



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 06:47 AM UTC

PDB ID : 4MQW / pdb_00004mqw
Title : Structure of follicle-stimulating hormone in complex with the entire ectodomain of its receptor (P31)
Authors : Jiang, X.; Liu, H.; Chen, X.; He, X.
Deposited on : 2013-09-16
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)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

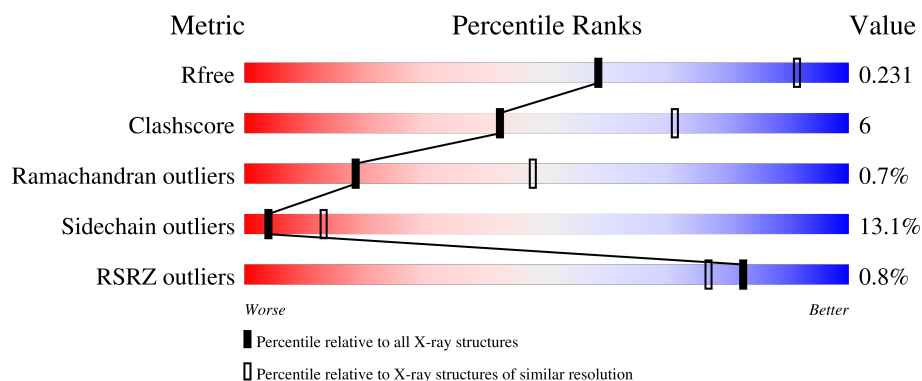
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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))
R_{free}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (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 $\leq 5\%$. 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	102	
1	D	102	
1	G	102	
2	B	111	
2	E	111	

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Mol	Chain	Length	Quality of chain
2	H	111	
3	X	361	
3	Y	361	
3	Z	361	

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	TYS	X	335	-	X	-	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11798 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 Glycoprotein hormones, alpha polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	88	Total	C	N	O	S	0	0	0
			675	417	118	127	13			
1	D	89	Total	C	N	O	S	0	0	0
			682	422	119	128	13			
1	G	88	Total	C	N	O	S	0	0	0
			675	417	118	127	13			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	93	ALA	-	expression tag	UNP Q96QJ4
A	94	ALA	-	expression tag	UNP Q96QJ4
A	95	ALA	-	expression tag	UNP Q96QJ4
A	96	HIS	-	expression tag	UNP Q96QJ4
A	97	HIS	-	expression tag	UNP Q96QJ4
A	98	HIS	-	expression tag	UNP Q96QJ4
A	99	HIS	-	expression tag	UNP Q96QJ4
A	100	HIS	-	expression tag	UNP Q96QJ4
A	101	HIS	-	expression tag	UNP Q96QJ4
A	102	HIS	-	expression tag	UNP Q96QJ4
D	93	ALA	-	expression tag	UNP Q96QJ4
D	94	ALA	-	expression tag	UNP Q96QJ4
D	95	ALA	-	expression tag	UNP Q96QJ4
D	96	HIS	-	expression tag	UNP Q96QJ4
D	97	HIS	-	expression tag	UNP Q96QJ4
D	98	HIS	-	expression tag	UNP Q96QJ4
D	99	HIS	-	expression tag	UNP Q96QJ4
D	100	HIS	-	expression tag	UNP Q96QJ4
D	101	HIS	-	expression tag	UNP Q96QJ4
D	102	HIS	-	expression tag	UNP Q96QJ4
G	93	ALA	-	expression tag	UNP Q96QJ4
G	94	ALA	-	expression tag	UNP Q96QJ4
G	95	ALA	-	expression tag	UNP Q96QJ4

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Chain	Residue	Modelled	Actual	Comment	Reference
G	96	HIS	-	expression tag	UNP Q96QJ4
G	97	HIS	-	expression tag	UNP Q96QJ4
G	98	HIS	-	expression tag	UNP Q96QJ4
G	99	HIS	-	expression tag	UNP Q96QJ4
G	100	HIS	-	expression tag	UNP Q96QJ4
G	101	HIS	-	expression tag	UNP Q96QJ4
G	102	HIS	-	expression tag	UNP Q96QJ4

- Molecule 2 is a protein called Follitropin subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	109	Total	C	N	O	S	0	0	0
			848	527	142	166	13			
2	E	108	Total	C	N	O	S	0	0	0
			840	522	141	165	12			
2	H	108	Total	C	N	O	S	0	0	0
			840	522	141	165	12			

