wwPDB X-ray Structure Validation Summary Report (i)

Jan 31, 2016 – 09:56 PM GMT

PDB ID	:	1R9N
Title	:	Crystal Structure of human dipeptidyl peptidase IV in complex with a decapeptide (tNPY) at 2.3 Ang. Resolution
Authors	:	Aertgeerts, K.; Ye, S.; Tennant, M.G.; Collins, B.; Rogers, J.; Sang, B.-C.; Skene, R.; Webb, D.R.; Prasad, G.S.
Deposited on	:	2003-10-30
Resolution	:	2.30 Å(reported)

This is a wwPDB X-ray Structure 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/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

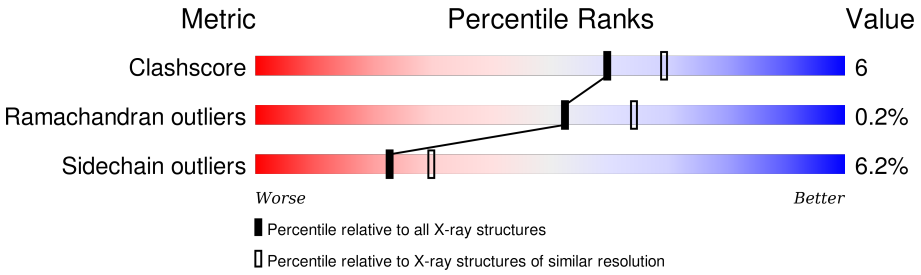
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)

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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	739	81% 15%
1	B	739	81% 16%
1	C	739	86% 11%
1	D	739	78% 19%
2	E	10	40% 60%
2	F	10	20% 40% 40%
2	G	10	40% 60%

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Mol	Chain	Length	Quality of chain
2	H	10	30% 20% 50%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	A	2811	X	-	-	-
3	NAG	A	6851	X	-	-	-
3	NAG	D	2811	X	-	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 25627 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 IV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	728	Total	C	N	O	S	0	0	0
			5963	3827	982	1128	26			
1	B	731	Total	C	N	O	S	0	0	0
			5993	3845	991	1131	26			
1	C	727	Total	C	N	O	S	0	0	0
			5957	3824	981	1126	26			
1	D	727	Total	C	N	O	S	0	0	0
			5957	3824	981	1126	26			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	ALA	-	CLONING ARTIFACT	UNP P27487
A	29	ASP	-	CLONING ARTIFACT	UNP P27487
A	30	PRO	-	CLONING ARTIFACT	UNP P27487
A	31	GLY	-	CLONING ARTIFACT	UNP P27487
A	32	GLY	-	CLONING ARTIFACT	UNP P27487
A	33	SER	-	CLONING ARTIFACT	UNP P27487
A	34	HIS	-	EXPRESSION TAG	UNP P27487
A	35	HIS	-	EXPRESSION TAG	UNP P27487
A	36	HIS	-	EXPRESSION TAG	UNP P27487
A	37	HIS	-	EXPRESSION TAG	UNP P27487
A	38	HIS	-	EXPRESSION TAG	UNP P27487
B	28	ALA	-	CLONING ARTIFACT	UNP P27487
B	29	ASP	-	CLONING ARTIFACT	UNP P27487
B	30	PRO	-	CLONING ARTIFACT	UNP P27487
B	31	GLY	-	CLONING ARTIFACT	UNP P27487
B	32	GLY	-	CLONING ARTIFACT	UNP P27487
B	33	SER	-	CLONING ARTIFACT	UNP P27487
B	34	HIS	-	EXPRESSION TAG	UNP P27487
B	35	HIS	-	EXPRESSION TAG	UNP P27487
B	36	HIS	-	EXPRESSION TAG	UNP P27487
B	37	HIS	-	EXPRESSION TAG	UNP P27487

