



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 10:17 AM UTC

PDB ID : 5CUS / pdb_00005cus
Title : Crystal Structure of sErbB3-Fab3379 Complex
Authors : Lee, S.; Schlessinger, J.
Deposited on : 2015-07-25
Resolution : 3.20 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)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

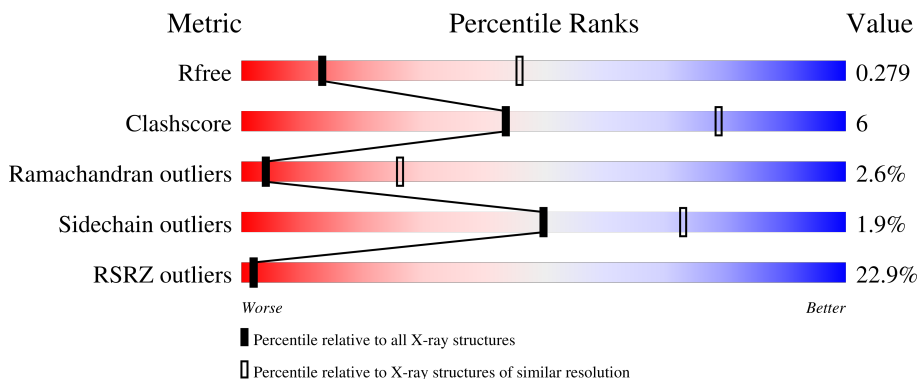
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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 $\leq 5\%$. 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	627	<div> <div>16%</div> <div> <div></div> <div>77%</div> <div>12%</div> <div>11%</div> </div> </div>
1	B	627	<div> <div>17%</div> <div> <div></div> <div>72%</div> <div>12%</div> <div>15%</div> </div> </div>
1	C	627	<div> <div>19%</div> <div> <div></div> <div>69%</div> <div>16%</div> <div>•</div> <div>14%</div> </div> </div>
1	D	627	<div> <div>24%</div> <div> <div></div> <div>70%</div> <div>10%</div> <div>•</div> <div>19%</div> </div> </div>
2	H	221	<div> <div>15%</div> <div> <div></div> <div>65%</div> <div>18%</div> <div>18%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	I	221	
2	J	221	
2	K	221	
3	L	216	
3	M	216	
3	N	216	
3	O	216	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 25896 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 Receptor tyrosine-protein kinase erbB-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	561	Total	C	N	O	S	23	0	0
			3927	2451	698	724	54			
1	B	530	Total	C	N	O	S	28	0	0
			3720	2317	654	698	51			
1	C	539	Total	C	N	O	S	14	0	0
			3839	2400	667	720	52			
1	D	509	Total	C	N	O	S	12	0	0
			3521	2188	617	666	50			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	623	HIS	-	expression tag	UNP P21860
A	624	HIS	-	expression tag	UNP P21860
A	625	HIS	-	expression tag	UNP P21860
A	626	HIS	-	expression tag	UNP P21860
A	627	HIS	-	expression tag	UNP P21860
B	623	HIS	-	expression tag	UNP P21860
B	624	HIS	-	expression tag	UNP P21860
B	625	HIS	-	expression tag	UNP P21860
B	626	HIS	-	expression tag	UNP P21860
B	627	HIS	-	expression tag	UNP P21860
C	623	HIS	-	expression tag	UNP P21860
C	624	HIS	-	expression tag	UNP P21860
C	625	HIS	-	expression tag	UNP P21860
C	626	HIS	-	expression tag	UNP P21860
C	627	HIS	-	expression tag	UNP P21860
D	623	HIS	-	expression tag	UNP P21860
D	624	HIS	-	expression tag	UNP P21860
D	625	HIS	-	expression tag	UNP P21860
D	626	HIS	-	expression tag	UNP P21860
D	627	HIS	-	expression tag	UNP P21860

- Molecule 2 is a protein called IgG H chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	182	Total	C	N	O	S	0	0	0
			1348	852	226	263	7			
2	I	198	Total	C	N	O	S	0	0	0
			1431	902	239	283	7			
2	J	175	Total	C	N	O	S	0	0	0
			1270	796	214	253	7			
2	K	180	Total	C	N	O	S	0	0	0
			1294	816	216	255	7			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	10	GLY	ASP	conflict	UNP S6B291
H	31	TYR	THR	conflict	UNP S6B291
H	33	TYR	ALA	conflict	UNP S6B291
H	35	GLN	SER	conflict	UNP S6B291
H	50	TYR	GLY	conflict	UNP S6B291
H	53	SER	ASP	conflict	UNP S6B291
H	56	GLY	HIS	conflict	UNP S6B291
H	57	VAL	SER	conflict	UNP S6B291
H	58	THR	ILE	conflict	UNP S6B291
H	59	ASN	TYR	conflict	UNP S6B291
H	98	ARG	-	insertion	UNP S6B291
H	99	VAL	THR	conflict	UNP S6B291
H	101	LEU	SER	conflict	UNP S6B291
H	102	GLY	GLN	conflict	UNP S6B291
H	103	ASP	TRP	conflict	UNP S6B291
H	104	ALA	PRO	conflict	UNP S6B291
H	105	PHE	GLY	conflict	UNP S6B291
H	107	ILE	TYR	conflict	UNP S6B291
H	113	MET	LEU	conflict	UNP S6B291
H	215	LYS	ARG	conflict	UNP S6B291
I	10	GLY	ASP	conflict	UNP S6B291
I	31	TYR	THR	conflict	UNP S6B291
I	33	TYR	ALA	conflict	UNP S6B291
I	35	GLN	SER	conflict	UNP S6B291
I	50	TYR	GLY	conflict	UNP S6B291
I	53	SER	ASP	conflict	UNP S6B291
I	56	GLY	HIS	conflict	UNP S6B291
I	57	VAL	SER	conflict	UNP S6B291
I	58	THR	ILE	conflict	UNP S6B291
I	59	ASN	TYR	conflict	UNP S6B291

