



wwPDB X-ray Structure Validation Summary Report i

Feb 26, 2014 – 03:49 PM GMT

PDB ID : 2ONC
Title : Crystal structure of human DPP-4
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Deposited on : 2007-01-23
Resolution : 2.55 Å(reported)

This is a wwPDB validation summary 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/ValidationPDFNotes.html>

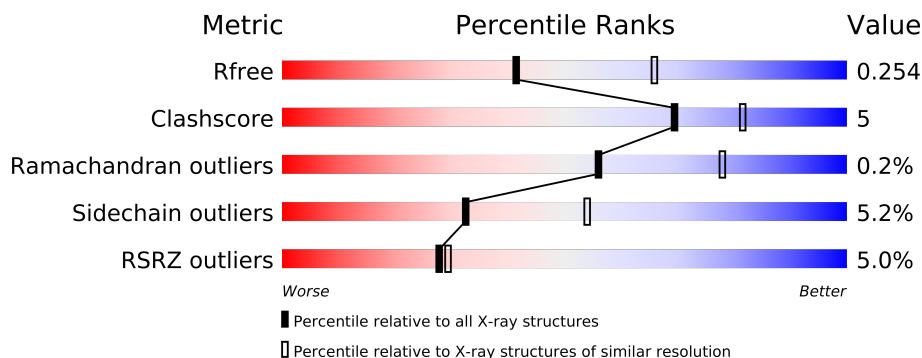
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.55 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}	66092	3413 (2.58-2.50)
Clashscore	79885	4284 (2.58-2.50)
Ramachandran outliers	78287	4193 (2.58-2.50)
Sidechain outliers	78261	4195 (2.58-2.50)
RSRZ outliers	66119	3414 (2.58-2.50)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	731	
1	B	731	
1	C	731	
1	D	731	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	NAG	A	804	-	X
2	NAG	A	807	-	X
2	NAG	B	804	-	X
2	NAG	C	807	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 25016 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

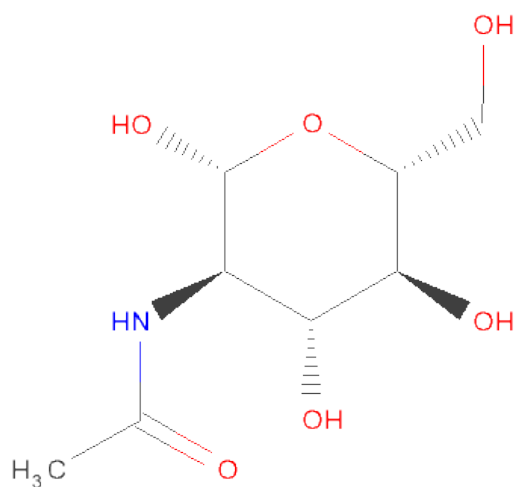
- Molecule 1 is a protein called Dipeptidyl peptidase 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	724	Total	C	N	O	S	0	1	0
			5925	3807	973	1119	26			
1	B	728	Total	C	N	O	S	0	1	0
			5958	3826	981	1125	26			
1	C	723	Total	C	N	O	S	0	1	0
			5918	3802	972	1118	26			
1	D	722	Total	C	N	O	S	0	0	0
			5907	3795	969	1117	26			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	36	HIS	-	EXPRESSION TAG	UNP P27487
A	37	HIS	-	EXPRESSION TAG	UNP P27487
A	38	ALA	-	EXPRESSION TAG	UNP P27487
A	39	SER	-	EXPRESSION TAG	UNP P27487
A	40	ALA	-	EXPRESSION TAG	UNP P27487
B	36	HIS	-	EXPRESSION TAG	UNP P27487
B	37	HIS	-	EXPRESSION TAG	UNP P27487
B	38	ALA	-	EXPRESSION TAG	UNP P27487
B	39	SER	-	EXPRESSION TAG	UNP P27487
B	40	ALA	-	EXPRESSION TAG	UNP P27487
C	36	HIS	-	EXPRESSION TAG	UNP P27487
C	37	HIS	-	EXPRESSION TAG	UNP P27487
C	38	ALA	-	EXPRESSION TAG	UNP P27487
C	39	SER	-	EXPRESSION TAG	UNP P27487
C	40	ALA	-	EXPRESSION TAG	UNP P27487
D	36	HIS	-	EXPRESSION TAG	UNP P27487
D	37	HIS	-	EXPRESSION TAG	UNP P27487
D	38	ALA	-	EXPRESSION TAG	UNP P27487
D	39	SER	-	EXPRESSION TAG	UNP P27487
D	40	ALA	-	EXPRESSION TAG	UNP P27487

