



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:56 PM GMT

PDB ID : 4N8D
Title : DPP4 complexed with syn-7aa
Authors : Ostermann, N.; Zink, F.; Kroemer, M.
Deposited on : 2013-10-17
Resolution : 1.65 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) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

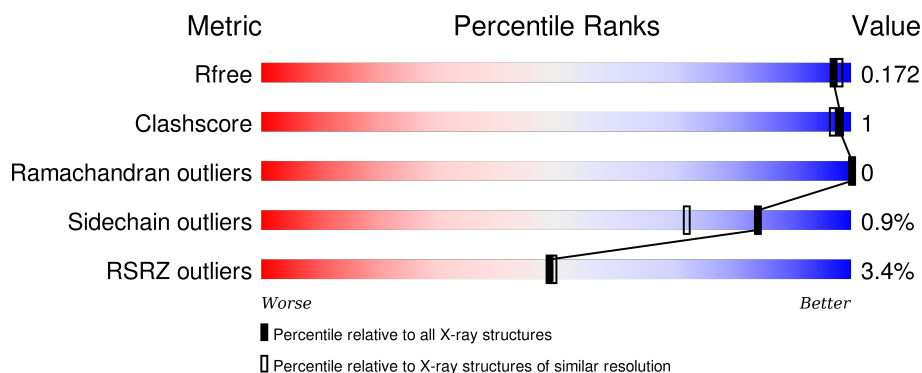
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

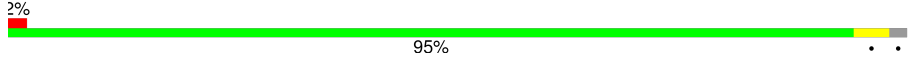
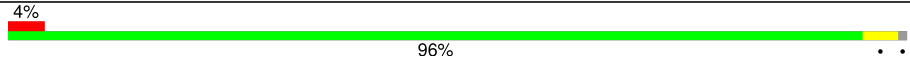
The reported resolution of this entry is 1.65 Å.

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}	91344	1226 (1.66-1.66)
Clashscore	102246	1323 (1.66-1.66)
Ramachandran outliers	100387	1295 (1.66-1.66)
Sidechain outliers	100360	1295 (1.66-1.66)
RSRZ outliers	91569	1227 (1.66-1.66)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	740	
1	B	740	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MAN	A	805	-	-	-	X
3	NAG	A	808	-	-	-	X
3	NAG	A	810	-	-	-	X
3	NAG	A	811	-	-	-	X
3	NAG	B	801	-	-	-	X
3	NAG	B	806	-	-	-	X
5	2KS	A	815	-	-	-	X
5	2KS	B	810	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 14344 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 Dipeptidyl peptidase 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	727	Total	C	N	O	S	0	8	0
			6015	3859	990	1140	26			
1	B	733	Total	C	N	O	S	0	8	0
			6062	3889	999	1148	26			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	437	ILE	SER	CONFLICT	UNP P27487
A	767	ALA	-	EXPRESSION TAG	UNP P27487
A	768	ALA	-	EXPRESSION TAG	UNP P27487
A	769	ALA	-	EXPRESSION TAG	UNP P27487
A	770	SER	-	EXPRESSION TAG	UNP P27487
A	771	TRP	-	EXPRESSION TAG	UNP P27487
A	772	SER	-	EXPRESSION TAG	UNP P27487
A	773	HIS	-	EXPRESSION TAG	UNP P27487
A	774	PRO	-	EXPRESSION TAG	UNP P27487
A	775	GLN	-	EXPRESSION TAG	UNP P27487
A	776	PHE	-	EXPRESSION TAG	UNP P27487
A	777	GLU	-	EXPRESSION TAG	UNP P27487
A	778	LYS	-	EXPRESSION TAG	UNP P27487
B	437	ILE	SER	CONFLICT	UNP P27487
B	767	ALA	-	EXPRESSION TAG	UNP P27487
B	768	ALA	-	EXPRESSION TAG	UNP P27487
B	769	ALA	-	EXPRESSION TAG	UNP P27487
B	770	SER	-	EXPRESSION TAG	UNP P27487
B	771	TRP	-	EXPRESSION TAG	UNP P27487
B	772	SER	-	EXPRESSION TAG	UNP P27487
B	773	HIS	-	EXPRESSION TAG	UNP P27487
B	774	PRO	-	EXPRESSION TAG	UNP P27487
B	775	GLN	-	EXPRESSION TAG	UNP P27487
B	776	PHE	-	EXPRESSION TAG	UNP P27487
B	777	GLU	-	EXPRESSION TAG	UNP P27487