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Chain	Residue	Modelled	Actual	Comment	Reference
I	98	ARG	-	insertion	UNP S6B291
I	99	VAL	THR	conflict	UNP S6B291
I	101	LEU	SER	conflict	UNP S6B291
I	102	GLY	GLN	conflict	UNP S6B291
I	103	ASP	TRP	conflict	UNP S6B291
I	104	ALA	PRO	conflict	UNP S6B291
I	105	PHE	GLY	conflict	UNP S6B291
I	107	ILE	TYR	conflict	UNP S6B291
I	113	MET	LEU	conflict	UNP S6B291
I	215	LYS	ARG	conflict	UNP S6B291
J	10	GLY	ASP	conflict	UNP S6B291
J	31	TYR	THR	conflict	UNP S6B291
J	33	TYR	ALA	conflict	UNP S6B291
J	35	GLN	SER	conflict	UNP S6B291
J	50	TYR	GLY	conflict	UNP S6B291
J	53	SER	ASP	conflict	UNP S6B291
J	56	GLY	HIS	conflict	UNP S6B291
J	57	VAL	SER	conflict	UNP S6B291
J	58	THR	ILE	conflict	UNP S6B291
J	59	ASN	TYR	conflict	UNP S6B291
J	98	ARG	-	insertion	UNP S6B291
J	99	VAL	THR	conflict	UNP S6B291
J	101	LEU	SER	conflict	UNP S6B291
J	102	GLY	GLN	conflict	UNP S6B291
J	103	ASP	TRP	conflict	UNP S6B291
J	104	ALA	PRO	conflict	UNP S6B291
J	105	PHE	GLY	conflict	UNP S6B291
J	107	ILE	TYR	conflict	UNP S6B291
J	113	MET	LEU	conflict	UNP S6B291
J	215	LYS	ARG	conflict	UNP S6B291
K	10	GLY	ASP	conflict	UNP S6B291
K	31	TYR	THR	conflict	UNP S6B291
K	33	TYR	ALA	conflict	UNP S6B291
K	35	GLN	SER	conflict	UNP S6B291
K	50	TYR	GLY	conflict	UNP S6B291
K	53	SER	ASP	conflict	UNP S6B291
K	56	GLY	HIS	conflict	UNP S6B291
K	57	VAL	SER	conflict	UNP S6B291
K	58	THR	ILE	conflict	UNP S6B291
K	59	ASN	TYR	conflict	UNP S6B291
K	98	ARG	-	insertion	UNP S6B291
K	99	VAL	THR	conflict	UNP S6B291

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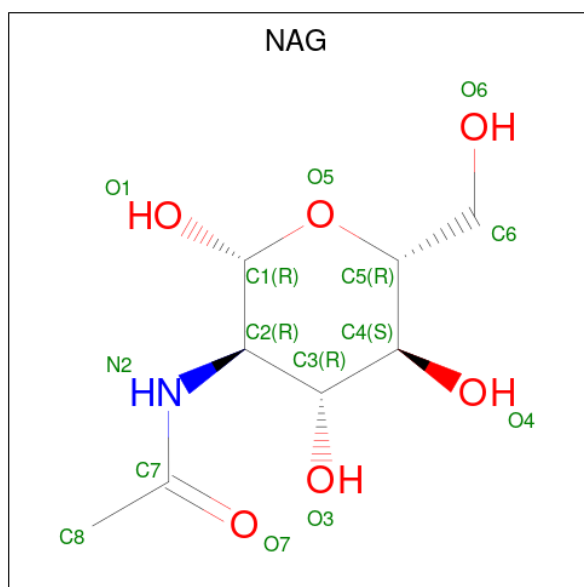
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Chain	Residue	Modelled	Actual	Comment	Reference
K	101	LEU	SER	conflict	UNP S6B291
K	102	GLY	GLN	conflict	UNP S6B291
K	103	ASP	TRP	conflict	UNP S6B291
K	104	ALA	PRO	conflict	UNP S6B291
K	105	PHE	GLY	conflict	UNP S6B291
K	107	ILE	TYR	conflict	UNP S6B291
K	113	MET	LEU	conflict	UNP S6B291
K	215	LYS	ARG	conflict	UNP S6B291

- Molecule 3 is a protein called Fab LC region of KTN3379.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	185	Total	C	N	O	S	0	0	0
			1327	829	226	269	3			
3	M	203	Total	C	N	O	S	0	0	0
			1410	873	241	292	4			
3	N	184	Total	C	N	O	S	0	0	0
			1275	790	217	264	4			
3	O	200	Total	C	N	O	S	0	0	0
			1380	858	235	283	4			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

