0.66
1:A:518:ARG:NH2	1:A:536:ASP:OD2	2.33	0.62
1:B:386:LYS:HG3	1:B:397:VAL:HG22	1.85	0.58
1:B:435:ARG:NH2	3:B:608:SO4:O1	2.40	0.55
1:B:421:PRO:HG2	1:B:424:VAL:HG21	1.91	0.53
1:B:510:SER:O	1:B:514:THR:OG1	2.23	0.51
1:B:267:LYS:HA	1:B:374:ILE:HB	1.91	0.51
1:A:416:GLU:CD	1:A:416:GLU:H	2.13	0.51
1:B:413:ARG:HE	1:B:421:PRO:HD3	1.75	0.51
1:B:522:LEU:HD12	1:B:526:THR:HB	1.93	0.51
1:A:282:ASP:HA	1:A:285:LYS:HG2	1.94	0.50
1:B:520:ARG:HB2	1:B:528:GLU:HB3	1.94	0.49
1:B:448:LEU:HD23	1:B:457:ASN:HB3	1.93	0.49
1:B:293:TRP:CD1	1:B:332:LEU:HD13	2.49	0.47
1:B:300:LEU:HD21	1:B:330:LEU:HD21	1.97	0.47
1:B:384:THR:OG1	1:B:386:LYS:NZ	2.49	0.46
1:B:276:CYS:HB2	1:B:293:TRP:CZ2	2.51	0.46
1:A:517:GLU:HB2	4:A:727:HOH:O	2.16	0.46
1:A:253:ASP:OD1	1:A:253:ASP:N	2.41	0.46
1:B:427:ASP:HB3	1:B:431:THR:H	1.82	0.45
1:A:276:CYS:HB2	1:A:293:TRP:CZ2	2.53	0.44
1:A:300:LEU:HD21	1:A:330:LEU:HD21	1.99	0.43
1:A:380:VAL:HA	1:A:381:PRO:HA	1.83	0.43
1:A:267:LYS:O	1:A:270:GLU:HB2	2.20	0.42
1:A:301:ARG:CZ	1:B:454:GLY:HA2	2.50	0.42
1:A:247:LEU:HD12	1:A:247:LEU:H	1.84	0.42
1:B:545:GLY:HA3	1:B:550:LEU:HD23	2.02	0.42
1:B:485:THR:HG22	1:B:530:ARG:HA	2.01	0.42
1:B:489:HIS:HB3	2:B:601:NAG:H83	2.02	0.41
1:B:480:THR:HG21	1:B:486:VAL:HG11	2.02	0.41
1:B:380:VAL:HA	1:B:381:PRO:HA	1.87	0.40
1:B:447:CYS:O	1:B:457:ASN:HA	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	294/569 (52%)	287 (98%)	7 (2%)	0	100	100
1	B	296/569 (52%)	291 (98%)	5 (2%)	0	100	100
All	All	590/1138 (52%)	578 (98%)	12 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	257/487 (53%)	256 (100%)	1 (0%)	91	90
1	B	258/487 (53%)	257 (100%)	1 (0%)	91	90
All	All	515/974 (53%)	513 (100%)	2 (0%)	91	90

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	500	ILE
1	B	416	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

19 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	606	1	14,14,15	0.26	0	17,19,21	0.46	0
3	SO4	A	607	-	4,4,4	0.14	0	6,6,6	0.05	0
2	NAG	A	602	1	14,14,15	0.30	0	17,19,21	0.43	0
2	NAG	A	603	1	14,14,15	0.21	0	17,19,21	0.45	0
2	NAG	B	603	1	14,14,15	0.27	0	17,19,21	0.42	0
3	SO4	A	610	-	4,4,4	0.17	0	6,6,6	0.10	0
2	NAG	B	604	1	14,14,15	0.24	0	17,19,21	0.45	0
2	NAG	A	604	1	14,14,15	0.26	0	17,19,21	0.47	0
2	NAG	B	606	1	14,14,15	0.28	0	17,19,21	0.53	0
3	SO4	B	609	-	4,4,4	0.14	0	6,6,6	0.10	0
3	SO4	A	609	-	4,4,4	0.14	0	6,6,6	0.04	0
3	SO4	B	607	-	4,4,4	0.14	0	6,6,6	0.07	0
2	NAG	B	605	1	14,14,15	0.48	0	17,19,21	0.44	0
2	NAG	A	605	1	14,14,15	0.42	0	17,19,21	0.72	1 (5%)
3	SO4	A	608	-	4,4,4	0.14	0	6,6,6	0.06	0
2	NAG	B	601	1	14,14,15	0.26	0	17,19,21	0.46	0
2	NAG	A	601	1	14,14,15	0.29	0	17,19,21	0.57	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	B	608	-	4,4,4	0.14	0	6,6,6	0.05	0
2	NAG	B	602	1	14,14,15	0.31	0	17,19,21	0.56	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
2	NAG	A	606	1	-	0/6/23/26	0/1/1/1
2	NAG	A	602	1	-	0/6/23/26	0/1/1/1
2	NAG	A	603	1	-	0/6/23/26	0/1/1/1
2	NAG	B	603	1	-	0/6/23/26	0/1/1/1
2	NAG	B	604	1	-	2/6/23/26	0/1/1/1
2	NAG	A	604	1	-	0/6/23/26	0/1/1/1
2	NAG	B	606	1	-	3/6/23/26	0/1/1/1
2	NAG	B	602	1	-	3/6/23/26	0/1/1/1
2	NAG	B	605	1	-	2/6/23/26	0/1/1/1
2	NAG	A	605	1	-	0/6/23/26	0/1/1/1
2	NAG	B	601	1	-	2/6/23/26	0/1/1/1
2	NAG	A	601	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	605	NAG	C1-O5-C5	2.52	115.61	112.19