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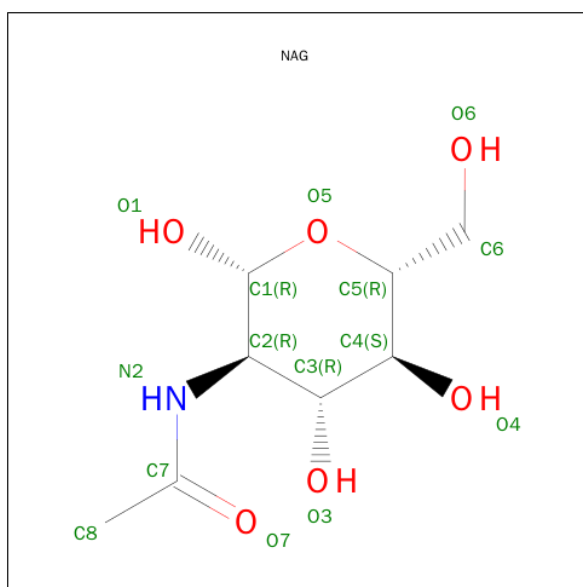
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Chain	Residue	Modelled	Actual	Comment	Reference
B	778	LYS	-	EXPRESSION TAG	UNP P27487

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	5	Total	C	N	O	0	0
			61	34	2	25		

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



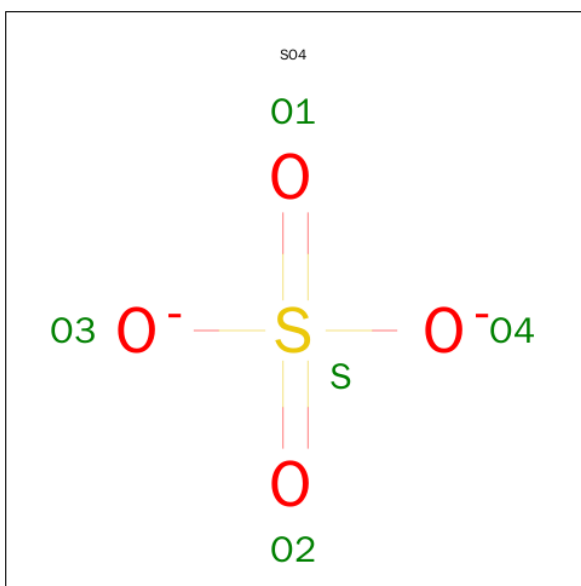
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

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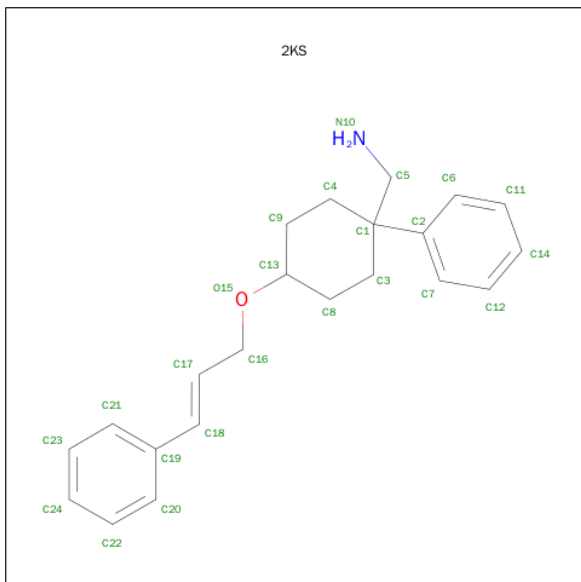
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 5 is 1-(CIS-1-PHENYL-4-{[(2E)-3-PHENYLPROP-2-EN-1-YL]OXY}CYCLOHEXYL)METHANAMINE (three-letter code: 2KS) (formula: C₂₂H₂₇NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			24	22	1	1		
5	B	1	Total	C	N	O	0	0
			24	22	1	1		

