



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 4, 2026 – 10:12 PM UTC

PDB ID : 1N73 / pdb_00001n73
Title : Fibrin D-Dimer, Lamprey complexed with the PEPTIDE LIGAND: GLY-HI
S-ARG-PRO-AMIDE
Authors : Yang, Z.; Pandi, L.; Doolittle, R.F.
Deposited on : 2002-11-12
Resolution : 2.90 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

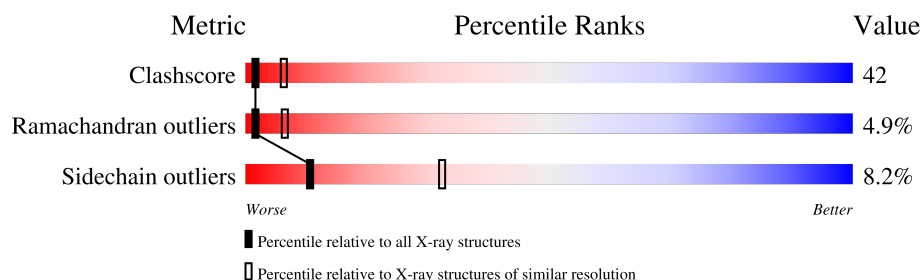
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)

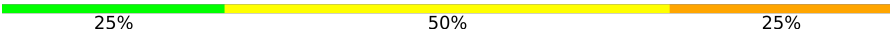
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively.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

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	119	20% 38% 18% • 24%
1	D	119	14% 42% 17% • 24%
2	B	323	41% 47% 9% ••
2	E	323	35% 52% 9% ••
3	C	330	43% 44% 10% ••
3	F	330	42% 48% 8% •
4	G	4	50% 50%
4	H	4	25% 75%

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Mol	Chain	Length	Quality of chain
4	I	4	 25%50%25%
4	J	4	 25%25%50%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12039 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 Fibrin alpha-1 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	91	Total	C	N	O	S	0	0	0
			763	480	143	137	3			
1	D	90	Total	C	N	O	S	0	0	0
			758	477	142	136	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	153	ALA	THR	SEE REMARK 999	UNP P02674
D	153	ALA	THR	SEE REMARK 999	UNP P02674

- Molecule 2 is a protein called Fibrin beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	315	Total	C	N	O	S	0	0	0
			2535	1579	453	482	21			
2	E	315	Total	C	N	O	S	0	0	0
			2535	1579	453	482	21			

- Molecule 3 is a protein called Fibrin gamma chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	322	Total	C	N	O	S	0	0	0
			2630	1658	457	502	13			
3	F	322	Total	C	N	O	S	0	0	0
			2630	1658	457	502	13			

- Molecule 4 is a protein called peptide ligand: Gly-his-Arg-Pro-amide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	4	Total	C	N	O	0	0	0
			32	19	9	4			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	H	4	Total	C	N	O	0	0	0
			32	19	9	4			
4	I	4	Total	C	N	O	0	0	0
			32	19	9	4			
4	J	4	Total	C	N	O	0	0	0
			32	19	9	4			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Ca	0	0
			1	1		
6	C	1	Total	Ca	0	0
			1	1		

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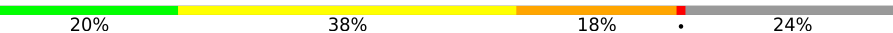
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	1	Total 1	Ca 1	0	0
6	F	1	Total 1	Ca 1	0	0

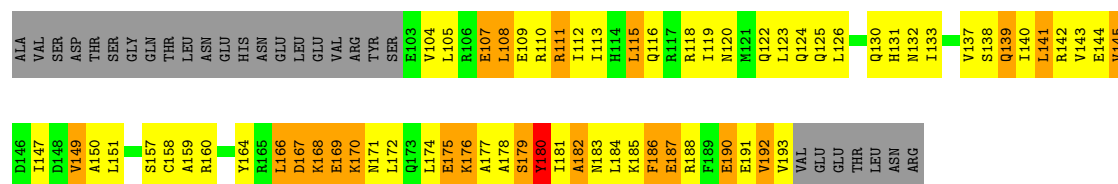
3 Residue-property plots

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. 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. 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.