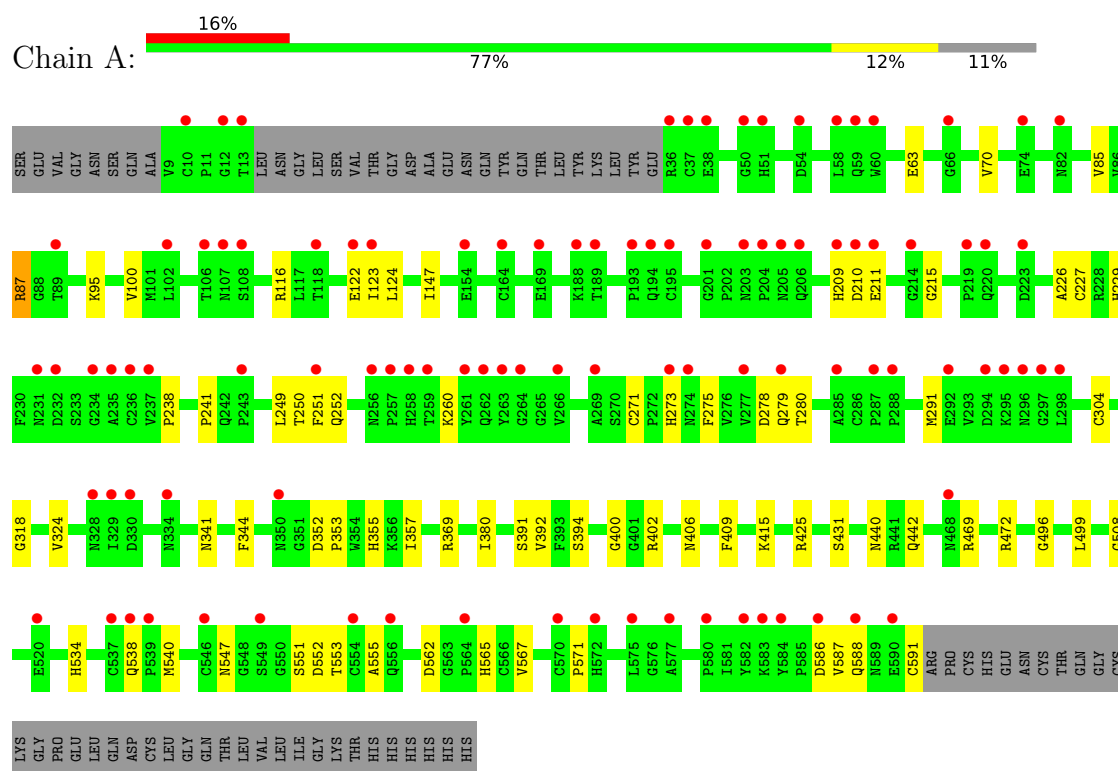


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1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

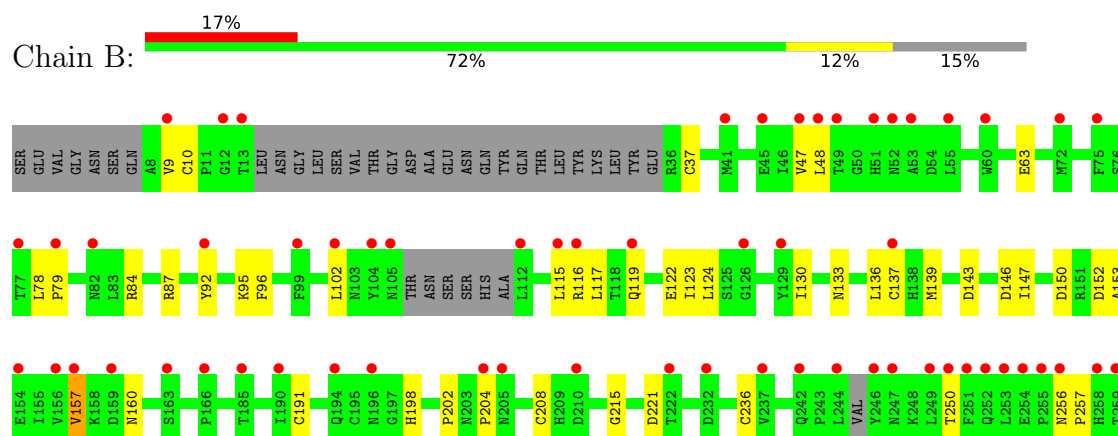
3 Residue-property plots [i](#)

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.