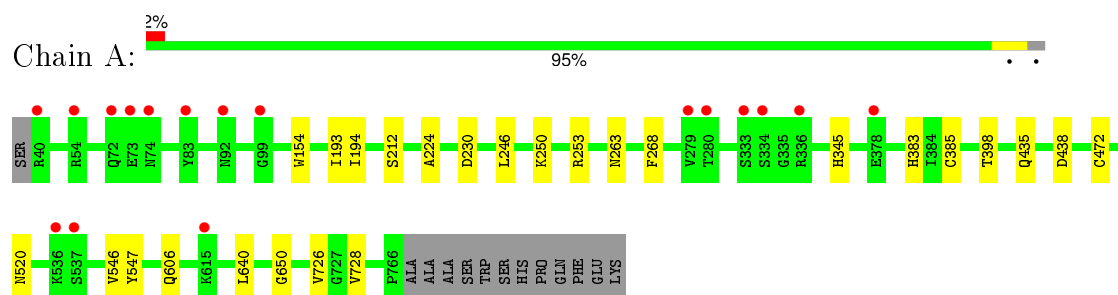
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1040	Total	O	0	0
			1040	1040		
6	B	920	Total	O	0	0
			920	920		

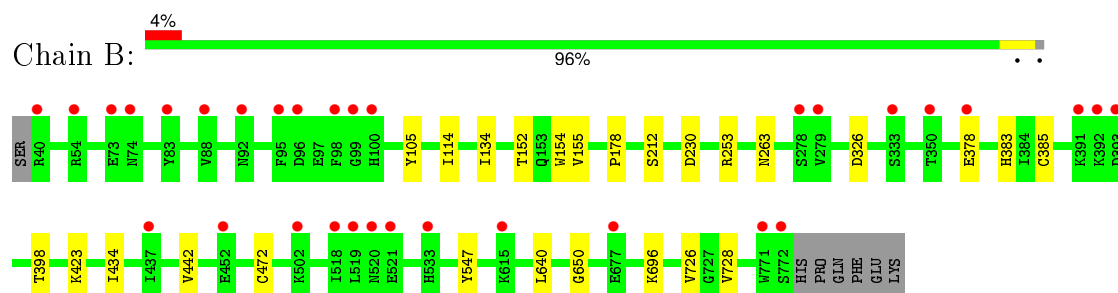
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ($\text{RSRZ} > 2$). 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: Dipeptidyl peptidase 4



- Molecule 1: Dipeptidyl peptidase 4



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	97.31Å 121.92Å 190.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.16 – 1.65 24.15 – 1.65	Depositor EDS
% Data completeness (in resolution range)	99.8 (24.16-1.65) 99.8 (24.15-1.65)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.15 (at 1.65Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.155 , 0.170 0.156 , 0.172	Depositor DCC
R_{free} test set	4879 reflections (1.83%)	DCC
Wilson B-factor (Å ²)	19.6	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 54.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 271022 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	14344	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.81% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: 2KS, NAG, SO4, MAN

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	0.54	0/6187	0.63	0/8415
1	B	0.50	0/6237	0.61	0/8483
All	All	0.52	0/12424	0.62	0/16898

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	6015	0	5723	14	0
1	B	6062	0	5763	12	0
2	A	61	0	52	0	0
3	A	84	0	78	2	0
3	B	84	0	78	0	0
4	A	15	0	0	0	0
4	B	15	0	0	0	0
5	A	24	0	27	0	0
5	B	24	0	27	0	0
6	A	1040	0	0	1	0
6	B	920	0	0	0	0
All	All	14344	0	11748	24	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 1.