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (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	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	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		

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

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

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

There are 25 discrepancies between the modelled and reference sequences:

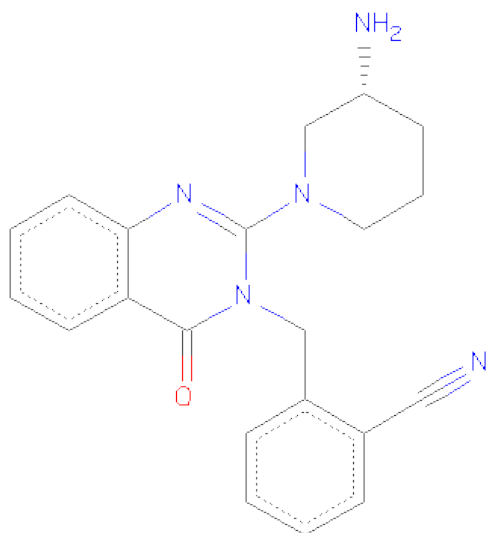
Chain	Residue	Modelled	Actual	Comment	Reference
A	36	HIS	-	EXPRESSION TAG	UNP P27487
A	37	HIS	-	EXPRESSION TAG	UNP P27487
A	38	ALA	-	EXPRESSION TAG	UNP P27487
A	39	SER	-	EXPRESSION TAG	UNP P27487
A	40	ALA	-	EXPRESSION TAG	UNP P27487
A	36	HIS	-	EXPRESSION TAG	UNP P27487
A	37	HIS	-	EXPRESSION TAG	UNP P27487
A	38	ALA	-	EXPRESSION TAG	UNP P27487
A	39	SER	-	EXPRESSION TAG	UNP P27487
A	40	ALA	-	EXPRESSION TAG	UNP P27487
B	36	HIS	-	EXPRESSION TAG	UNP P27487
B	37	HIS	-	EXPRESSION TAG	UNP P27487
B	38	ALA	-	EXPRESSION TAG	UNP P27487
B	39	SER	-	EXPRESSION TAG	UNP P27487
B	40	ALA	-	EXPRESSION TAG	UNP P27487
C	36	HIS	-	EXPRESSION TAG	UNP P27487
C	37	HIS	-	EXPRESSION TAG	UNP P27487
C	38	ALA	-	EXPRESSION TAG	UNP P27487
C	39	SER	-	EXPRESSION TAG	UNP P27487
C	40	ALA	-	EXPRESSION TAG	UNP P27487

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Chain	Residue	Modelled	Actual	Comment	Reference
D	36	HIS	-	EXPRESSION TAG	UNP P27487
D	37	HIS	-	EXPRESSION TAG	UNP P27487
D	38	ALA	-	EXPRESSION TAG	UNP P27487
D	39	SER	-	EXPRESSION TAG	UNP P27487
D	40	ALA	-	EXPRESSION TAG	UNP P27487

- Molecule 4 is 2-({2-[(3R)-3-AMINOPIPERIDIN-1-YL]-4-OXOQUINAZOLIN-3(4H)-YL}METHYL)BENZONITRILE (three-letter code: SY1) (formula: C₂₁H₂₁N₅O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			27	21	5	1		
4	A	1	Total	C	N	O	0	0
			27	21	5	1		
4	B	1	Total	C	N	O	0	0
			27	21	5	1		
4	B	1	Total	C	N	O	0	0
			27	21	5	1		
4	C	1	Total	C	N	O	0	0
			27	21	5	1		
4	C	1	Total	C	N	O	0	0
			27	21	5	1		
4	D	1	Total	C	N	O	0	0
			27	21	5	1		
4	D	1	Total	C	N	O	0	0
			27	21	5	1		

- Molecule 5 is water.