- Molecule 3 is a protein called Follicle-stimulating hormone receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	X	289	Total	C	N	O	S	0	0	0
			2275	1439	397	427	12			
3	Y	284	Total	C	N	O	S	0	0	0
			2258	1428	392	428	10			
3	Z	290	Total	C	N	O	S	0	0	0
			2312	1463	406	431	12			

There are 33 discrepancies between the modelled and reference sequences:

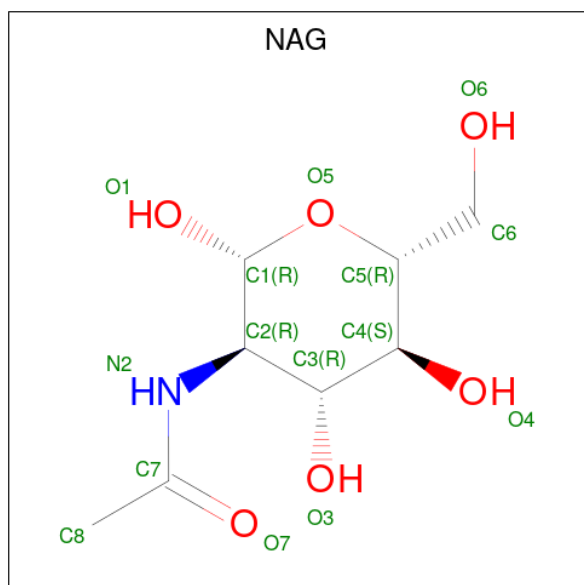
Chain	Residue	Modelled	Actual	Comment	Reference
X	188	SER	CYS	engineered mutation	UNP P23945
X	367	ALA	-	expression tag	UNP P23945
X	368	ALA	-	expression tag	UNP P23945
X	369	ALA	-	expression tag	UNP P23945
X	370	HIS	-	expression tag	UNP P23945
X	371	HIS	-	expression tag	UNP P23945
X	372	HIS	-	expression tag	UNP P23945
X	373	HIS	-	expression tag	UNP P23945
X	374	HIS	-	expression tag	UNP P23945
X	375	HIS	-	expression tag	UNP P23945
X	376	HIS	-	expression tag	UNP P23945

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Chain	Residue	Modelled	Actual	Comment	Reference
Y	188	SER	CYS	engineered mutation	UNP P23945
Y	367	ALA	-	expression tag	UNP P23945
Y	368	ALA	-	expression tag	UNP P23945
Y	369	ALA	-	expression tag	UNP P23945
Y	370	HIS	-	expression tag	UNP P23945
Y	371	HIS	-	expression tag	UNP P23945
Y	372	HIS	-	expression tag	UNP P23945
Y	373	HIS	-	expression tag	UNP P23945
Y	374	HIS	-	expression tag	UNP P23945
Y	375	HIS	-	expression tag	UNP P23945
Y	376	HIS	-	expression tag	UNP P23945
Z	188	SER	CYS	engineered mutation	UNP P23945
Z	367	ALA	-	expression tag	UNP P23945
Z	368	ALA	-	expression tag	UNP P23945
Z	369	ALA	-	expression tag	UNP P23945
Z	370	HIS	-	expression tag	UNP P23945
Z	371	HIS	-	expression tag	UNP P23945
Z	372	HIS	-	expression tag	UNP P23945
Z	373	HIS	-	expression tag	UNP P23945
Z	374	HIS	-	expression tag	UNP P23945
Z	375	HIS	-	expression tag	UNP P23945
Z	376	HIS	-	expression tag	UNP P23945