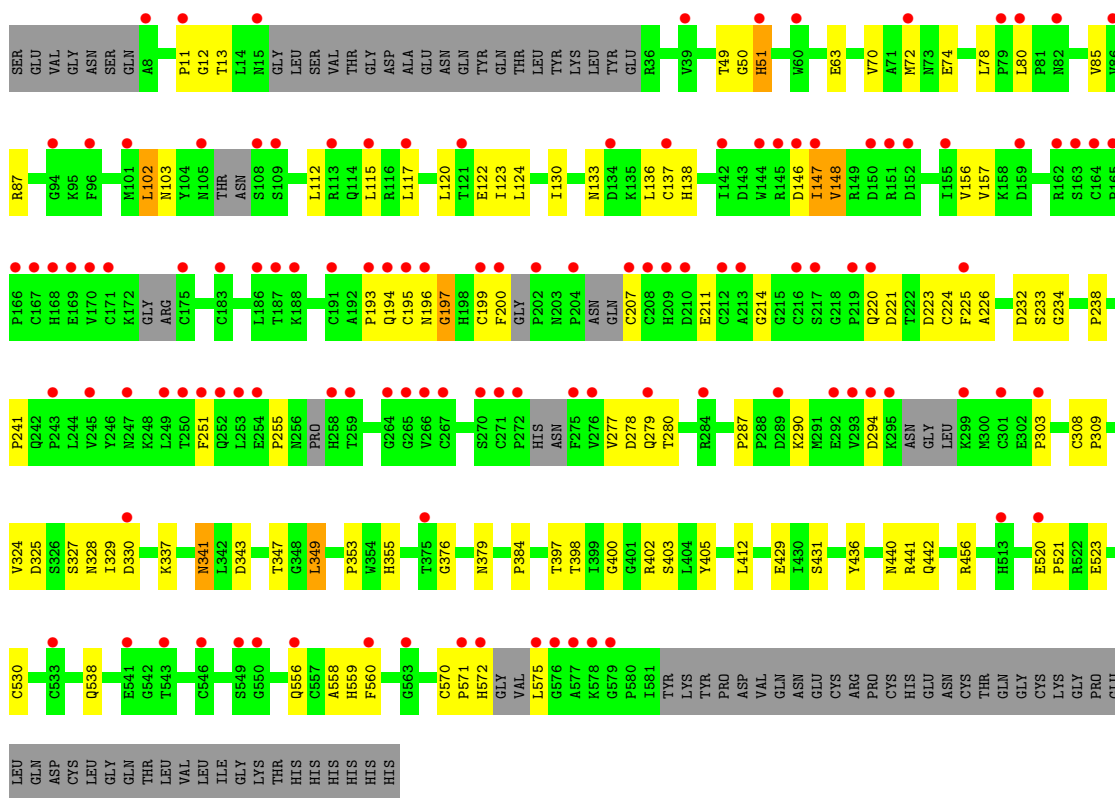
- Molecule 1: Receptor tyrosine-protein kinase erbB-3



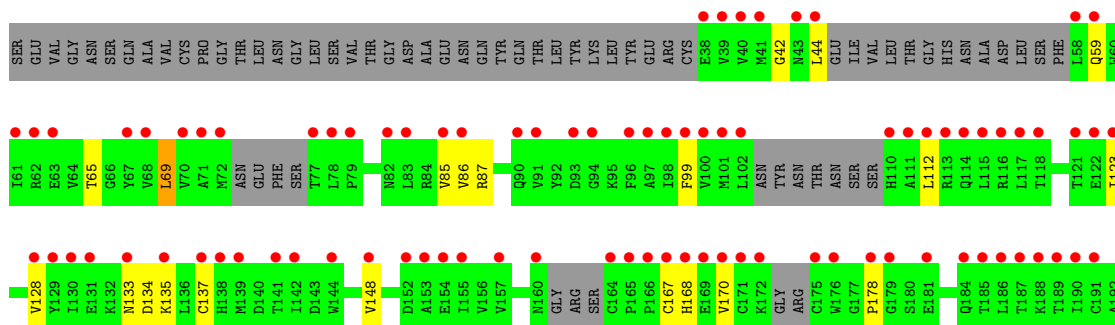
- Molecule 1: Receptor tyrosine-protein kinase erbB-3