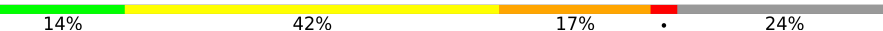
Note EDS was not executed.

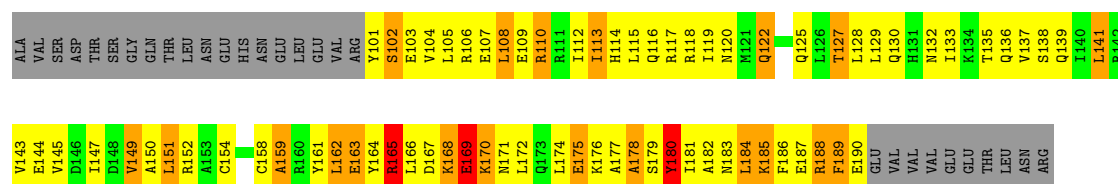
• Molecule 1: Fibrin alpha-1 chain

Chain A: 

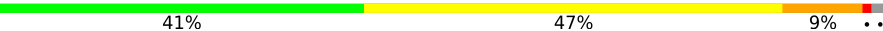


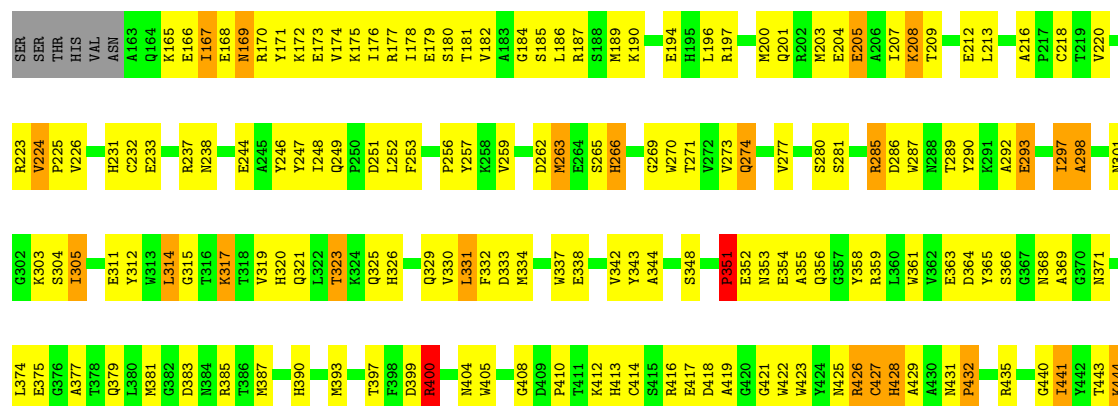
• Molecule 1: Fibrin alpha-1 chain

Chain D: 