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



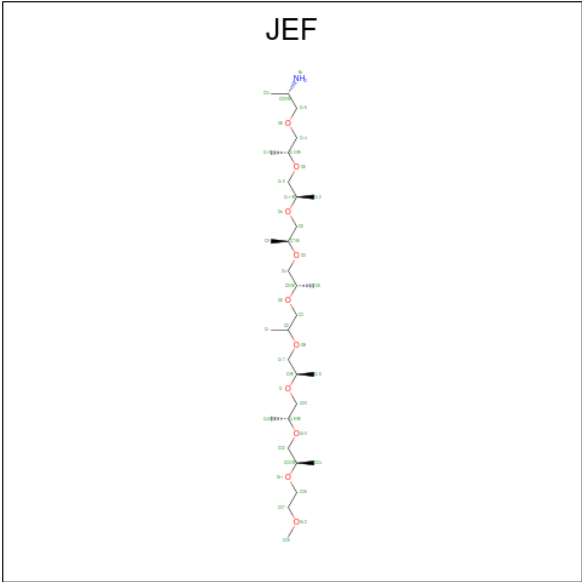
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	X	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	E	1	Total	C	N	O	0	0
			14	8	1	5		
4	E	1	Total	C	N	O	0	0
			14	8	1	5		
4	Y	1	Total	C	N	O	0	0
			14	8	1	5		
4	G	1	Total	C	N	O	0	0
			14	8	1	5		
4	G	1	Total	C	N	O	0	0
			14	8	1	5		
4	H	1	Total	C	N	O	0	0
			14	8	1	5		
4	H	1	Total	C	N	O	0	0
			14	8	1	5		
4	Z	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	X	1	Total	C	O	0	0
			4	2	2		
5	X	1	Total	C	O	0	0
			4	2	2		
5	Y	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is O-(O-(2-AMINOPROPYL)-O'-(2-METHOXYETHYL)POLYPROPYLENE GLYCOL 500) (CCD ID: JEF) (formula: $C_{30}H_{63}NO_{10}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	Z	1	Total	C	O	0	0
			8	5	3		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	13	Total	O	0	0
			13	13		
7	B	16	Total	O	0	0
			16	16		
7	X	22	Total	O	0	0
			22	22		
7	D	10	Total	O	0	0
			10	10		
7	E	13	Total	O	0	0
			13	13		
7	Y	28	Total	O	0	0
			28	28		
7	G	15	Total	O	0	0
			15	15		
7	H	20	Total	O	0	0
			20	20		
7	Z	18	Total	O	0	0
			18	18		

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: Glycoprotein hormones, alpha polypeptide

Chain A: 



- Molecule 1: Glycoprotein hormones, alpha polypeptide

Chain D: 



- Molecule 1: Glycoprotein hormones, alpha polypeptide

Chain G: 



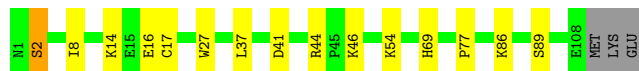
- Molecule 2: Follitropin subunit beta

Chain B: 



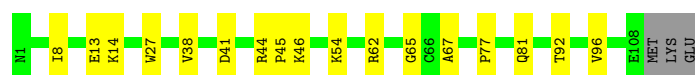
- Molecule 2: Follitropin subunit beta

Chain E: 

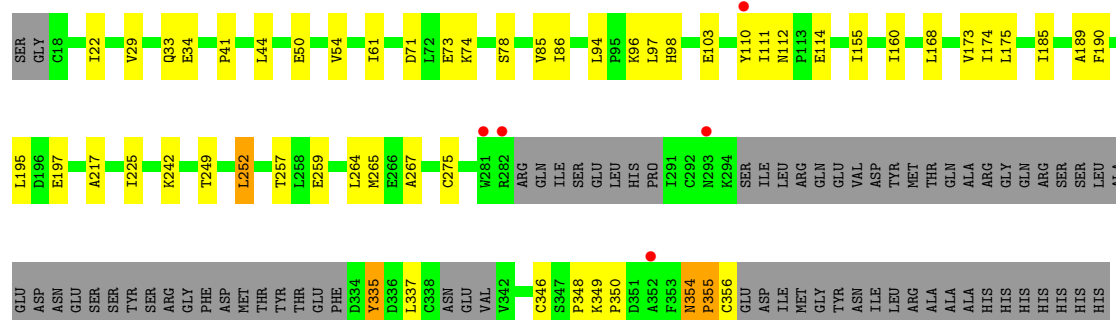


- Molecule 2: Follitropin subunit beta

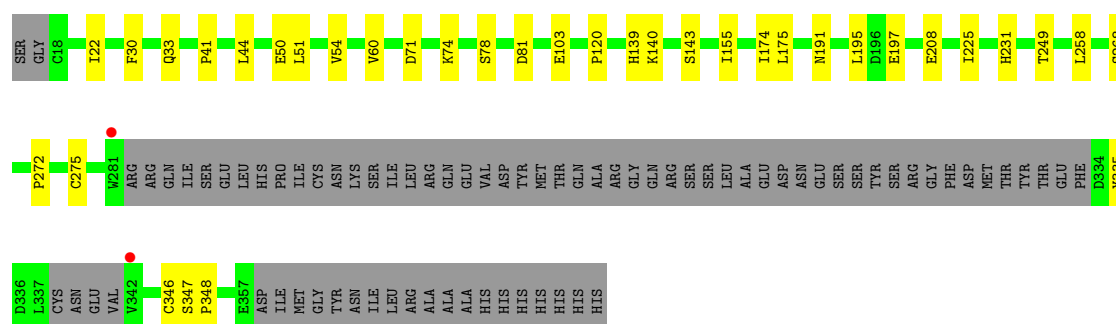
Chain H: 