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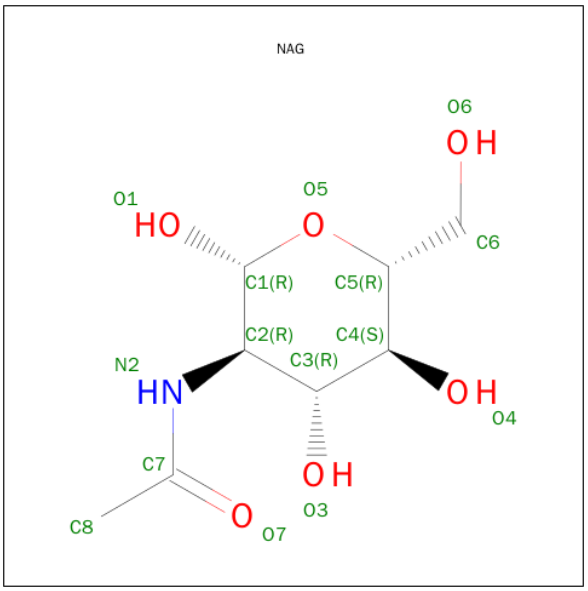
Chain	Residue	Modelled	Actual	Comment	Reference
B	38	HIS	-	EXPRESSION TAG	UNP P27487
C	28	ALA	-	CLONING ARTIFACT	UNP P27487
C	29	ASP	-	CLONING ARTIFACT	UNP P27487
C	30	PRO	-	CLONING ARTIFACT	UNP P27487
C	31	GLY	-	CLONING ARTIFACT	UNP P27487
C	32	GLY	-	CLONING ARTIFACT	UNP P27487
C	33	SER	-	CLONING ARTIFACT	UNP P27487
C	34	HIS	-	EXPRESSION TAG	UNP P27487
C	35	HIS	-	EXPRESSION TAG	UNP P27487
C	36	HIS	-	EXPRESSION TAG	UNP P27487
C	37	HIS	-	EXPRESSION TAG	UNP P27487
C	38	HIS	-	EXPRESSION TAG	UNP P27487
D	28	ALA	-	CLONING ARTIFACT	UNP P27487
D	29	ASP	-	CLONING ARTIFACT	UNP P27487
D	30	PRO	-	CLONING ARTIFACT	UNP P27487
D	31	GLY	-	CLONING ARTIFACT	UNP P27487
D	32	GLY	-	CLONING ARTIFACT	UNP P27487
D	33	SER	-	CLONING ARTIFACT	UNP P27487
D	34	HIS	-	EXPRESSION TAG	UNP P27487
D	35	HIS	-	EXPRESSION TAG	UNP P27487
D	36	HIS	-	EXPRESSION TAG	UNP P27487
D	37	HIS	-	EXPRESSION TAG	UNP P27487
D	38	HIS	-	EXPRESSION TAG	UNP P27487

- Molecule 2 is a protein called Neuropeptide Y.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	4	Total	C	N	O	0	0	0
			34	23	5	6			
2	F	6	Total	C	N	O	0	0	0
			49	32	7	10			
2	G	4	Total	C	N	O	0	0	0
			34	23	5	6			
2	H	5	Total	C	N	O	0	0	0
			41	28	6	7			

- 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 14 8 1 5	0	0
3	A	1	Total C N O 14 8 1 5	0	0
3	A	1	Total C N O 14 8 1 5	0	0
3	A	1	Total C N O 14 8 1 5	0	0
3	A	1	Total C N O 14 8 1 5	0	0
3	A	1	Total C N O 14 8 1 5	0	0
3	B	1	Total C N O 14 8 1 5	0	0
3	B	1	Total C N O 14 8 1 5	0	0
3	B	1	Total C N O 14 8 1 5	0	0
3	B	1	Total C N O 14 8 1 5	0	0
3	B	1	Total C N O 14 8 1 5	0	0
3	C	1	Total C N O 14 8 1 5	0	0
3	C	1	Total C N O 14 8 1 5	0	0
3	C	1	Total C N O 14 8 1 5	0	0

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

- Molecule 4 is a polymer of unknown type called SUGAR (2-MER).

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	342	Total O 342 342	0	0
5	B	361	Total O 361 361	0	0
5	C	277	Total O 277 277	0	0
5	D	254	Total O 254 254	0	0
5	E	3	Total O 3 3	0	0
5	F	4	Total O 4 4	0	0
5	G	6	Total O 6 6	0	0
5	H	2	Total O 2 2	0	0