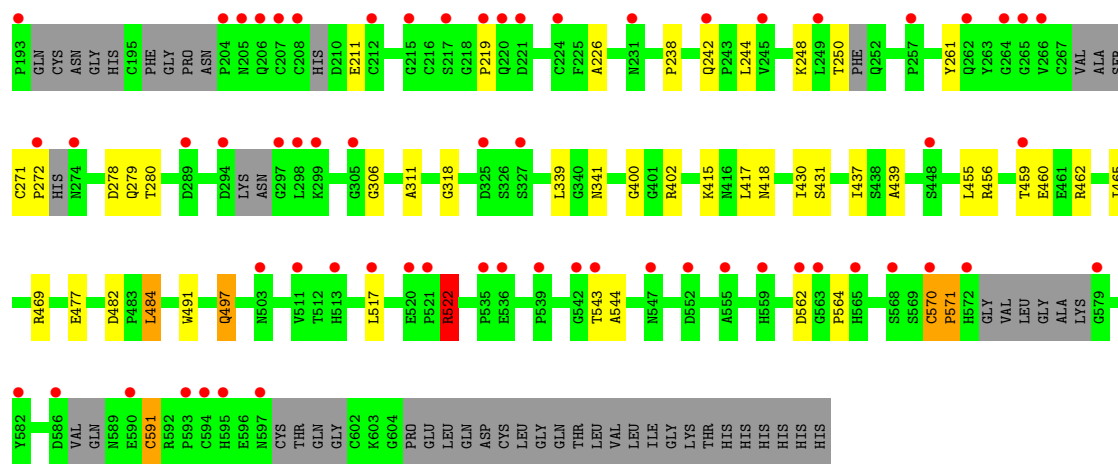


- Molecule 1: Receptor tyrosine-protein kinase erbB-3

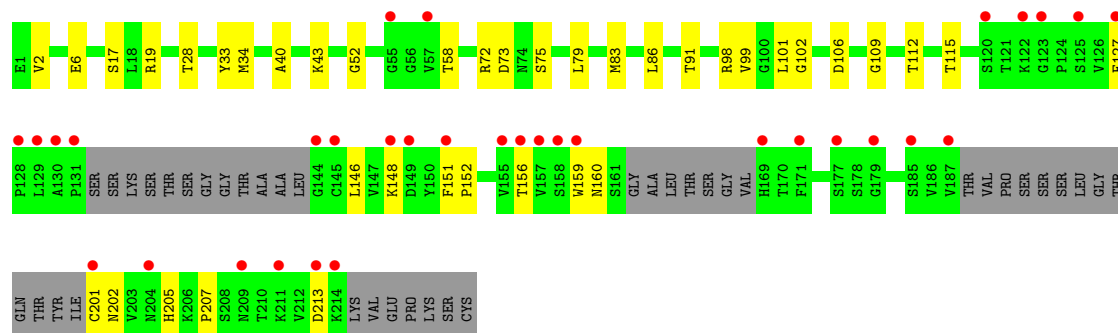


- Molecule 1: Receptor tyrosine-protein kinase erbB-3

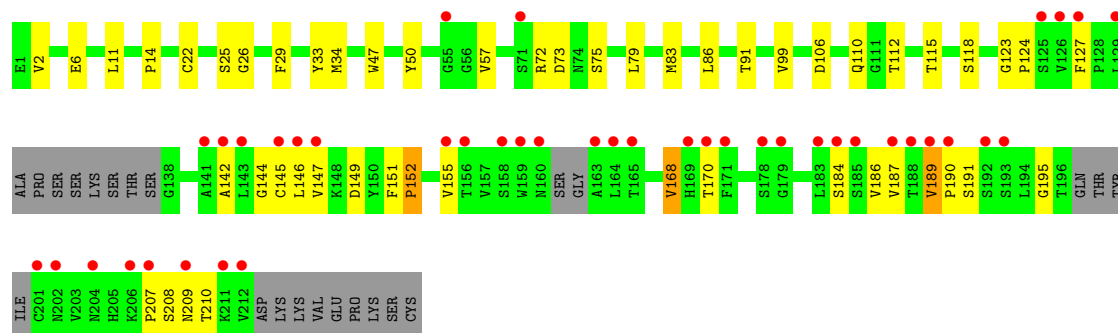




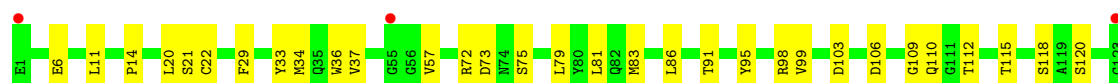
• Molecule 2: IgG H chain