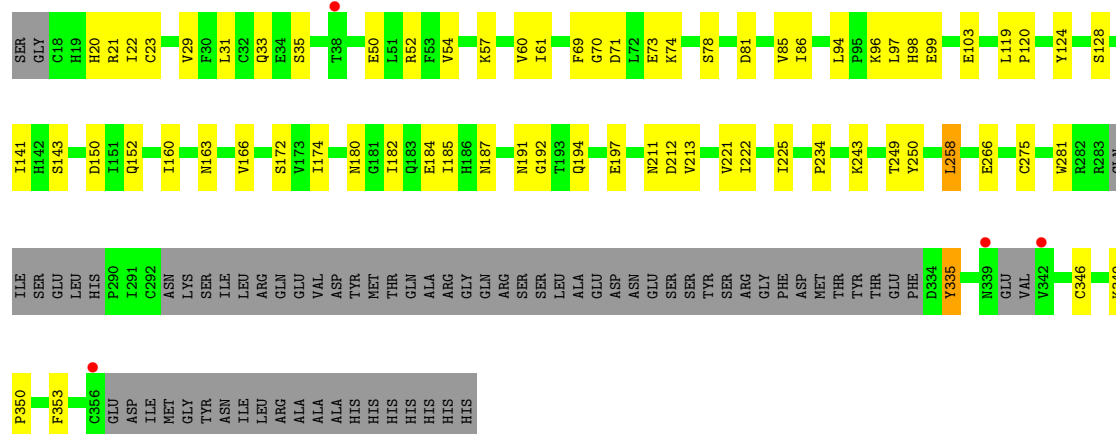
• Molecule 3: Follicle-stimulating hormone receptor



• Molecule 3: Follicle-stimulating hormone receptor



• Molecule 3: Follicle-stimulating hormone receptor



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	95.90Å 95.90Å 204.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.93 – 2.90 24.93 – 2.90	Depositor EDS
% Data completeness (in resolution range)	95.6 (24.93-2.90) 95.4 (24.93-2.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.71 (at 2.89Å)	Xtriage
Refinement program	REFMAC 5.5.0066, BUSTER 2.11.5	Depositor
R, R_{free}	0.174 , 0.237 (Not available) , 0.231	Depositor DCC
R_{free} test set	2233 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	57.3	Xtriage
Anisotropy	0.278	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 72.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,l 0.000 for h,-h-k,-l 0.000 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11798	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 29.94 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4222e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, EDO, JEF, TYS

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	0.81	0/690	1.14	0/933
1	D	0.76	0/697	1.18	1/943 (0.1%)
1	G	0.79	0/690	1.21	3/933 (0.3%)
2	B	0.73	0/867	1.26	3/1177 (0.3%)
2	E	0.76	0/859	1.24	3/1167 (0.3%)
2	H	0.75	0/859	1.20	1/1167 (0.1%)
3	X	0.80	0/2299	1.24	4/3115 (0.1%)
3	Y	0.81	0/2283	1.27	6/3094 (0.2%)
3	Z	0.80	0/2339	1.29	9/3168 (0.3%)
All	All	0.79	0/11583	1.24	30/15697 (0.2%)

There are no bond length outliers.