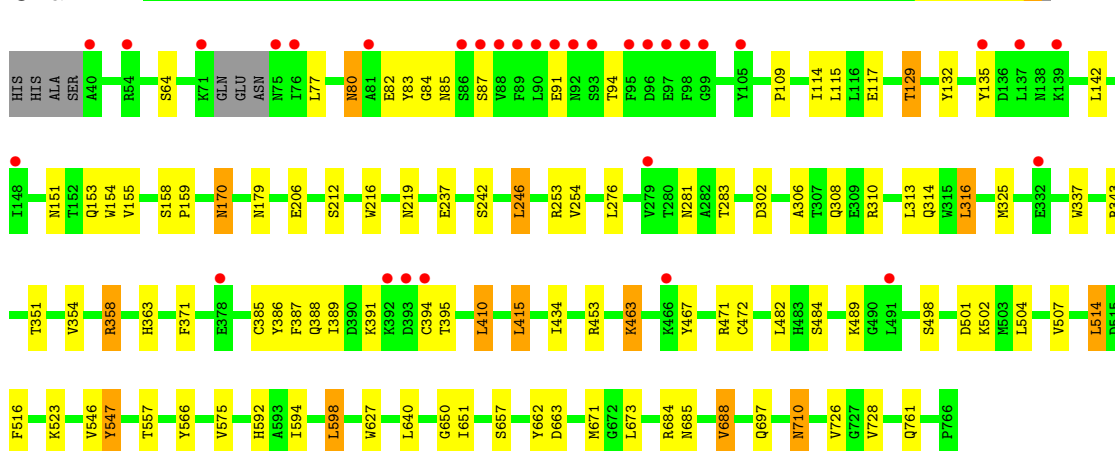
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	227	Total 227	O 227	0	0
5	B	213	Total 213	O 213	0	0
5	C	219	Total 219	O 219	0	0
5	D	97	Total 97	O 97	0	0

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.

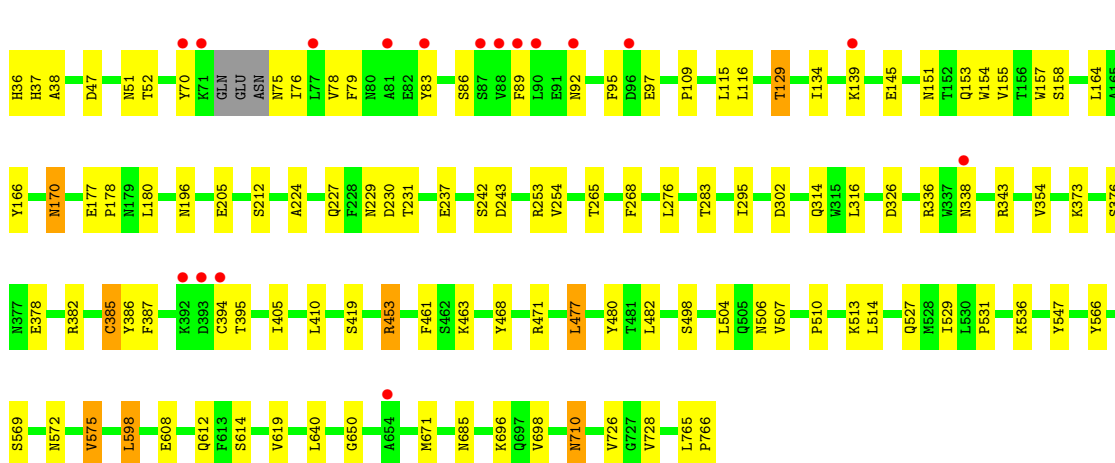
• Molecule 1: Dipeptidyl peptidase 4

Chain A:



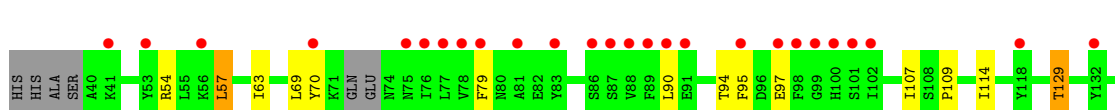
• Molecule 1: Dipeptidyl peptidase 4

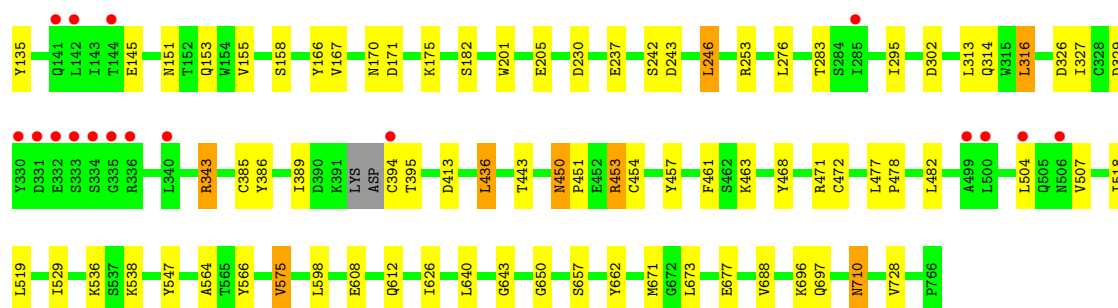
Chain B:



• Molecule 1: Dipeptidyl peptidase 4

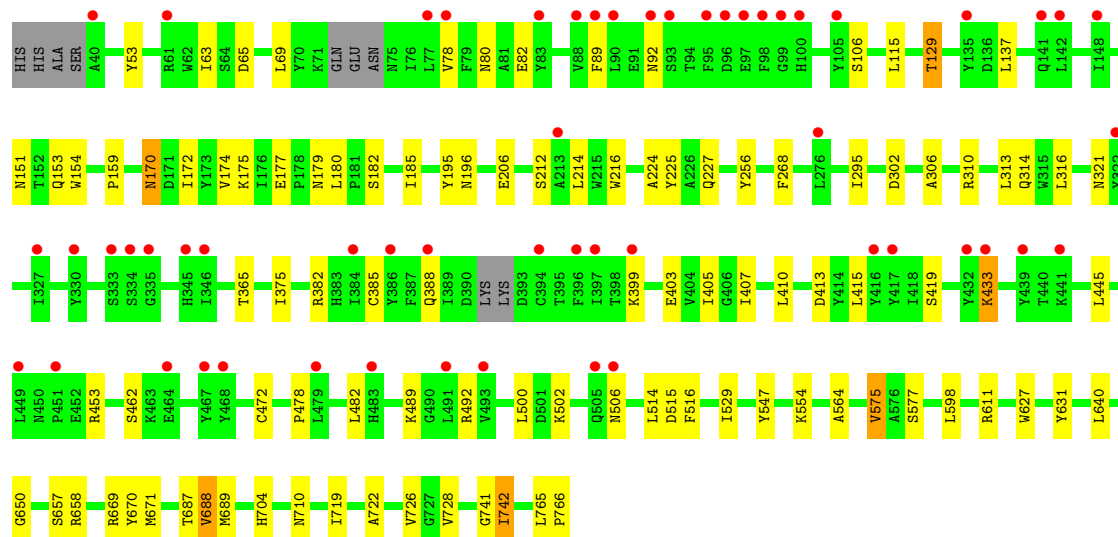
Chain C:





• Molecule 1: Dipeptidyl peptidase 4

Chain D:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	122.36Å 123.70Å 145.36Å 90.00° 114.89° 90.00°	Depositor
Resolution (Å)	50.00 – 2.55 38.65 – 2.55	Depositor EDS
% Data completeness (in resolution range)	92.8 (50.00-2.55) 92.8 (38.65-2.55)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.61 (at 2.54Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.195 , 0.254 0.196 , 0.254	Depositor DCC
R_{free} test set	5942 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	46.8	Xtriage
Anisotropy	0.526	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 38.5	EDS
Estimated twinning fraction	0.012 for h,-k,-h-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 118368 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	25016	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.26% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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: SY1, NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.44	0/6096	0.59	2/8291 (0.0%)
1	B	0.42	0/6135	0.58	0/8344
1	C	0.43	0/6092	0.59	2/8285 (0.0%)
1	D	0.40	0/6077	0.55	0/8266
All	All	0.42	0/24400	0.58	4/33186 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	316	LEU	CA-CB-CG	5.45	127.84	115.30
1	C	57	LEU	CA-CB-CG	5.37	127.66	115.30
1	A	316	LEU	CA-CB-CG	5.09	127.00	115.30
1	A	142	LEU	CA-CB-CG	5.03	126.88	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts i