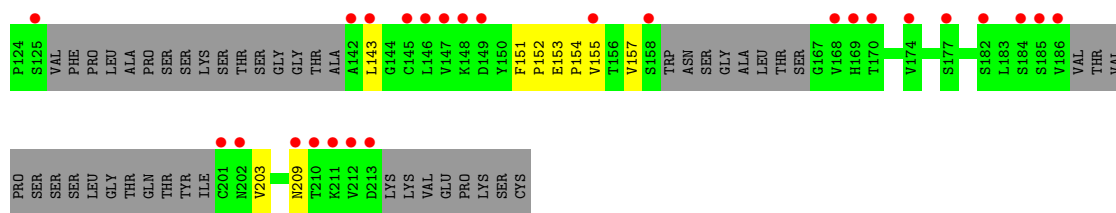


• Molecule 2: IgG H chain

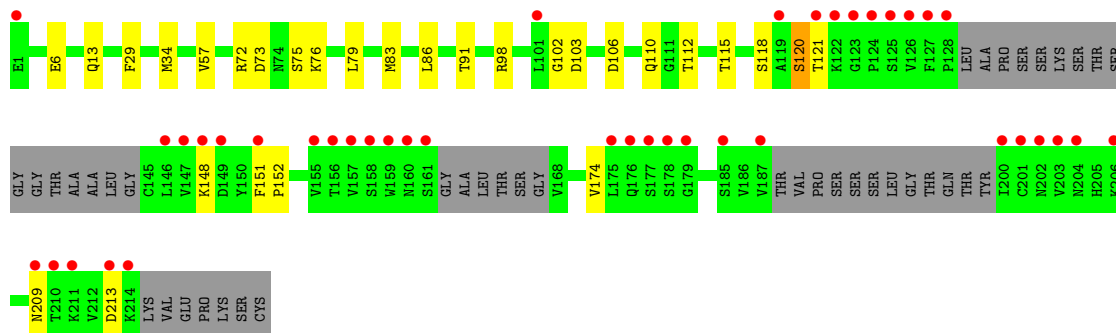


• Molecule 2: IgG H chain

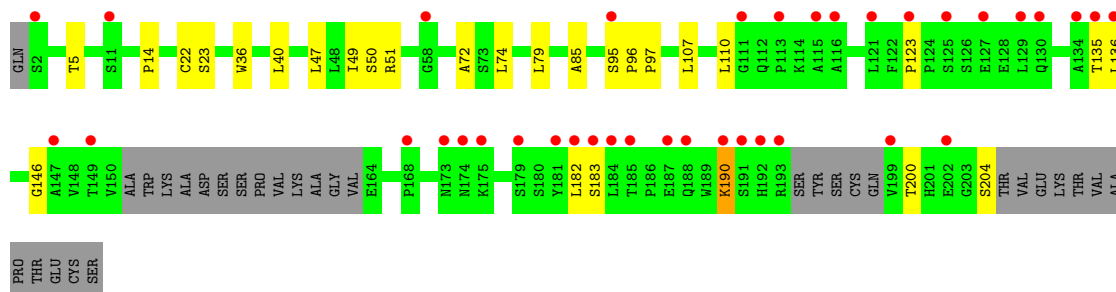
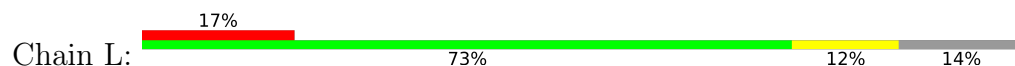




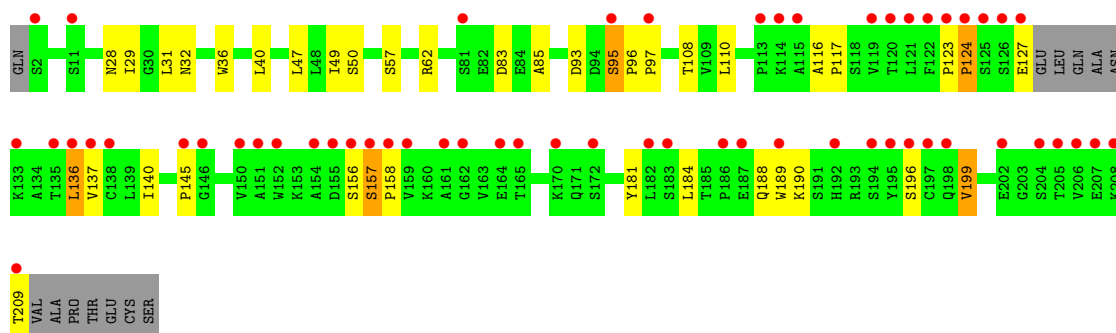
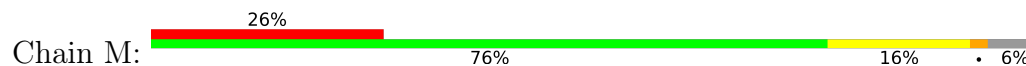
● Molecule 2: IgG H chain