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	Z	163	ASN	CA-CB-CG	6.90	119.50	112.60
3	Z	150	ASP	CA-CB-CG	6.73	119.33	112.60
2	B	24	ASN	CA-CB-CG	6.56	119.16	112.60
2	B	71	ASP	CA-CB-CG	6.44	119.04	112.60
3	X	34	GLU	CA-C-N	6.10	129.28	120.38

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	675	0	647	14	0
1	D	682	0	656	12	0
1	G	675	0	647	15	0
2	B	848	0	798	4	0
2	E	840	0	789	12	0
2	H	840	0	789	14	0
3	X	2275	0	2240	35	0
3	Y	2258	0	2236	19	0
3	Z	2312	0	2293	36	0
4	A	28	0	26	1	0
4	B	28	0	26	0	0
4	D	28	0	26	0	0
4	E	28	0	26	0	0
4	G	28	0	26	1	0
4	H	28	0	26	0	0
4	X	14	0	13	0	0
4	Y	14	0	13	0	0
4	Z	14	0	13	0	0
5	B	8	0	12	0	0
5	X	8	0	12	0	0
5	Y	4	0	6	0	0
6	Z	8	0	8	0	0
7	A	13	0	0	0	0
7	B	16	0	0	0	0
7	D	10	0	0	0	0
7	E	13	0	0	0	0
7	G	15	0	0	0	0
7	H	20	0	0	0	0
7	X	22	0	0	0	0
7	Y	28	0	0	0	0
7	Z	18	0	0	1	0
All	All	11798	0	11328	141	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 141 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:Z:275:CYS:HG	3:Z:346:CYS:HG	0.89	0.85
1:G:32:CYS:HB3	1:G:58:THR:HG23	1.62	0.81
3:Y:275:CYS:HG	3:Y:346:CYS:HG	1.12	0.80
2:E:41:ASP:O	2:E:44:ARG:HD2	1.85	0.76
1:A:32:CYS:HB3	1:A:58:THR:HG23	1.71	0.73

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	86/102 (84%)	80 (93%)	6 (7%)	0	100	100
1	D	87/102 (85%)	80 (92%)	7 (8%)	0	100	100
1	G	86/102 (84%)	79 (92%)	7 (8%)	0	100	100
2	B	107/111 (96%)	103 (96%)	4 (4%)	0	100	100
2	E	106/111 (96%)	103 (97%)	2 (2%)	1 (1%)	14	41
2	H	106/111 (96%)	101 (95%)	3 (3%)	2 (2%)	6	23
3	X	280/361 (78%)	244 (87%)	32 (11%)	4 (1%)	9	30
3	Y	277/361 (77%)	246 (89%)	30 (11%)	1 (0%)	30	59
3	Z	281/361 (78%)	241 (86%)	38 (14%)	2 (1%)	18	48
All	All	1416/1722 (82%)	1277 (90%)	129 (9%)	10 (1%)	18	48

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	X	354	ASN
2	H	67	ALA
3	Z	70	GLY
3	X	252	LEU
3	X	337	LEU

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	80/90 (89%)	71 (89%)	9 (11%)	5	19
2	B	95/99 (96%)	81 (85%)	14 (15%)	3	10
All	All	175/189 (93%)	152 (87%)	23 (13%)	4	13

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	41	ASP
2	B	47	ILE
2	B	46	LYS
2	B	59	GLU
1	A	63	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	GLN
2	B	69	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 non-standard protein/DNA/RNA residues 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	TYS	Y	335	3	15,16,17	3.20	8 (53%)	15,22,24	2.12	5 (33%)
3	TYS	Z	335	3	15,16,17	2.89	9 (60%)	15,22,24	1.49	1 (6%)
3	TYS	X	335	3	15,16,17	2.68	6 (40%)	15,22,24	2.26	9 (60%)

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	TYS	Y	335	3	-	4/10/11/13	0/1/1/1
3	TYS	Z	335	3	-	3/10/11/13	0/1/1/1
3	TYS	X	335	3	-	8/10/11/13	0/1/1/1

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	Y	335	TYS	OH-S	-7.11	1.44	1.58
3	X	335	TYS	OH-S	-6.67	1.45	1.58
3	Z	335	TYS	OH-S	-6.58	1.45	1.58
3	Y	335	TYS	CE1-CZ	5.44	1.48	1.38
3	Y	335	TYS	CD2-CG	4.11	1.47	1.38

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Y	335	TYS	OH-CZ-CE1	4.97	128.45	118.70
3	X	335	TYS	O2-S-O1	4.67	130.23	112.24
3	Z	335	TYS	O2-S-O1	4.04	127.81	112.24
3	Y	335	TYS	OH-CZ-CE2	-3.91	111.03	118.70
3	X	335	TYS	OH-CZ-CE2	3.33	125.23	118.70

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	X	335	TYS	C-CA-CB-CG

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Mol	Chain	Res	Type	Atoms
3	X	335	TYS	CE1-CZ-OH-S
3	X	335	TYS	CE2-CZ-OH-S
3	Y	335	TYS	CA-CB-CG-CD2
3	Y	335	TYS	CA-CB-CG-CD1