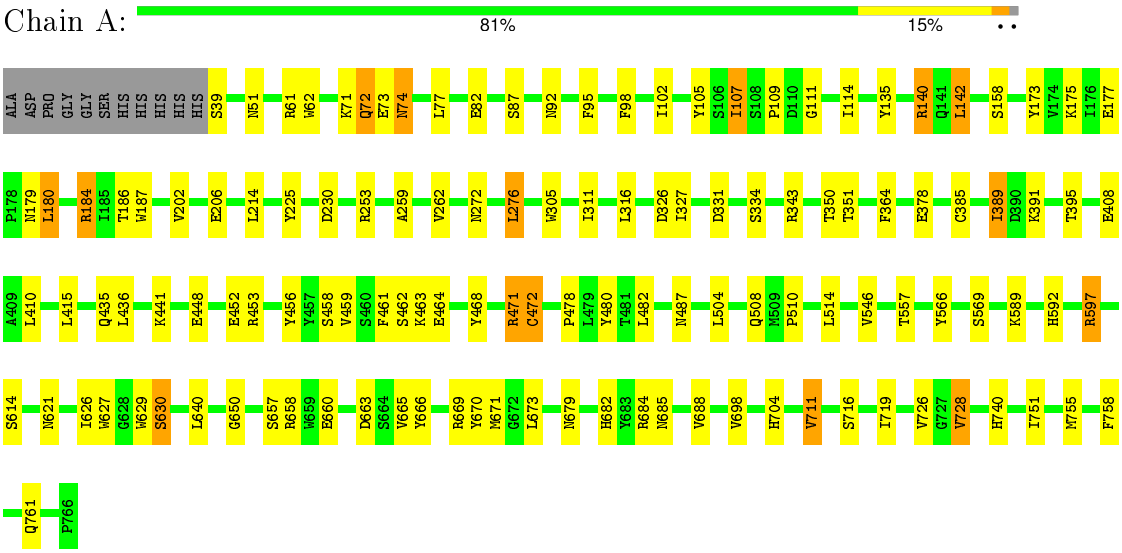
3 Residue-property plots (i)

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 (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

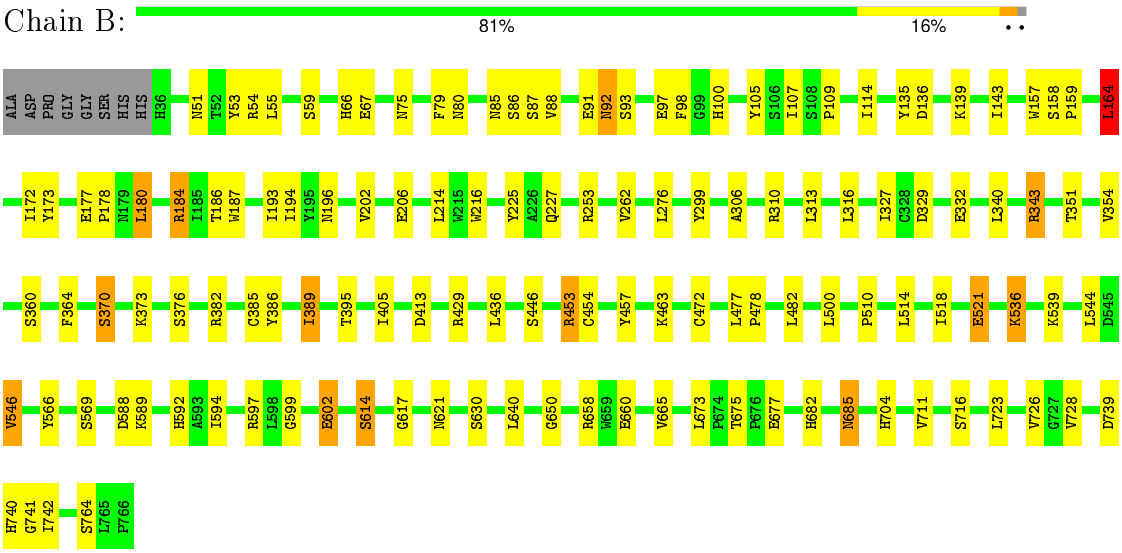
- Molecule 1: Dipeptidyl peptidase IV

Chain A:



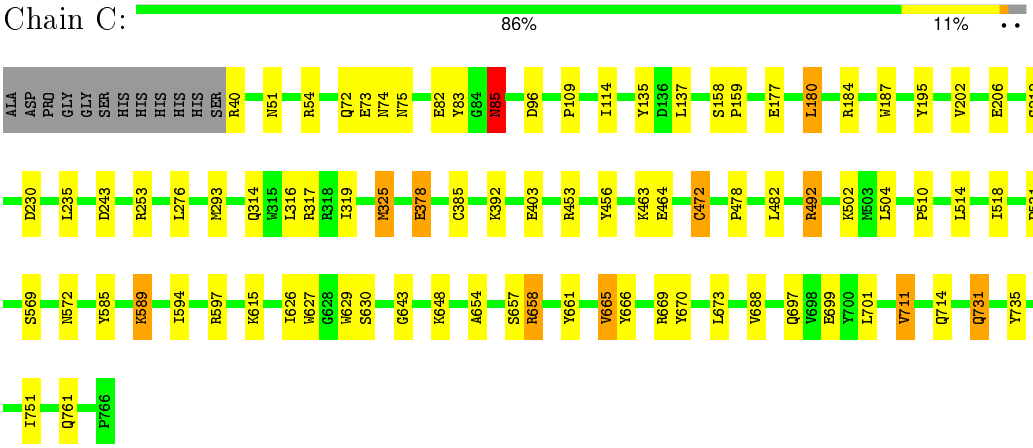
- Molecule 1: Dipeptidyl peptidase IV

Chain B:



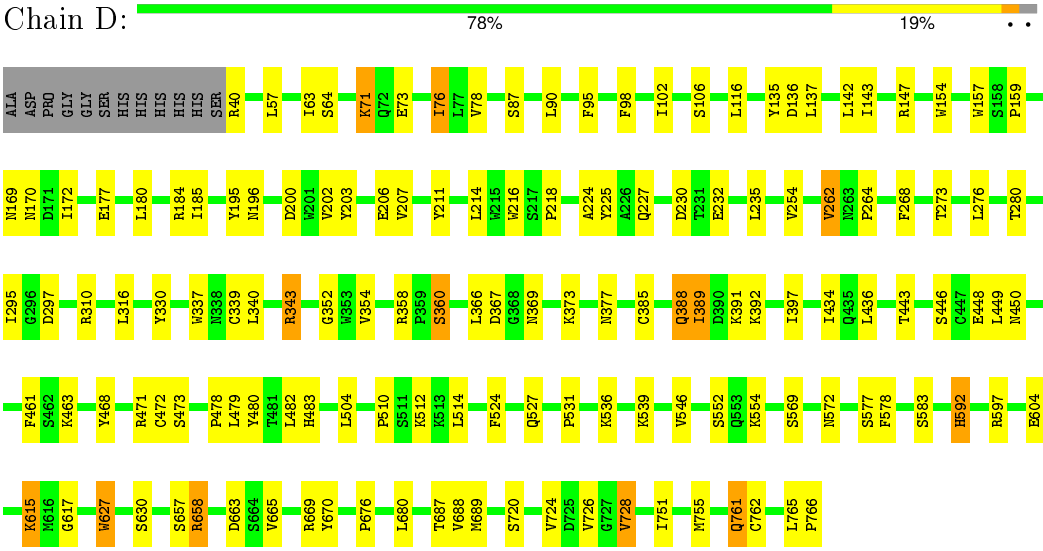
• Molecule 1: Dipeptidyl peptidase IV

Chain C:



• Molecule 1: Dipeptidyl peptidase IV

Chain D:

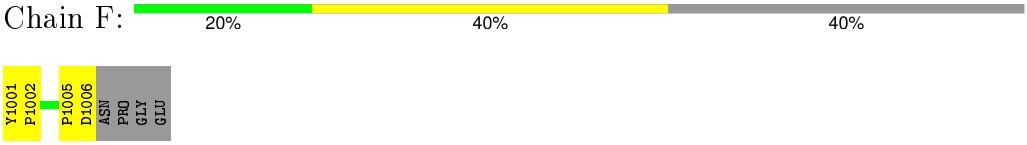


• Molecule 2: Neuropeptide Y

Chain E:

• Molecule 2: Neuropeptide Y

Chain F:

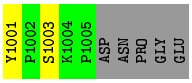


• Molecule 2: Neuropeptide Y

Chain G:

• Molecule 2: Neuropeptide Y

Chain H:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	122.61Å 122.70Å 145.41Å 90.00° 114.88° 90.00°	Depositor
Resolution (Å)	41.17 – 2.30	Depositor
% Data completeness (in resolution range)	100.0 (41.17-2.30)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.05	Depositor
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.211 , 0.251	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	25627	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.52	0/6135	0.65	0/8344
1	B	0.49	0/6168	0.63	2/8389 (0.0%)
1	C	0.49	0/6129	0.61	0/8336
1	D	0.48	0/6129	0.60	0/8336
2	E	0.77	0/35	0.64	0/46
2	F	0.76	0/51	0.73	0/69
2	G	0.62	0/35	0.78	0/46
2	H	0.61	0/43	0.71	0/58
All	All	0.50	0/24725	0.62	2/33624 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	739	ASP	CB-CG-OD2	6.74	124.37	118.30
1	B	164	LEU	CA-CB-CG	5.20	127.27	115.30

