



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 17, 2018 – 09:55 pm GMT

PDB ID : 1F6A  
Title : Structure of the human ige-fc bound to its high affinity receptor  
fc(epsilon)ri(alpha)  
Authors : Garman, S.C.; Wurzburg, B.A.; Tarchevskaya, S.S.; Kinet, J.P.; Jardetzky,  
T.S.  
Deposited on : 2000-06-20  
Resolution : 3.50 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30686

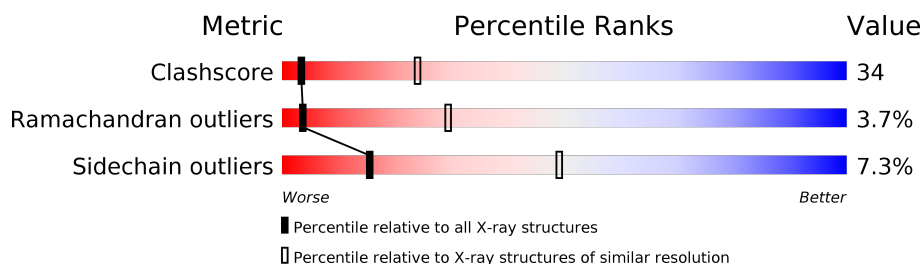
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.50 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	122078	1485 (3.60-3.40)
Ramachandran outliers	120005	1446 (3.60-3.40)
Sidechain outliers	119972	1447 (3.60-3.40)

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  $\geq 3$ , 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  $\leq 5\%$ . 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	176	
2	B	222	
2	D	222	

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
4	MAN	A	223	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MAN	A	244	X	-	-	-
4	MAN	B	696	X	-	X	-
4	MAN	B	697	-	-	X	-
4	MAN	D	696	X	-	-	-

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5251 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 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR ALPHA-SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	173	Total	C	N	O	S	0	0	0
			1406	902	229	270	5			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	74	ALA	ASN	ENGINEERED	UNP P12319
A	135	ALA	ASN	ENGINEERED	UNP P12319
A	142	ALA	THR	ENGINEERED	UNP P12319
A	143	ALA	VAL	CLONING ARTIFACT	UNP P12319

- Molecule 2 is a protein called IG EPSILON CHAIN C REGION.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	217	Total	C	N	O	S	0	0	0
			1711	1067	317	320	7			
2	D	216	Total	C	N	O	S	0	0	0
			1704	1062	316	319	7			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	326	ALA	-	CLONING ARTIFACT	UNP P01854
B	327	ASP	-	CLONING ARTIFACT	UNP P01854
B	328	PRO	-	CLONING ARTIFACT	UNP P01854
B	329	CYS	-	CLONING ARTIFACT	UNP P01854
D	326	ALA	-	CLONING ARTIFACT	UNP P01854
D	327	ASP	-	CLONING ARTIFACT	UNP P01854
D	328	PRO	-	CLONING ARTIFACT	UNP P01854
D	329	CYS	-	CLONING ARTIFACT	UNP P01854

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

- Molecule 4 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula:  $C_6H_{12}O_6$ ).



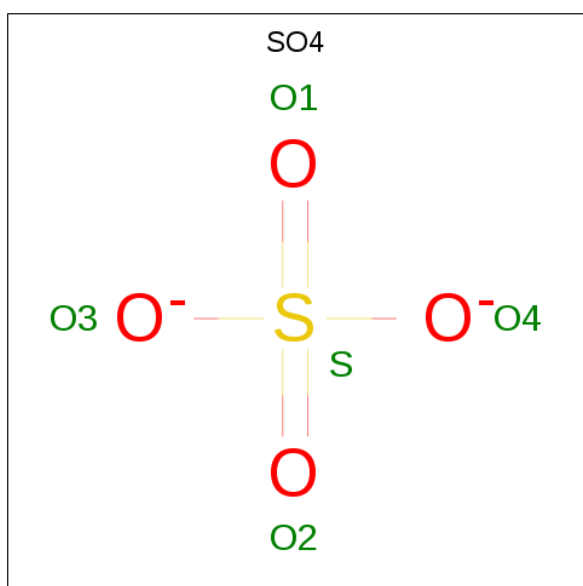
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			11	6	5		
4	A	1	Total	C	O	0	0
			11	6	5		
4	B	1	Total	C	O	0	0
			11	6	5		
4	B	1	Total	C	O	0	0
			11	6	5		
4	B	1	Total	C	O	0	0
			11	6	5		
4	B	1	Total	C	O	0	0
			11	6	5		
4	D	1	Total	C	O	0	0
			11	6	5		

- Molecule 5 is ALPHA-L-FUCOSE (three-letter code: FUC) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			10	6	4		
5	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