All (24) 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:253:ARG:HH21	1:B:253:ARG:HH21	1.20	0.89
1:B:434[A]:ILE:HG22	1:B:442:VAL:HG22	1.67	0.76
1:A:520:ASN:HD22	3:A:811:NAG:H83	1.63	0.63
1:A:726:VAL:HG23	1:A:728:VAL:HG23	1.88	0.55
1:B:726:VAL:HG23	1:B:728:VAL:HG23	1.90	0.53
1:A:546[B]:VAL:HG12	1:A:606:GLN:OE1	2.10	0.51
1:A:435:GLN:HE21	1:A:438:ASP:HB3	1.77	0.49
1:B:378:GLU:CD	1:B:378:GLU:H	2.15	0.49
1:A:345:HIS:HD2	6:A:955:HOH:O	1.95	0.49
1:A:383:HIS:HD2	1:A:398:THR:OG1	1.97	0.47
1:A:154:TRP:CE2	1:A:212[A]:SER:HB3	2.51	0.45
1:A:640:LEU:HD11	1:A:650:GLY:HA3	1.98	0.45
1:B:640:LEU:HD11	1:B:650:GLY:HA3	1.98	0.45
1:A:253:ARG:NH2	1:B:253:ARG:HH21	2.02	0.45
1:B:383:HIS:HD2	1:B:398:THR:OG1	2.00	0.44
1:B:105:TYR:HB2	1:B:114:ILE:HD11	2.00	0.44
1:A:193[B]:ILE:HG22	1:A:194:ILE:HG12	2.00	0.43
1:B:152:THR:HG21	1:B:155:VAL:HG22	2.01	0.43
1:B:696:LYS:HG2	1:B:728:VAL:HG22	2.02	0.42
1:A:224:ALA:HB1	1:A:268:PHE:CZ	2.55	0.42
1:B:154:TRP:CE2	1:B:212[B]:SER:HB3	2.54	0.42
1:B:134:ILE:HD13	1:B:178:PRO:HB3	2.03	0.41
1:A:520:ASN:ND2	3:A:811:NAG:H83	2.31	0.41
1:A:246:LEU:HD21	1:A:250:LYS:HG3	2.03	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	733/740 (99%)	711 (97%)	22 (3%)	0	100	100
1	B	739/740 (100%)	719 (97%)	20 (3%)	0	100	100
All	All	1472/1480 (100%)	1430 (97%)	42 (3%)	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	660/662 (100%)	655 (99%)	5 (1%)	86	76
1	B	663/662 (100%)	656 (99%)	7 (1%)	80	64
All	All	1323/1324 (100%)	1311 (99%)	12 (1%)	84	72

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	230	ASP
1	A	263	ASN
1	A	385	CYS
1	A	472	CYS
1	A	547	TYR
1	B	230	ASP
1	B	263	ASN
1	B	326	ASP
1	B	385	CYS
1	B	423	LYS
1	B	472	CYS
1	B	547	TYR

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

Mol	Chain	Res	Type
1	A	138	ASN

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Mol	Chain	Res	Type
1	A	263	ASN
1	A	345	HIS
1	A	363	HIS
1	A	383	HIS
1	A	435	GLN
1	A	572	ASN
1	B	263	ASN
1	B	344	GLN
1	B	363	HIS
1	B	383	HIS
1	B	388	GLN
1	B	435	GLN
1	B	572	ASN

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 ⓘ

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	$\# Z > 2$
2	NAG	A	801	1,2	14,14,15	0.33	0	15,19,21	0.42	0
2	NAG	A	802	2	14,14,15	0.38	0	15,19,21	0.78	1 (6%)
2	MAN	A	803	2	11,11,12	0.39	0	14,15,17	1.75	3 (21%)
2	MAN	A	804	2	11,11,12	0.32	0	14,15,17	0.83	1 (7%)
2	MAN	A	805	2	11,11,12	0.35	0	14,15,17	0.79	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	801	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	802	2	-	0/6/23/26	0/1/1/1
2	MAN	A	803	2	-	0/2/19/22	1/1/1/1
2	MAN	A	804	2	-	0/2/19/22	0/1/1/1
2	MAN	A	805	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	803	MAN	O2-C2-C1	-3.02	103.14	109.21
2	A	802	NAG	O4-C4-C5	-2.60	102.35	109.24
2	A	803	MAN	C1-C2-C3	2.36	112.33	109.54
2	A	804	MAN	C1-O5-C5	2.95	115.99	112.25
2	A	803	MAN	C1-O5-C5	4.98	118.57	112.25

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	803	MAN	C1-C2-C3-C4-C5-O5

No monomer is involved in short contacts.