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	5963	0	5677	80	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	5993	0	5700	70	0
1	C	5957	0	5674	45	0
1	D	5957	0	5677	72	0
2	E	34	0	33	6	0
2	F	49	0	44	4	0
2	G	34	0	33	5	0
2	H	41	0	40	1	0
3	A	84	0	78	3	0
3	B	70	0	65	1	0
3	C	56	0	52	0	0
3	D	28	0	26	0	0
4	A	28	0	25	0	0
4	B	28	0	25	0	0
4	C	28	0	25	0	0
4	D	28	0	25	0	0
5	A	342	0	0	0	0
5	B	361	0	0	0	0
5	C	277	0	0	2	0
5	D	254	0	0	0	0
5	E	3	0	0	0	0
5	F	4	0	0	0	0
5	G	6	0	0	0	0
5	H	2	0	0	0	0
All	All	25627	0	23199	269	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 6.

The worst 5 of 269 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	1.08	0.97
1:C:711:VAL:HG13	1:C:740:HIS:CE1	2.03	0.93
1:A:711:VAL:HG13	1:A:740:HIS:CE1	2.04	0.93
1:C:589:LYS:HD3	5:C:5477:HOH:O	1.70	0.90
1:A:74:ASN:HD21	1:A:92:ASN:HD22	1.17	0.88

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	726/739 (98%)	695 (96%)	29 (4%)	2 (0%)	46 57
1	B	729/739 (99%)	695 (95%)	34 (5%)	0	100 100
1	C	725/739 (98%)	688 (95%)	33 (5%)	4 (1%)	30 36
1	D	725/739 (98%)	683 (94%)	41 (6%)	1 (0%)	56 68
2	E	2/10 (20%)	2 (100%)	0	0	100 100
2	F	4/10 (40%)	3 (75%)	1 (25%)	0	100 100
2	G	2/10 (20%)	1 (50%)	1 (50%)	0	100 100
2	H	3/10 (30%)	3 (100%)	0	0	100 100
All	All	2916/2996 (97%)	2770 (95%)	139 (5%)	7 (0%)	52 64

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	72	GLN
1	C	85	ASN
1	A	630	SER
1	C	74	ASN
1	D	630	SER

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	653/661 (99%)	612 (94%)	41 (6%)	22 29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	656/661 (99%)	614 (94%)	42 (6%)	22 28
1	C	652/661 (99%)	616 (94%)	36 (6%)	27 36
1	D	652/661 (99%)	607 (93%)	45 (7%)	19 24
2	E	4/9 (44%)	4 (100%)	0	100 100
2	F	6/9 (67%)	6 (100%)	0	100 100
2	G	4/9 (44%)	4 (100%)	0	100 100
2	H	5/9 (56%)	5 (100%)	0	100 100
All	All	2632/2680 (98%)	2468 (94%)	164 (6%)	23 30

5 of 164 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	602	GLU
1	C	230	ASP
1	D	482	LEU
1	B	658	ARG
1	C	40	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	51	ASN
1	C	138	ASN
1	D	505	GLN
1	C	75	ASN
1	C	85	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 (i)

8 carbohydrates are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	NAG	A	2291	1,4	14,14,15	0.63	0	15,19,21	1.18	1 (6%)
4	NAG	A	2292	4	14,14,15	0.52	0	15,19,21	1.29	1 (6%)
4	NAG	B	2291	1,4	14,14,15	0.57	0	15,19,21	1.17	1 (6%)
4	NAG	B	2292	4	14,14,15	0.50	0	15,19,21	0.89	0
4	NAG	C	2291	1,4	14,14,15	0.61	0	15,19,21	1.07	1 (6%)
4	NAG	C	2292	4	14,14,15	0.59	0	15,19,21	1.68	2 (13%)
4	NAG	D	2291	1,4	14,14,15	0.52	0	15,19,21	1.02	1 (6%)
4	NAG	D	2292	4	14,14,15	0.48	0	15,19,21	1.34	4 (26%)