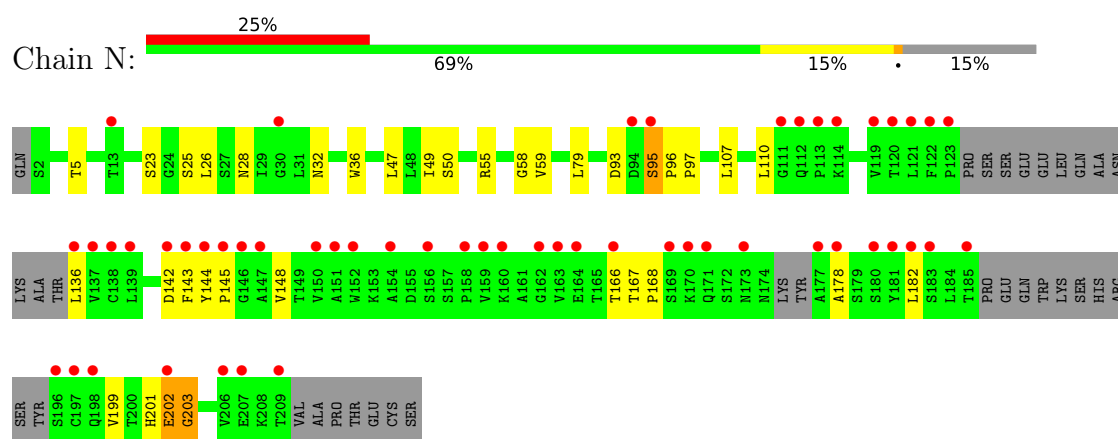
● Molecule 3: Fab LC region of KTN3379



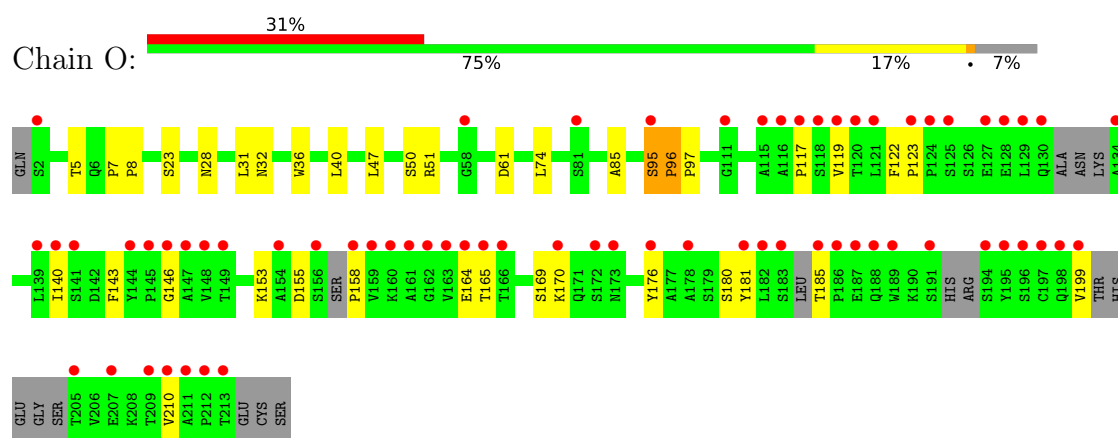
● Molecule 3: Fab LC region of KTN3379



● Molecule 3: Fab LC region of KTN3379



• Molecule 3: Fab LC region of KTN3379



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	84.38Å 127.14Å 138.08Å 87.10° 85.54° 89.92°	Depositor
Resolution (Å)	69.39 – 3.20 69.39 – 3.20	Depositor EDS
% Data completeness (in resolution range)	98.3 (69.39-3.20) 98.3 (69.39-3.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 3.19Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.252 , 0.278 0.255 , 0.279	Depositor DCC
R_{free} test set	4593 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	52.7	Xtriage
Anisotropy	0.367	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 82.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.048 for -h,k,-l	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	25896	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% 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

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	0.26	0/4023	0.75	0/5502
1	B	0.27	0/3801	0.74	2/5195 (0.0%)
1	C	0.27	0/3924	0.75	3/5355 (0.1%)
1	D	0.26	0/3596	0.74	2/4906 (0.0%)
2	H	0.27	0/1379	0.66	0/1878
2	I	0.28	0/1463	0.73	3/1994 (0.2%)
2	J	0.27	0/1295	0.67	0/1761
2	K	0.27	0/1321	0.66	0/1800
3	L	0.27	0/1359	0.72	1/1860 (0.1%)
3	M	0.29	0/1443	0.78	2/1984 (0.1%)
3	N	0.28	0/1301	0.77	2/1782 (0.1%)
3	O	0.28	0/1408	0.73	2/1926 (0.1%)
All	All	0.27	0/26313	0.74	17/35943 (0.0%)

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	95	SER	CA-C-N	-9.07	111.04	120.38
3	N	95	SER	C-N-CA	-9.07	111.04	120.38
3	M	95	SER	CA-C-N	-8.73	111.39	120.38
3	M	95	SER	C-N-CA	-8.73	111.39	120.38
1	D	570	CYS	CA-C-N	8.11	129.98	119.84

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	3927	0	3437	39	0
1	B	3720	0	3310	36	0
1	C	3839	0	3426	50	0
1	D	3521	0	2985	36	0
2	H	1348	0	1268	23	0
2	I	1431	0	1329	26	0
2	J	1270	0	1174	23	0
2	K	1294	0	1175	16	0
3	L	1327	0	1253	16	0
3	M	1410	0	1283	20	0
3	N	1275	0	1170	18	0
3	O	1380	0	1258	21	0
4	A	28	0	26	0	0
4	B	28	0	26	0	0
4	C	42	0	39	1	0
4	D	42	0	39	2	0
4	M	14	0	13	0	0
All	All	25896	0	23211	297	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 297 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:D:517:LEU:O	1:D:522:ARG:NH1	2.11	0.83
1:B:63:GLU:OE2	1:B:87:ARG:NE	2.16	0.77
2:K:98:ARG:NH2	2:K:106:ASP:OD2	2.12	0.74
2:H:19:ARG:NH2	2:J:11:LEU:O	2.23	0.71
2:H:52:GLY:O	2:H:72:ARG:NH1	2.23	0.71

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	557/627 (89%)	491 (88%)	58 (10%)	8 (1%)	9	39
1	B	522/627 (83%)	447 (86%)	65 (12%)	10 (2%)	6	33
1	C	519/627 (83%)	424 (82%)	76 (15%)	19 (4%)	2	18
1	D	478/627 (76%)	402 (84%)	60 (13%)	16 (3%)	3	21
2	H	174/221 (79%)	166 (95%)	6 (3%)	2 (1%)	11	43
2	I	190/221 (86%)	166 (87%)	17 (9%)	7 (4%)	2	18
2	J	167/221 (76%)	150 (90%)	14 (8%)	3 (2%)	6	34
2	K	172/221 (78%)	149 (87%)	17 (10%)	6 (4%)	3	20
3	L	179/216 (83%)	157 (88%)	17 (10%)	5 (3%)	4	25
3	M	199/216 (92%)	166 (83%)	25 (13%)	8 (4%)	2	17
3	N	176/216 (82%)	147 (84%)	23 (13%)	6 (3%)	3	20
3	O	188/216 (87%)	166 (88%)	19 (10%)	3 (2%)	7	36
All	All	3521/4256 (83%)	3031 (86%)	397 (11%)	93 (3%)	4	26

5 of 93 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	148	VAL
1	C	255	PRO
1	D	134	ASP
1	D	167	CYS
1	D	571	PRO

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	379/543 (70%)	371 (98%)	8 (2%)	47	71
1	B	371/543 (68%)	365 (98%)	6 (2%)	55	75
1	C	390/543 (72%)	380 (97%)	10 (3%)	40	69
1	D	338/543 (62%)	330 (98%)	8 (2%)	43	70
2	H	144/183 (79%)	140 (97%)	4 (3%)	38	68
2	I	149/183 (81%)	147 (99%)	2 (1%)	61	78
2	J	131/183 (72%)	130 (99%)	1 (1%)	73	82
2	K	130/183 (71%)	129 (99%)	1 (1%)	73	82
3	L	143/180 (79%)	141 (99%)	2 (1%)	59	77
3	M	146/180 (81%)	141 (97%)	5 (3%)	32	64
3	N	131/180 (73%)	130 (99%)	1 (1%)	73	82
3	O	140/180 (78%)	138 (99%)	2 (1%)	59	77
All	All	2592/3624 (72%)	2542 (98%)	50 (2%)	50	73