5.6 Ligand geometry

20 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	806	1	14,14,15	0.27	0	15,19,21	0.47	0
3	NAG	A	807	1	14,14,15	0.24	0	15,19,21	0.53	0
3	NAG	A	808	1	14,14,15	0.31	0	15,19,21	0.47	0
3	NAG	A	809	1	14,14,15	0.28	0	15,19,21	0.36	0
3	NAG	A	810	1	14,14,15	0.27	0	15,19,21	1.01	1 (6%)
3	NAG	A	811	1	14,14,15	0.39	0	15,19,21	0.52	0
4	SO4	A	812	-	4,4,4	0.13	0	6,6,6	0.18	0
4	SO4	A	813	-	4,4,4	0.23	0	6,6,6	0.16	0
4	SO4	A	814	-	4,4,4	0.11	0	6,6,6	0.11	0
5	2KS	A	815	-	25,26,26	1.51	4 (16%)	29,34,34	0.88	1 (3%)
3	NAG	B	801	1	14,14,15	0.28	0	15,19,21	0.82	1 (6%)
3	NAG	B	802	1	14,14,15	0.32	0	15,19,21	0.60	1 (6%)
3	NAG	B	803	1	14,14,15	0.26	0	15,19,21	0.41	0
3	NAG	B	804	1	14,14,15	0.29	0	15,19,21	0.50	0
3	NAG	B	805	1	14,14,15	0.30	0	15,19,21	0.49	0
3	NAG	B	806	1	14,14,15	0.26	0	15,19,21	0.84	1 (6%)
4	SO4	B	807	-	4,4,4	0.27	0	6,6,6	0.24	0
4	SO4	B	808	-	4,4,4	0.13	0	6,6,6	0.10	0
4	SO4	B	809	-	4,4,4	0.06	0	6,6,6	0.07	0
5	2KS	B	810	-	25,26,26	1.65	4 (16%)	29,34,34	1.13	2 (6%)

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	806	1	-	0/6/23/26	0/1/1/1
3	NAG	A	807	1	-	0/6/23/26	0/1/1/1
3	NAG	A	808	1	-	0/6/23/26	0/1/1/1
3	NAG	A	809	1	-	0/6/23/26	0/1/1/1
3	NAG	A	810	1	-	0/6/23/26	0/1/1/1
3	NAG	A	811	1	-	0/6/23/26	0/1/1/1
4	SO4	A	812	-	-	0/0/0/0	0/0/0/0
4	SO4	A	813	-	-	0/0/0/0	0/0/0/0
4	SO4	A	814	-	-	0/0/0/0	0/0/0/0
5	2KS	A	815	-	-	0/16/28/28	0/3/3/3
3	NAG	B	801	1	-	0/6/23/26	0/1/1/1
3	NAG	B	802	1	-	0/6/23/26	0/1/1/1
3	NAG	B	803	1	-	0/6/23/26	0/1/1/1
3	NAG	B	804	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	B	805	1	-	0/6/23/26	0/1/1/1
3	NAG	B	806	1	-	0/6/23/26	0/1/1/1
4	SO4	B	807	-	-	0/0/0/0	0/0/0/0
4	SO4	B	808	-	-	0/0/0/0	0/0/0/0
4	SO4	B	809	-	-	0/0/0/0	0/0/0/0
5	2KS	B	810	-	-	0/16/28/28	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	815	2KS	C1-C2	2.20	1.56	1.53
5	A	815	2KS	C8-C13	2.21	1.56	1.51
5	B	810	2KS	C8-C13	2.32	1.57	1.51
5	B	810	2KS	C7-C2	2.37	1.43	1.39
5	A	815	2KS	C9-C13	2.40	1.57	1.51
5	A	815	2KS	C7-C2	2.73	1.43	1.39
5	B	810	2KS	C9-C13	2.86	1.58	1.51
5	B	810	2KS	C1-C2	3.61	1.58	1.53

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	815	2KS	C4-C9-C13	2.01	113.86	110.23
3	B	802	NAG	C1-O5-C5	2.06	114.87	112.25
5	B	810	2KS	C11-C6-C2	2.18	123.16	120.76
5	B	810	2KS	C4-C9-C13	2.61	114.94	110.23
3	B	801	NAG	C1-O5-C5	2.79	115.80	112.25
3	B	806	NAG	C1-O5-C5	3.10	116.19	112.25
3	A	810	NAG	C1-O5-C5	3.44	116.62	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	811	NAG	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