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	NAG	A	2291	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	2292	4	-	0/6/23/26	0/1/1/1
4	NAG	B	2291	1,4	-	0/6/23/26	0/1/1/1
4	NAG	B	2292	4	-	0/6/23/26	0/1/1/1
4	NAG	C	2291	1,4	-	0/6/23/26	0/1/1/1
4	NAG	C	2292	4	-	0/6/23/26	0/1/1/1
4	NAG	D	2291	1,4	-	0/6/23/26	0/1/1/1
4	NAG	D	2292	4	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	D	2292	NAG	O7-C7-C8	-2.40	117.66	122.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	D	2292	NAG	C1-O5-C5	2.10	114.91	112.25
4	B	2291	NAG	C3-C4-C5	2.23	114.08	110.20
4	C	2291	NAG	C1-O5-C5	2.24	115.09	112.25
4	D	2292	NAG	C8-C7-N2	2.30	120.51	116.11

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry

17 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	1501	1	14,14,15	0.66	0	15,19,21	2.40	4 (26%)
3	NAG	A	2191	1	14,14,15	0.53	0	15,19,21	1.11	1 (6%)
3	NAG	A	2811	1	14,14,15	0.54	0	15,19,21	2.40	3 (20%)
3	NAG	A	3211	1	14,14,15	0.55	0	15,19,21	1.09	1 (6%)
3	NAG	A	6851	1	14,14,15	0.69	1 (7%)	15,19,21	2.44	3 (20%)
3	NAG	A	851	1	14,14,15	0.49	0	15,19,21	1.22	1 (6%)
3	NAG	B	1501	1	14,14,15	0.49	0	15,19,21	2.13	4 (26%)
3	NAG	B	2191	1	14,14,15	0.52	0	15,19,21	1.02	1 (6%)
3	NAG	B	2811	1	14,14,15	0.44	0	15,19,21	1.27	1 (6%)
3	NAG	B	3211	1	14,14,15	0.49	0	15,19,21	1.74	1 (6%)
3	NAG	B	851	1	14,14,15	0.59	0	15,19,21	2.10	2 (13%)
3	NAG	C	2191	1	14,14,15	0.69	0	15,19,21	1.21	2 (13%)
3	NAG	C	2811	1	14,14,15	0.93	1 (7%)	15,19,21	1.18	2 (13%)
3	NAG	C	3211	1	14,14,15	0.50	0	15,19,21	2.18	4 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	NAG	C	5201	1	14,14,15	0.60	0	15,19,21	1.81	1 (6%)
3	NAG	D	2191	1	14,14,15	0.52	0	15,19,21	0.96	1 (6%)
3	NAG	D	2811	1	14,14,15	0.49	0	15,19,21	1.56	3 (20%)

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	1501	1	-	0/6/23/26	0/1/1/1
3	NAG	A	2191	1	-	0/6/23/26	0/1/1/1
3	NAG	A	2811	1	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	A	3211	1	-	0/6/23/26	0/1/1/1
3	NAG	A	6851	1	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	A	851	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1501	1	-	0/6/23/26	0/1/1/1
3	NAG	B	2191	1	-	0/6/23/26	0/1/1/1
3	NAG	B	2811	1	-	0/6/23/26	0/1/1/1
3	NAG	B	3211	1	-	0/6/23/26	0/1/1/1
3	NAG	B	851	1	-	0/6/23/26	0/1/1/1
3	NAG	C	2191	1	-	2/6/23/26	0/1/1/1
3	NAG	C	2811	1	-	0/6/23/26	0/1/1/1
3	NAG	C	3211	1	-	0/6/23/26	0/1/1/1
3	NAG	C	5201	1	-	2/6/23/26	0/1/1/1
3	NAG	D	2191	1	-	0/6/23/26	0/1/1/1
3	NAG	D	2811	1	1/1/5/7	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	6851	NAG	C1-C2	2.03	1.55	1.52
3	C	2811	NAG	O6-C6	2.46	1.53	1.42

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1501	NAG	C4-C3-C2	-4.02	104.98	111.23
3	B	1501	NAG	C4-C3-C2	-3.41	105.93	111.23
3	A	2811	NAG	C4-C3-C2	-2.59	107.21	111.23
3	B	851	NAG	C6-C5-C4	-2.52	106.79	113.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	6851	NAG	C4-C3-C2	-2.16	107.88	111.23

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	D	2811	NAG	C1
3	A	6851	NAG	C1
3	A	2811	NAG	C1

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	5201	NAG	O7-C7-N2-C2
3	C	2191	NAG	O7-C7-N2-C2
3	C	5201	NAG	C8-C7-N2-C2
3	C	2191	NAG	C8-C7-N2-C2

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	6851	NAG	2	0
3	A	851	NAG	1	0
3	B	851	NAG	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

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

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

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

6.3 Carbohydrates

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

6.4 Ligands

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

6.5 Other polymers

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