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	Z	335	TYS	1	0
3	X	335	TYS	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

21 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	G	202	1	14,14,15	0.29	0	17,19,21	0.49	0
4	NAG	Z	402	3	14,14,15	0.28	0	17,19,21	0.49	0
4	NAG	H	202	2	14,14,15	0.30	0	17,19,21	0.51	0
5	EDO	X	402	-	3,3,3	0.59	0	2,2,2	0.29	0
4	NAG	X	403	3	14,14,15	0.28	0	17,19,21	0.63	0
4	NAG	A	202	1	14,14,15	0.31	0	17,19,21	0.77	0
4	NAG	B	201	2	14,14,15	0.34	0	17,19,21	1.22	2 (11%)
5	EDO	B	203	-	3,3,3	0.71	0	2,2,2	0.10	0
4	NAG	H	201	2	14,14,15	0.32	0	17,19,21	0.72	1 (5%)
4	NAG	E	201	2	14,14,15	0.33	0	17,19,21	0.73	1 (5%)
4	NAG	A	201	1	14,14,15	0.27	0	17,19,21	2.29	4 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	D	201	1	14,14,15	0.27	0	17,19,21	1.72	3 (17%)
6	JEF	Z	401	-	7,7,40	1.30	2 (28%)	7,7,48	1.41	1 (14%)
4	NAG	G	201	1	14,14,15	0.31	0	17,19,21	1.97	3 (17%)
4	NAG	Y	402	3	14,14,15	0.31	0	17,19,21	0.70	0
5	EDO	Y	401	-	3,3,3	0.60	0	2,2,2	0.33	0
4	NAG	B	202	2	14,14,15	0.38	0	17,19,21	0.74	0
4	NAG	D	202	1	14,14,15	0.30	0	17,19,21	0.75	1 (5%)
5	EDO	X	401	-	3,3,3	0.70	0	2,2,2	0.06	0
5	EDO	B	204	-	3,3,3	0.60	0	2,2,2	0.21	0
4	NAG	E	202	2	14,14,15	0.32	0	17,19,21	0.85	2 (11%)

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	G	202	1	-	0/6/23/26	0/1/1/1
4	NAG	Z	402	3	-	0/6/23/26	0/1/1/1
4	NAG	H	202	2	-	0/6/23/26	0/1/1/1
5	EDO	X	402	-	-	0/1/1/1	-
4	NAG	X	403	3	-	0/6/23/26	0/1/1/1
4	NAG	A	202	1	-	2/6/23/26	0/1/1/1
4	NAG	B	201	2	-	1/6/23/26	0/1/1/1
5	EDO	B	203	-	-	1/1/1/1	-
4	NAG	H	201	2	-	0/6/23/26	0/1/1/1
4	NAG	E	201	2	-	2/6/23/26	0/1/1/1
4	NAG	A	201	1	-	2/6/23/26	0/1/1/1
4	NAG	D	201	1	-	1/6/23/26	0/1/1/1
6	JEF	Z	401	-	-	3/6/6/46	-
4	NAG	G	201	1	-	1/6/23/26	0/1/1/1
4	NAG	Y	402	3	-	0/6/23/26	0/1/1/1
5	EDO	Y	401	-	-	0/1/1/1	-
4	NAG	B	202	2	-	2/6/23/26	0/1/1/1
4	NAG	D	202	1	-	0/6/23/26	0/1/1/1
5	EDO	X	401	-	-	1/1/1/1	-
5	EDO	B	204	-	-	0/1/1/1	-
4	NAG	E	202	2	-	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)
6	Z	401	JEF	O4-C11	2.11	1.47	1.44
6	Z	401	JEF	C10-C11	2.02	1.55	1.51

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	201	NAG	O5-C1-C2	-6.36	101.44	111.29
4	G	201	NAG	C1-C2-N2	5.97	119.84	110.43
4	A	201	NAG	C1-C2-N2	5.52	119.14	110.43
4	D	201	NAG	O5-C1-C2	-4.67	104.06	111.29
4	D	201	NAG	C1-C2-N2	4.56	117.62	110.43