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	NAG	O5-C5-C6-O6
2	B	604	NAG	O5-C5-C6-O6
2	B	604	NAG	C4-C5-C6-O6
2	B	605	NAG	C4-C5-C6-O6
2	B	606	NAG	C4-C5-C6-O6
2	B	605	NAG	O5-C5-C6-O6
2	B	601	NAG	C4-C5-C6-O6
2	B	602	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
2	B	602	NAG	C3-C2-N2-C7
2	A	601	NAG	C3-C2-N2-C7
2	B	602	NAG	O5-C5-C6-O6
2	B	606	NAG	O5-C5-C6-O6
2	B	606	NAG	C3-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	NAG	1	0
3	B	608	SO4	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

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	298/569 (52%)	0.44	8 (2%) 54 63	23, 40, 73, 101	0
1	B	300/569 (52%)	0.91	33 (11%) 5 9	24, 47, 106, 145	0
All	All	598/1138 (52%)	0.67	41 (6%) 16 25	23, 43, 89, 145	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	246	ALA	6.3
1	B	535	GLU	6.1
1	B	480	THR	5.5
1	B	557	LEU	5.5
1	A	327	ASP	5.4
1	B	534	VAL	5.4
1	B	559	VAL	4.9
1	B	533	GLN	4.3
1	A	561	THR	4.1
1	B	479	GLU	4.1
1	B	483	GLN	4.1
1	B	538	GLY	4.0
1	B	506	LEU	3.9
1	B	556	GLN	3.9
1	B	558	VAL	3.7
1	B	531	ASN	3.4
1	B	536	ASP	3.4
1	B	478	ILE	3.4
1	B	482	GLU	3.4
1	A	534	VAL	3.2
1	B	481	SER	3.0
1	B	416	GLU	2.9
1	B	422	ASP	2.9
1	B	485	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	394	VAL	2.8
1	B	484	GLY	2.7
1	A	533	GLN	2.7
1	B	511	GLU	2.6
1	B	529	ILE	2.6
1	A	559	VAL	2.5
1	B	440	GLU	2.5
1	A	394	VAL	2.5
1	B	537	GLU	2.5
1	B	325	ARG	2.4
1	B	522	LEU	2.4
1	B	415	GLY	2.4
1	B	393	VAL	2.4
1	B	517	GLU	2.4
1	B	532	VAL	2.2
1	A	535	GLU	2.2
1	B	516	ARG	2.1

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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	SO4	A	607	5/5	0.70	0.31	129,131,132,133	0
2	NAG	B	606	14/15	0.74	0.33	93,109,117,119	0
2	NAG	B	603	14/15	0.76	0.19	75,88,101,102	0
2	NAG	B	605	14/15	0.77	0.25	83,95,109,113	0
2	NAG	B	602	14/15	0.79	0.19	87,94,103,105	0
2	NAG	A	606	14/15	0.80	0.36	99,109,120,123	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	B	604	14/15	0.86	0.31	80,87,103,103	0
3	SO4	B	608	5/5	0.87	0.17	111,111,112,112	0
2	NAG	B	601	14/15	0.88	0.17	78,86,94,99	0
2	NAG	A	601	14/15	0.89	0.15	48,60,69,72	0
3	SO4	B	609	5/5	0.92	0.11	50,57,59,68	0
3	SO4	A	609	5/5	0.92	0.18	94,97,99,100	0
2	NAG	A	603	14/15	0.94	0.12	38,46,56,64	0
2	NAG	A	604	14/15	0.95	0.13	35,46,56,58	0
3	SO4	A	608	5/5	0.95	0.10	60,65,70,75	0
2	NAG	A	602	14/15	0.96	0.10	33,38,44,47	0
3	SO4	B	607	5/5	0.96	0.14	74,75,76,77	0
2	NAG	A	605	14/15	0.97	0.11	23,30,36,43	0
3	SO4	A	610	5/5	0.97	0.19	41,46,52,54	0

6.5 Other polymers ⓘ

There are no such residues in this entry.