• Molecule 2: Fibrin beta chain

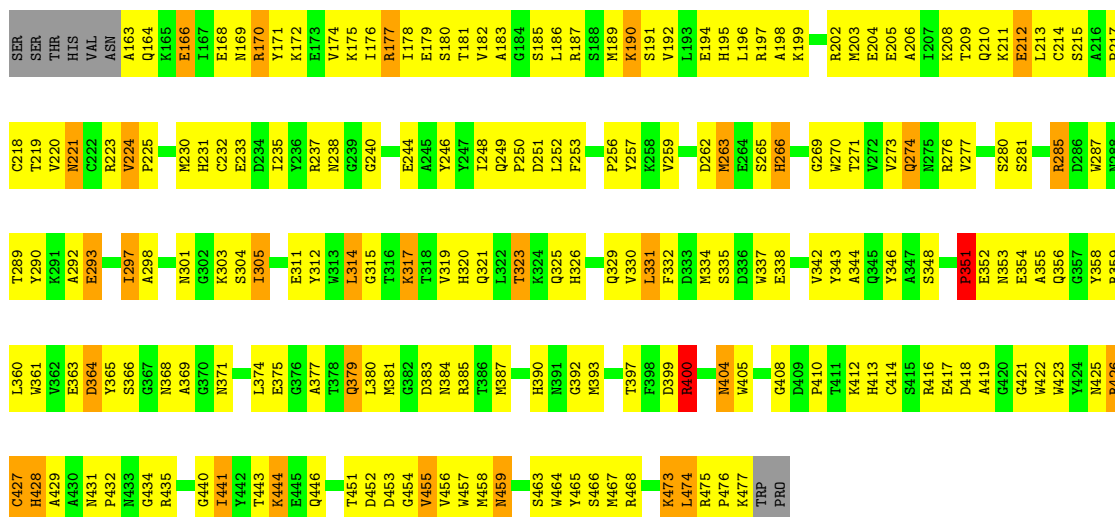
Chain B: 





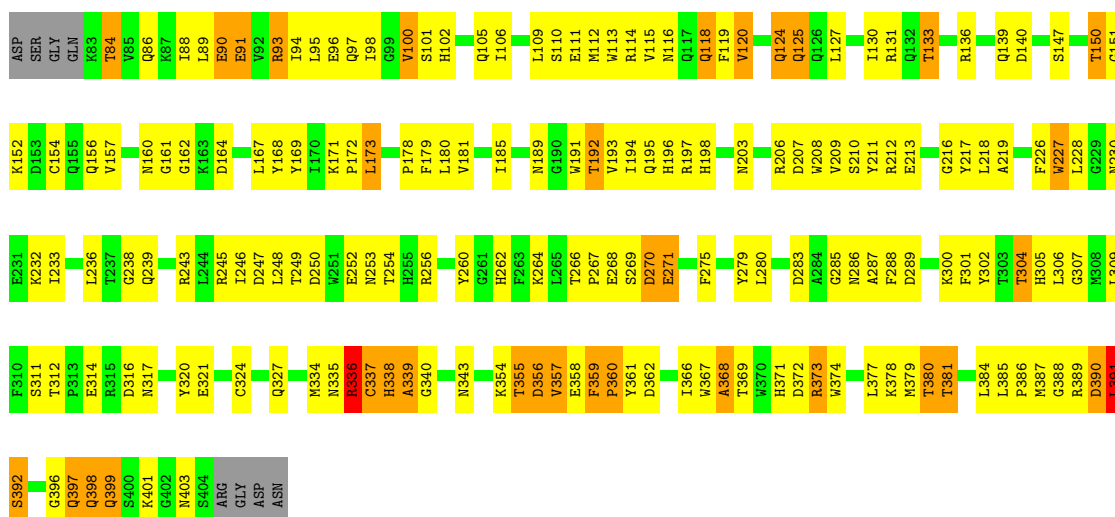
• Molecule 2: Fibrin beta chain

Chain E: 35% 52% 9% ..