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

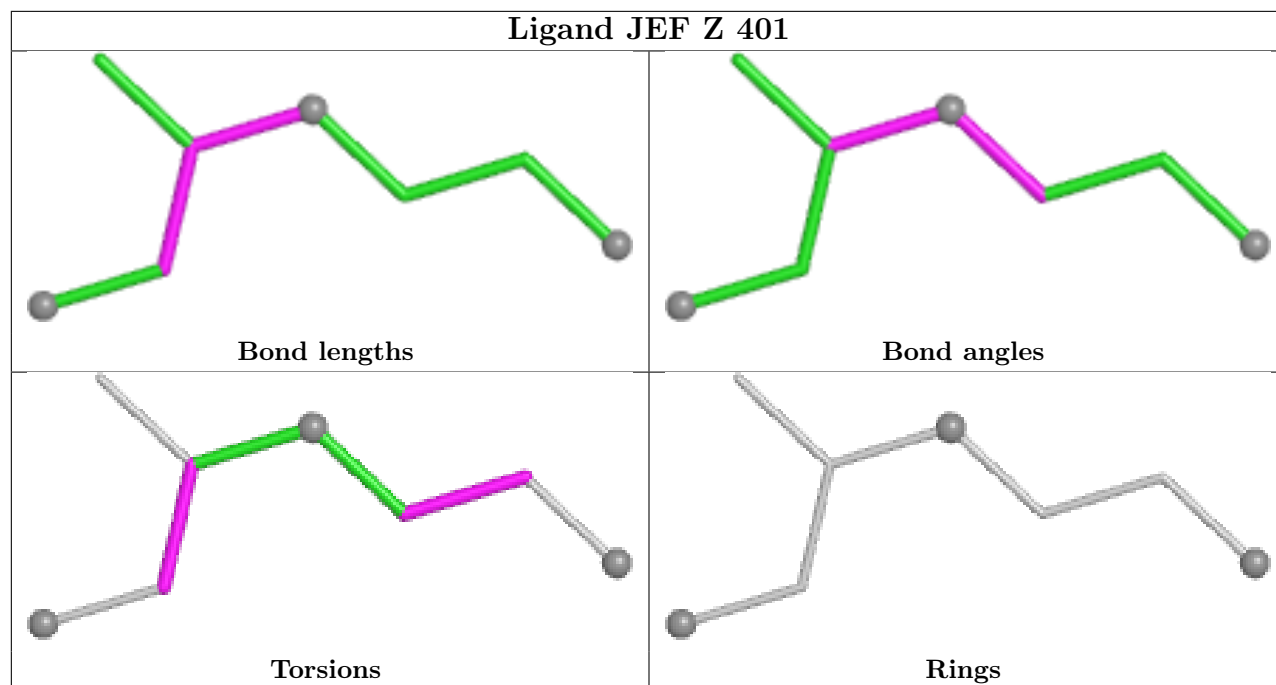
Mol	Chain	Res	Type	Atoms
4	A	201	NAG	C1-C2-N2-C7
4	B	201	NAG	C1-C2-N2-C7
4	D	201	NAG	C1-C2-N2-C7
4	G	201	NAG	C1-C2-N2-C7
6	Z	401	JEF	O5-C10-C11-O4

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	202	NAG	1	0
4	A	202	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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 [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	88/102 (86%)	-0.56	0 100 100	40, 67, 114, 147	0
1	D	89/102 (87%)	-0.51	1 (1%) 78 71	41, 67, 121, 159	0
1	G	88/102 (86%)	-0.50	0 100 100	48, 71, 114, 145	0
2	B	109/111 (98%)	-0.48	0 100 100	43, 72, 126, 162	0
2	E	108/111 (97%)	-0.36	0 100 100	48, 75, 116, 158	0
2	H	108/111 (97%)	-0.32	0 100 100	49, 76, 126, 152	0
3	X	288/361 (79%)	-0.35	5 (1%) 69 61	41, 86, 140, 210	0
3	Y	283/361 (78%)	-0.39	2 (0%) 84 79	44, 86, 144, 187	0
3	Z	289/361 (80%)	-0.30	4 (1%) 73 65	42, 92, 143, 195	0
All	All	1450/1722 (84%)	-0.39	12 (0%) 82 77	40, 82, 139, 210	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	Y	281	TRP	3.1
3	X	293	ASN	2.6
3	Z	356	CYS	2.6
1	D	4	VAL	2.5
3	Z	342	VAL	2.4