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	727/740 (98%)	-0.20	17 (2%) 64 65	12, 21, 43, 69	0
1	B	733/740 (99%)	-0.11	32 (4%) 38 37	13, 25, 51, 71	0
All	All	1460/1480 (98%)	-0.16	49 (3%) 49 49	12, 23, 48, 71	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	279	VAL	6.7
1	A	74	ASN	6.2
1	B	615	LYS	5.8
1	B	279	VAL	5.2
1	B	74	ASN	5.0
1	B	437	ILE	4.7
1	B	96	ASP	4.6
1	A	73	GLU	4.5
1	B	772	SER	4.3
1	B	73	GLU	4.2
1	B	98	PHE	4.2
1	A	92	ASN	4.1
1	B	771	TRP	3.9
1	B	521	GLU	3.7
1	A	72	GLN	3.7
1	A	40	ARG	3.7
1	B	40	ARG	3.6
1	B	278	SER	3.3
1	A	83	TYR	3.2
1	B	393	ASP	3.1
1	B	99	GLY	3.1
1	A	333	SER	3.1
1	B	88	VAL	3.0
1	A	336	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	537	SER	3.0
1	B	333	SER	2.9
1	B	520	ASN	2.9
1	B	92	ASN	2.6
1	B	83	TYR	2.6
1	B	519	LEU	2.6
1	B	452	GLU	2.6
1	B	677	GLU	2.5
1	A	54	ARG	2.5
1	A	615	LYS	2.5
1	B	391	LYS	2.5
1	A	334	SER	2.4
1	A	378	GLU	2.4
1	B	378	GLU	2.3
1	B	95	PHE	2.3
1	B	100	HIS	2.3
1	A	536	LYS	2.3
1	A	99	GLY	2.2
1	B	533	HIS	2.2
1	B	518	ILE	2.2
1	A	280	THR	2.2
1	B	502	LYS	2.1
1	B	54	ARG	2.1
1	B	392	LYS	2.0
1	B	350	THR	2.0

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 ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	MAN	A	805	11/12	0.86	0.16	4.29	27,30,33,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	NAG	A	801	14/15	0.89	0.15	1.06	28,31,33,39	0
2	NAG	A	802	14/15	0.85	0.16	-	30,35,39,41	0
2	MAN	A	804	11/12	0.92	0.26	-	43,47,49,51	0
2	MAN	A	803	11/12	0.80	0.20	-	30,34,40,41	0

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	A	811	14/15	0.89	0.16	6.54	21,29,37,41	0
5	2KS	B	810	24/24	0.78	0.21	6.00	19,29,53,54	0
5	2KS	A	815	24/24	0.80	0.19	4.72	16,23,47,48	0
3	NAG	B	806	14/15	0.86	0.26	3.77	33,39,49,50	0
3	NAG	A	810	14/15	0.87	0.21	3.34	23,32,40,41	0
3	NAG	B	801	14/15	0.77	0.24	3.07	45,54,62,66	0
3	NAG	A	808	14/15	0.95	0.13	2.04	24,31,37,37	0
3	NAG	B	804	14/15	0.94	0.13	1.42	24,31,36,36	0
3	NAG	B	805	14/15	0.92	0.19	-	33,41,44,46	0
4	SO4	A	814	5/5	0.77	0.36	-	72,76,76,78	0
3	NAG	A	806	14/15	0.86	0.23	-	33,39,44,45	0
4	SO4	A	812	5/5	0.94	0.18	-	60,61,62,63	0
3	NAG	A	809	14/15	0.87	0.17	-	37,43,48,49	0
3	NAG	A	807	14/15	0.84	0.26	-	30,42,57,58	0
4	SO4	B	809	5/5	0.70	0.35	-	91,92,92,93	0
4	SO4	B	808	5/5	0.91	0.19	-	87,87,89,89	0
4	SO4	B	807	5/5	0.90	0.23	-	52,59,59,61	0
4	SO4	A	813	5/5	0.99	0.21	-	46,46,48,48	0
3	NAG	B	803	14/15	0.77	0.25	-	33,41,51,53	0
3	NAG	B	802	14/15	0.86	0.25	-	35,38,45,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.