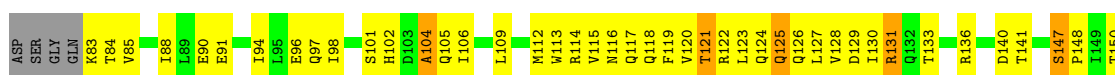
• Molecule 3: Fibrin gamma chain

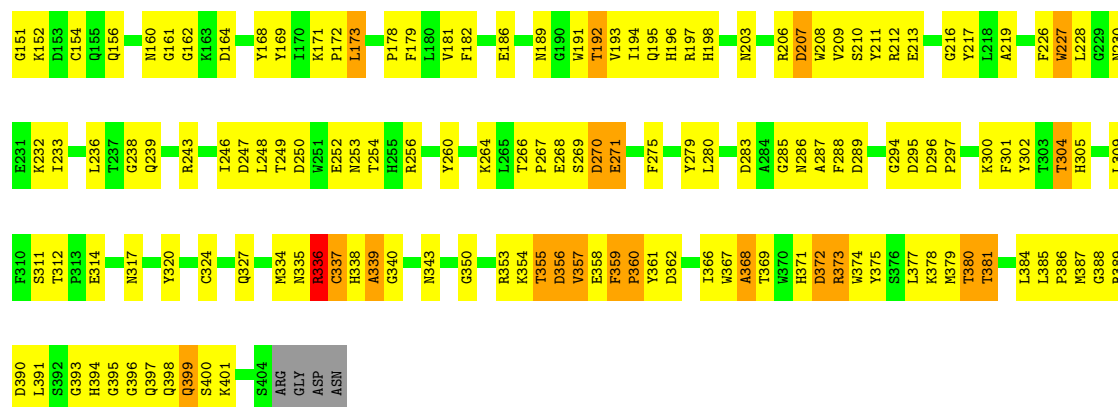
Chain C: 43% 44% 10% ..



• Molecule 3: Fibrin gamma chain

Chain F: 42% 48% 8% .





- Molecule 4: peptide ligand: Gly-his-Arg-Pro-amide

Chain G: 50% 50%

G1
H2
R3
P4

- Molecule 4: peptide ligand: Gly-his-Arg-Pro-amide

Chain H: 25% 75%

G1
H2
R3
P4

- Molecule 4: peptide ligand: Gly-his-Arg-Pro-amide

Chain I: 25% 50% 25%

G1
H2
R3
P4

- Molecule 4: peptide ligand: Gly-his-Arg-Pro-amide

Chain J: 25% 25% 50%

G1
H2
R3
P4

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	49.73Å 99.30Å 120.73Å 99.58° 101.46° 92.36°	Depositor
Resolution (Å)	20.00 – 2.90	Depositor
% Data completeness (in resolution range)	81.7 (20.00-2.90)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.258 , 0.289	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12039	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

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: NAG, CA

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	0.50	0/769	1.09	6/1030 (0.6%)
1	D	0.44	0/765	1.05	6/1024 (0.6%)
2	B	0.51	0/2602	0.98	10/3517 (0.3%)
2	E	0.48	1/2602 (0.0%)	1.00	11/3517 (0.3%)
3	C	0.51	0/2701	1.07	18/3653 (0.5%)
3	F	0.48	0/2701	1.02	14/3653 (0.4%)
4	G	0.48	0/33	0.83	0/43
4	H	0.47	0/33	0.75	0/43
4	I	0.49	0/33	0.70	0/43
4	J	0.51	0/33	0.80	0/43
All	All	0.49	1/12272 (0.0%)	1.02	65/16566 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	384	ASN	CA-CB	6.18	1.63	1.53

The worst 5 of 65 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	428	HIS	N-CA-C	11.78	124.28	108.38
2	B	428	HIS	N-CA-C	11.53	123.94	108.38
1	D	170	LYS	N-CA-C	-10.33	100.86	113.15
3	F	336	ARG	N-CA-C	-10.25	97.05	111.81
3	C	336	ARG	N-CA-C	-9.93	96.88	110.68

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	763	0	799	94	0
1	D	758	0	789	123	0
2	B	2535	0	2363	228	0
2	E	2535	0	2363	228	0
3	C	2630	0	2455	185	0
3	F	2630	0	2453	207	0
4	G	32	0	32	14	0
4	H	32	0	32	7	0
4	I	32	0	32	3	0
4	J	32	0	32	8	0
5	B	14	0	13	3	0
5	C	14	0	13	2	0
5	E	14	0	13	4	0
5	F	14	0	13	3	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	E	1	0	0	0	0
6	F	1	0	0	0	0
All	All	12039	0	11402	982	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 42.