6.2 Non-standard residues in protein, DNA, RNA chains [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($\text{\AA}^2$)	Q<0.9
3	TYS	Y	335	16/17	0.83	0.16	114,125,145,147	0
3	TYS	Z	335	16/17	0.83	0.15	105,114,138,139	0
3	TYS	X	335	16/17	0.90	0.14	107,121,139,141	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

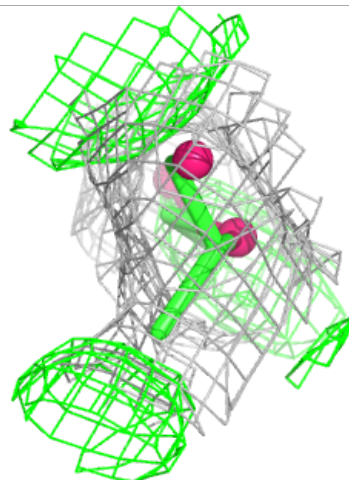
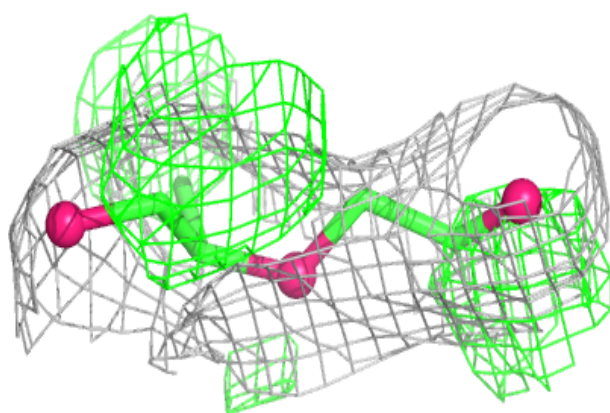
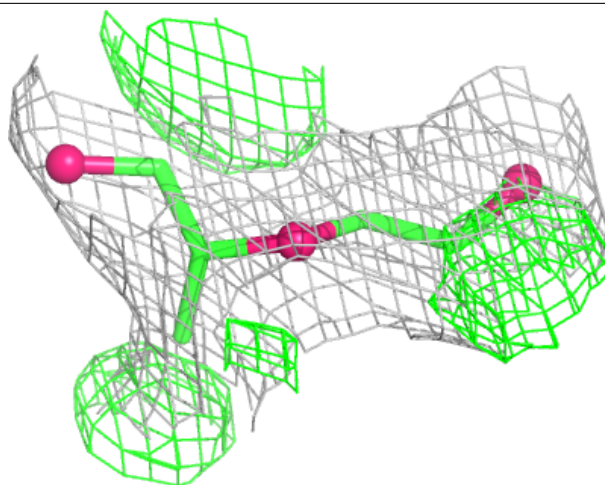
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	JEF	Z	401	8/41	0.34	0.20	108,114,116,117	0
5	EDO	B	204	4/4	0.45	0.12	109,109,110,110	0
4	NAG	B	202	14/15	0.48	0.12	162,171,176,179	0
4	NAG	H	201	14/15	0.54	0.13	140,145,153,154	0
4	NAG	H	202	14/15	0.60	0.12	135,143,151,154	0
4	NAG	E	201	14/15	0.62	0.15	145,152,158,163	0
5	EDO	X	402	4/4	0.63	0.18	97,98,99,99	0
4	NAG	E	202	14/15	0.74	0.09	144,150,159,164	0
4	NAG	B	201	14/15	0.74	0.11	126,136,146,146	0
5	EDO	X	401	4/4	0.77	0.15	66,67,68,68	0
5	EDO	B	203	4/4	0.81	0.14	76,77,78,79	0
5	EDO	Y	401	4/4	0.82	0.09	74,76,77,77	0
4	NAG	D	201	14/15	0.84	0.10	71,76,80,83	0
4	NAG	A	201	14/15	0.87	0.10	70,77,86,89	0
4	NAG	Z	402	14/15	0.87	0.09	103,118,123,124	0
4	NAG	G	201	14/15	0.88	0.10	69,79,88,92	0
4	NAG	X	403	14/15	0.89	0.08	109,117,127,127	0
4	NAG	Y	402	14/15	0.91	0.08	106,118,125,127	0
4	NAG	G	202	14/15	0.92	0.10	85,88,95,98	0
4	NAG	D	202	14/15	0.94	0.08	75,78,86,87	0
4	NAG	A	202	14/15	0.95	0.06	72,78,86,92	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around JEF Z 401:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.