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	417	LEU
2	H	156	THR
3	O	165	THR
1	D	484	LEU
2	H	2	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	82	ASN
3	M	173	ASN
1	D	389	ASN
3	O	32	ASN
2	I	77	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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](#)

11 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	NAG	C	702	-	14,14,15	0.47	0	17,19,21	1.36	2 (11%)
4	NAG	D	702	-	14,14,15	0.24	0	17,19,21	0.42	0
4	NAG	M	301	-	14,14,15	0.30	0	17,19,21	0.38	0
4	NAG	A	702	-	14,14,15	0.26	0	17,19,21	0.43	0
4	NAG	A	701	-	14,14,15	0.31	0	17,19,21	0.35	0
4	NAG	D	703	-	14,14,15	0.27	0	17,19,21	0.38	0
4	NAG	C	701	-	14,14,15	0.24	0	17,19,21	0.41	0
4	NAG	B	702	-	14,14,15	0.24	0	17,19,21	0.41	0
4	NAG	B	701	-	14,14,15	0.24	0	17,19,21	0.42	0
4	NAG	D	701	-	14,14,15	0.26	0	17,19,21	0.40	0
4	NAG	C	703	-	14,14,15	0.24	0	17,19,21	0.41	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
4	NAG	C	702	-	-	6/6/23/26	0/1/1/1
4	NAG	D	702	-	-	2/6/23/26	0/1/1/1
4	NAG	M	301	-	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	702	-	-	0/6/23/26	0/1/1/1
4	NAG	A	701	-	-	2/6/23/26	0/1/1/1
4	NAG	D	703	-	-	0/6/23/26	0/1/1/1
4	NAG	C	701	-	-	2/6/23/26	0/1/1/1
4	NAG	B	702	-	-	2/6/23/26	0/1/1/1
4	NAG	B	701	-	-	4/6/23/26	0/1/1/1
4	NAG	D	701	-	-	2/6/23/26	0/1/1/1
4	NAG	C	703	-	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	702	NAG	C2-N2-C7	4.66	129.15	122.90
4	C	702	NAG	C1-C2-N2	2.13	113.80	110.43

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	702	NAG	O5-C5-C6-O6
4	B	701	NAG	O5-C5-C6-O6
4	C	701	NAG	O5-C5-C6-O6
4	B	702	NAG	O5-C5-C6-O6
4	C	702	NAG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	702	NAG	1	0
4	D	701	NAG	2	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	561/627 (89%)	1.13	100 (17%) 4 3	15, 64, 126, 188	14 (2%)
1	B	530/627 (84%)	1.10	108 (20%) 3 2	13, 64, 122, 187	16 (3%)
1	C	539/627 (85%)	1.23	118 (21%) 2 2	12, 68, 139, 209	8 (1%)
1	D	509/627 (81%)	1.42	150 (29%) 1 1	12, 75, 142, 227	8 (1%)
2	H	182/221 (82%)	0.93	33 (18%) 3 3	15, 42, 144, 194	0
2	I	198/221 (89%)	0.95	42 (21%) 2 2	15, 40, 152, 176	0
2	J	175/221 (79%)	0.85	29 (16%) 4 3	16, 39, 129, 189	0
2	K	180/221 (81%)	1.00	41 (22%) 2 2	17, 41, 149, 187	0
3	L	185/216 (85%)	1.09	37 (20%) 3 2	19, 57, 145, 209	0
3	M	203/216 (93%)	1.39	57 (28%) 1 1	22, 62, 156, 215	0
3	N	184/216 (85%)	1.28	53 (28%) 1 1	15, 56, 144, 194	0
3	O	200/216 (92%)	1.47	67 (33%) 1 1	18, 65, 165, 221	0
All	All	3646/4256 (85%)	1.18	835 (22%) 2 2	12, 62, 143, 227	46 (1%)

The worst 5 of 835 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	M	135	THR	9.9
1	C	200	PHE	7.9
1	C	15	ASN	7.5
1	A	294	ASP	7.0
1	D	189	THR	6.9

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

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. 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(\AA^2)	Q<0.9
4	NAG	C	702	14/15	0.64	0.22	26,46,57,59	0
4	NAG	M	301	14/15	0.75	0.22	85,94,103,106	0
4	NAG	C	703	14/15	0.77	0.17	37,58,70,87	0
4	NAG	A	702	14/15	0.79	0.16	21,34,53,71	0
4	NAG	B	701	14/15	0.79	0.16	29,44,51,51	0
4	NAG	B	702	14/15	0.79	0.17	54,59,85,91	0
4	NAG	C	701	14/15	0.80	0.16	25,47,67,71	0
4	NAG	D	702	14/15	0.82	0.17	30,37,49,53	0
4	NAG	D	703	14/15	0.85	0.12	23,45,56,68	0
4	NAG	A	701	14/15	0.86	0.14	35,45,54,56	0
4	NAG	D	701	14/15	0.87	0.14	30,47,62,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.