The worst 5 of 982 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)
3:C:203:ASN:HD21	5:C:480:NAG:C1	1.30	1.40
3:F:203:ASN:ND2	5:F:480:NAG:O5	1.70	1.23
2:E:381:MET:HB2	5:E:480:NAG:C8	1.67	1.22
2:B:381:MET:HB2	5:B:480:NAG:C8	1.73	1.18
1:D:168:LYS:HD2	1:D:169:GLU:H	0.97	1.10

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	89/119 (75%)	62 (70%)	16 (18%)	11 (12%)	0	0
1	D	88/119 (74%)	58 (66%)	20 (23%)	10 (11%)	0	1
2	B	313/323 (97%)	261 (83%)	41 (13%)	11 (4%)	3	12
2	E	313/323 (97%)	259 (83%)	43 (14%)	11 (4%)	3	12
3	C	320/330 (97%)	268 (84%)	36 (11%)	16 (5%)	1	6
3	F	320/330 (97%)	264 (82%)	44 (14%)	12 (4%)	2	10
4	G	2/4 (50%)	1 (50%)	1 (50%)	0	100	100
4	H	2/4 (50%)	1 (50%)	1 (50%)	0	100	100
4	I	2/4 (50%)	2 (100%)	0	0	100	100
4	J	2/4 (50%)	2 (100%)	0	0	100	100
All	All	1451/1560 (93%)	1178 (81%)	202 (14%)	71 (5%)	1	6

5 of 71 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	179	SER
1	A	182	ALA
1	A	186	PHE
2	B	455	VAL
3	C	337	CYS

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	84/110 (76%)	73 (87%)	11 (13%)	4	13
1	D	83/110 (76%)	70 (84%)	13 (16%)	2	9
2	B	266/274 (97%)	246 (92%)	20 (8%)	12	37
2	E	266/274 (97%)	246 (92%)	20 (8%)	12	37
3	C	280/286 (98%)	260 (93%)	20 (7%)	13	40
3	F	280/286 (98%)	265 (95%)	15 (5%)	20	51
4	G	3/3 (100%)	1 (33%)	2 (67%)	0	0
4	H	3/3 (100%)	3 (100%)	0	100	100
4	I	3/3 (100%)	2 (67%)	1 (33%)	0	0
4	J	3/3 (100%)	1 (33%)	2 (67%)	0	0
All	All	1271/1352 (94%)	1167 (92%)	104 (8%)	10	32

5 of 104 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	168	LYS
2	E	303	LYS
4	G	3	ARG
1	D	175	GLU
2	E	212	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 77 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	394	GLN
3	F	305	HIS
2	E	459	ASN
3	F	160	ASN
3	F	398	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

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	$\# Z > 2$
5	NAG	C	480	3	14,14,15	0.49	0	17,19,21	0.93	1 (5%)
5	NAG	B	480	2	14,14,15	0.78	0	17,19,21	0.69	0
5	NAG	E	480	2	14,14,15	0.76	0	17,19,21	0.70	0
5	NAG	F	480	3	14,14,15	0.57	0	17,19,21	0.68	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
5	NAG	C	480	3	-	2/6/23/26	0/1/1/1
5	NAG	B	480	2	-	5/6/23/26	0/1/1/1
5	NAG	E	480	2	-	5/6/23/26	0/1/1/1
5	NAG	F	480	3	-	5/6/23/26	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(°)
5	C	480	NAG	C2-N2-C7	-2.65	119.35	122.90

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	480	NAG	C8-C7-N2-C2
5	B	480	NAG	O7-C7-N2-C2
5	E	480	NAG	C8-C7-N2-C2
5	E	480	NAG	O7-C7-N2-C2
5	F	480	NAG	C1-C2-N2-C7

There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	480	NAG	2	0
5	B	480	NAG	3	0
5	E	480	NAG	4	0
5	F	480	NAG	3	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 is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.