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5925	0	5639	53	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	5958	0	5670	58	0
1	C	5918	0	5635	43	0
1	D	5907	0	5621	46	0
2	A	56	0	52	0	0
2	B	56	0	52	0	0
2	C	56	0	52	0	0
2	D	28	0	26	0	0
3	A	56	0	50	1	0
3	B	28	0	25	0	0
3	C	28	0	25	0	0
3	D	28	0	25	0	0
4	A	54	0	42	6	0
4	B	54	0	42	6	0
4	C	54	0	42	6	0
4	D	54	0	42	5	0
5	A	227	0	0	5	0
5	B	213	0	0	5	0
5	C	219	0	0	0	0
5	D	97	0	0	2	0
All	All	25016	0	23040	220	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

The worst 5 of 220 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:153:GLN:HE22	1:B:170:ASN:H	1.07	1.00
1:C:153:GLN:HE22	1:C:170:ASN:H	1.13	0.95
1:A:153:GLN:HE22	1:A:170:ASN:H	1.20	0.89
4:B:800:SY1:H52	4:B:800:SY1:H191	1.57	0.87
1:D:153:GLN:HE22	1:D:170:ASN:H	1.25	0.81

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	720/731 (98%)	681 (95%)	37 (5%)	2 (0%)	50	71
1	B	725/731 (99%)	686 (95%)	37 (5%)	2 (0%)	50	71
1	C	718/731 (98%)	678 (94%)	39 (5%)	1 (0%)	59	81
1	D	716/731 (98%)	671 (94%)	44 (6%)	1 (0%)	59	81
All	All	2879/2924 (98%)	2716 (94%)	157 (6%)	6 (0%)	56	78

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	85	ASN
1	A	87	SER
1	B	463	LYS
1	B	83	TYR
1	C	536	LYS

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	648/654 (99%)	611 (94%)	37 (6%)	29	48
1	B	652/654 (100%)	616 (94%)	36 (6%)	30	50
1	C	648/654 (99%)	614 (95%)	34 (5%)	32	54
1	D	646/654 (99%)	618 (96%)	28 (4%)	40	64
All	All	2594/2616 (99%)	2459 (95%)	135 (5%)	32	54

5 of 135 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	498	SER
1	C	94	THR
1	D	489	LYS
1	B	504	LEU
1	B	566	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	506	ASN
1	C	169	ASN
1	D	506	ASN
1	B	572	ASN
1	B	710	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

10 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	$\# Z > 2$
3	NAG	A	805	3	12,14,15	0.71	0	15,19,21	1.52	3 (20%)
3	NAG	A	806	3	12,14,15	0.59	0	15,19,21	0.98	1 (6%)
3	NAG	A	808	1,3	12,14,15	0.75	1 (8%)	15,19,21	0.66	0
3	NAG	A	809	3	12,14,15	0.52	0	15,19,21	0.79	1 (6%)
3	NAG	B	805	1,3	12,14,15	0.68	0	15,19,21	0.75	1 (6%)
3	NAG	B	806	3	12,14,15	0.61	0	15,19,21	1.34	2 (13%)
3	NAG	C	804	1,3	12,14,15	0.69	1 (8%)	15,19,21	1.19	1 (6%)
3	NAG	C	805	3	12,14,15	0.57	0	15,19,21	0.80	0
3	NAG	D	803	1,3	12,14,15	0.54	0	15,19,21	0.88	0
3	NAG	D	804	3	12,14,15	0.55	0	15,19,21	0.95	1 (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	805	3	-	0/6/23/26	0/1/1/1
3	NAG	A	806	3	-	0/6/23/26	0/1/1/1
3	NAG	A	808	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	809	3	-	0/6/23/26	0/1/1/1
3	NAG	B	805	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	806	3	-	0/6/23/26	0/1/1/1
3	NAG	C	804	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	805	3	-	0/6/23/26	0/1/1/1
3	NAG	D	803	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	804	3	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	808	NAG	O5-C5	-2.22	1.41	1.45
3	C	804	NAG	O5-C5	-2.06	1.41	1.45

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	805	NAG	C3-C4-C5	3.59	116.62	110.20
3	B	806	NAG	O5-C5-C6	3.19	110.33	106.98
3	B	806	NAG	C3-C2-N2	-3.18	106.92	111.76
3	C	804	NAG	C2-N2-C7	-2.70	118.56	123.09
3	A	805	NAG	O5-C5-C4	2.49	113.81	110.65

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.6 Ligand geometry

22 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link

column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SY1	A	800	-	30,30,30	2.31	4 (13%)	40,42,42	2.28	10 (25%)
4	SY1	A	801	-	30,30,30	2.24	5 (16%)	40,42,42	2.22	11 (27%)
2	NAG	A	802	1	12,14,15	0.64	0	15,19,21	1.09	1 (6%)
2	NAG	A	803	1	12,14,15	0.54	0	15,19,21	1.09	1 (6%)
2	NAG	A	804	1	12,14,15	0.61	0	15,19,21	0.88	0
2	NAG	A	807	1	12,14,15	0.57	0	15,19,21	0.81	0
4	SY1	B	800	-	30,30,30	2.21	4 (13%)	40,42,42	2.18	10 (25%)
4	SY1	B	801	-	30,30,30	2.22	4 (13%)	40,42,42	1.83	6 (15%)
2	NAG	B	802	1	12,14,15	0.64	0	15,19,21	1.40	2 (13%)
2	NAG	B	803	1	12,14,15	0.55	0	15,19,21	0.85	0
2	NAG	B	804	1	12,14,15	0.56	0	15,19,21	0.95	1 (6%)
2	NAG	B	807	1	12,14,15	0.50	0	15,19,21	1.29	1 (6%)
4	SY1	C	800	-	30,30,30	2.26	4 (13%)	40,42,42	2.18	9 (22%)
4	SY1	C	801	-	30,30,30	2.40	5 (16%)	40,42,42	2.56	9 (22%)
2	NAG	C	802	1	12,14,15	0.59	0	15,19,21	1.11	1 (6%)
2	NAG	C	803	1	12,14,15	0.61	0	15,19,21	0.94	1 (6%)
2	NAG	C	806	1	12,14,15	0.56	0	15,19,21	1.34	2 (13%)
2	NAG	C	807	1	12,14,15	0.66	0	15,19,21	1.16	2 (13%)
4	SY1	D	800	-	30,30,30	2.31	4 (13%)	40,42,42	2.05	10 (25%)
4	SY1	D	801	-	30,30,30	2.21	5 (16%)	40,42,42	2.32	10 (25%)
2	NAG	D	802	1	12,14,15	0.59	0	15,19,21	1.14	2 (13%)
2	NAG	D	805	1	12,14,15	0.52	0	15,19,21	1.09	1 (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
4	SY1	A	800	-	-	0/10/20/20	0/2/4/4
4	SY1	A	801	-	-	0/10/20/20	0/2/4/4
2	NAG	A	802	1	-	0/6/23/26	0/1/1/1
2	NAG	A	803	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	804	1	-	0/6/23/26	0/1/1/1
2	NAG	A	807	1	-	0/6/23/26	0/1/1/1
4	SY1	B	800	-	-	0/10/20/20	0/2/4/4
4	SY1	B	801	-	-	0/10/20/20	0/2/4/4
2	NAG	B	802	1	-	0/6/23/26	0/1/1/1
2	NAG	B	803	1	-	0/6/23/26	0/1/1/1
2	NAG	B	804	1	-	0/6/23/26	0/1/1/1
2	NAG	B	807	1	-	0/6/23/26	0/1/1/1
4	SY1	C	800	-	-	0/10/20/20	0/2/4/4
4	SY1	C	801	-	-	0/10/20/20	0/2/4/4
2	NAG	C	802	1	-	0/6/23/26	0/1/1/1
2	NAG	C	803	1	-	0/6/23/26	0/1/1/1
2	NAG	C	806	1	-	0/6/23/26	0/1/1/1
2	NAG	C	807	1	-	0/6/23/26	0/1/1/1
4	SY1	D	800	-	-	0/10/20/20	0/2/4/4
4	SY1	D	801	-	-	0/10/20/20	0/2/4/4
2	NAG	D	802	1	-	0/6/23/26	0/1/1/1
2	NAG	D	805	1	-	0/6/23/26	0/1/1/1

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	800	SY1	C25-C26	-9.87	1.28	1.44
4	B	801	SY1	C25-C26	-9.67	1.28	1.44
4	D	800	SY1	C25-C26	-9.64	1.29	1.44
4	A	800	SY1	C25-C26	-9.59	1.29	1.44
4	B	800	SY1	C25-C26	-9.41	1.29	1.44

The worst 5 of 90 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	801	SY1	C25-C26-N27	-10.66	159.03	177.80
4	D	801	SY1	C25-C26-N27	-7.84	164.00	177.80
4	C	800	SY1	C5-N6-C8	-5.74	109.64	122.01
4	D	800	SY1	C5-N6-C8	-5.67	109.80	122.01
4	B	800	SY1	C5-N6-C8	-5.66	109.82	122.01

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	724/731 (99%)	0.14	32 (4%)	33	35	28, 45, 76, 113	1 (0%)
1	B	728/731 (99%)	0.03	17 (2%)	57	61	32, 49, 74, 102	0
1	C	723/731 (98%)	0.13	43 (5%)	22	23	31, 49, 77, 94	0
1	D	722/731 (98%)	0.42	55 (7%)	14	14	35, 62, 91, 133	0
All	All	2897/2924 (99%)	0.18	147 (5%)	28	28	28, 51, 83, 133	1 (0%)

The worst 5 of 147 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	88	VAL	6.0
1	D	83	TYR	6.0
1	C	89	PHE	5.9
1	A	392	LYS	5.8
1	D	77	LEU	5.7

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	C	805	14/15	0.29	6.94	74,77,80,80	0
3	NAG	B	806	14/15	0.22	1.64	80,82,83,83	0
3	NAG	A	808	14/15	0.15	1.35	57,61,63,65	0
3	NAG	D	804	14/15	0.18	1.22	74,75,76,76	0
3	NAG	B	805	14/15	0.15	0.71	68,70,73,77	0
3	NAG	A	805	14/15	0.18	-0.06	97,99,101,101	0
3	NAG	C	804	14/15	0.12	-0.38	62,65,68,72	0
3	NAG	A	806	14/15	0.19	-0.53	101,102,103,103	0
3	NAG	D	803	14/15	0.13	-0.69	67,69,70,72	0
3	NAG	A	809	14/15	0.12	-45.00	67,68,69,69	0

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. 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	NAG	B	804	14/15	0.26	8.57	72,74,76,77	0
2	NAG	A	807	14/15	0.37	5.65	60,64,66,66	0
2	NAG	C	807	14/15	0.29	3.76	70,74,75,76	0
2	NAG	A	804	14/15	0.27	3.21	70,72,76,77	0
4	SY1	A	800	27/27	0.24	1.98	36,41,42,43	0
4	SY1	C	801	27/27	0.17	1.58	62,63,64,64	0
4	SY1	B	800	27/27	0.22	1.49	38,40,44,45	0
4	SY1	C	800	27/27	0.19	1.38	33,37,41,41	0
2	NAG	C	803	14/15	0.24	1.33	69,71,74,75	0
2	NAG	A	803	14/15	0.27	1.19	72,75,77,78	0
4	SY1	D	801	27/27	0.21	1.07	56,58,62,65	0
4	SY1	D	800	27/27	0.22	0.58	43,46,47,47	0
2	NAG	B	803	14/15	0.15	0.56	62,64,66,67	0
4	SY1	B	801	27/27	0.16	0.53	48,49,51,52	0
4	SY1	A	801	27/27	0.16	0.51	47,50,53,53	0
2	NAG	C	802	14/15	0.25	0.44	72,73,74,75	0
2	NAG	D	802	14/15	0.21	-0.01	78,80,81,81	0
2	NAG	A	802	14/15	0.18	-0.24	105,105,106,106	0
2	NAG	B	807	14/15	0.11	-0.85	75,77,78,79	0
2	NAG	C	806	14/15	0.14	-1.19	82,84,86,86	0
2	NAG	B	802	14/15	0.12	-1.46	98,100,100,100	0
2	NAG	D	805	14/15	0.13	-1.64	80,81,82,83	0

6.5 Other polymers ⓘ

There are no such residues in this entry.