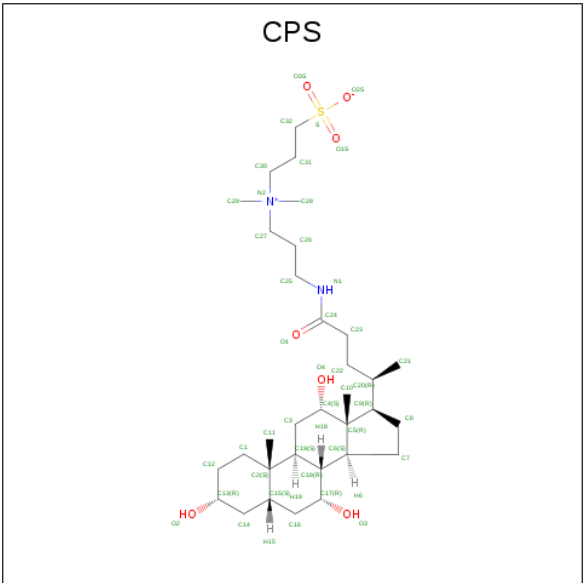
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is 3-[(3-CHOLAMIDOPROPYL)DIMETHYLAMMONIO]-1-PROPANESULFO NATE (three-letter code: CPS) (formula: C<sub>32</sub>H<sub>58</sub>N<sub>2</sub>O<sub>7</sub>S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	O		0	0
			26	23	3			
7	A	1	Total	C	N	O	S	0
			42	32	2	7	1	
7	D	1	Total	C	O		0	0
			26	23	3			
7	D	1	Total	C	O		0	0
			26	23	3			
7	D	1	Total	C	O		0	0
			26	23	3			

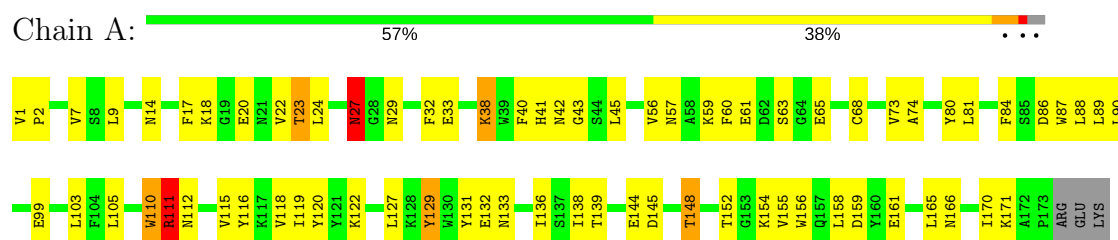


### 3 Residue-property plots

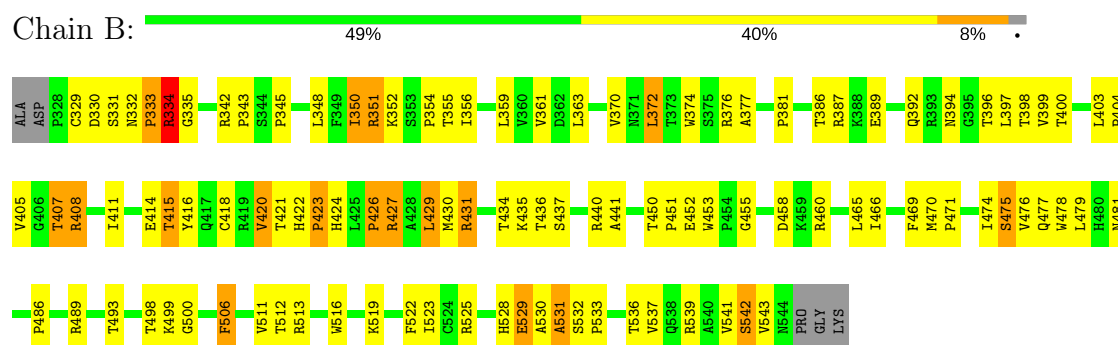
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

Note EDS was not executed.

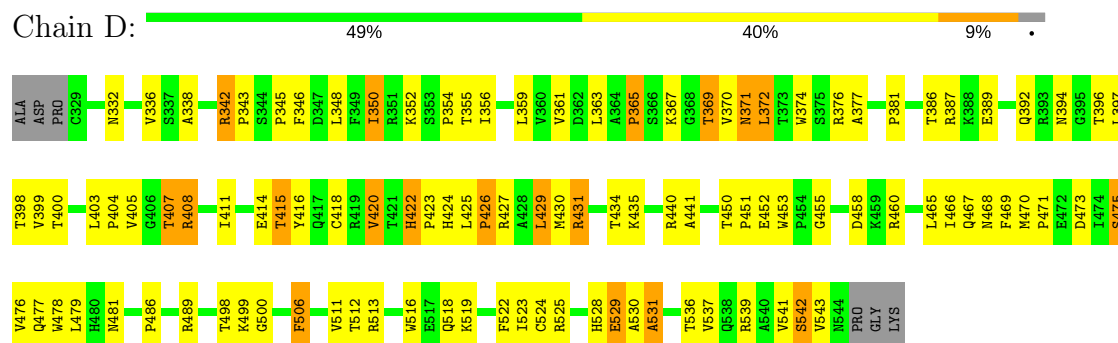
#### • Molecule 1: HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR ALPHA-SUBUNIT



#### • Molecule 2: IG EPSILON CHAIN C REGION



#### • Molecule 2: IG EPSILON CHAIN C REGION



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	192.80 Å   192.80 Å   302.40 Å 90.00°   90.00°   120.00°	Depositor
Resolution (Å)	36.87 – 3.50	Depositor
% Data completeness (in resolution range)	99.6 (36.87-3.50)	Depositor
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS 0.9	Depositor
R, $R_{free}$	0.254 , 0.273	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5251	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	89.0	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: FUC, CPS, NAG, SO4, MAN

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	0/1448	0.73	1/1974 (0.1%)
2	B	0.49	2/1755 (0.1%)	0.77	2/2389 (0.1%)
2	D	0.48	2/1747 (0.1%)	0.76	2/2378 (0.1%)
All	All	0.49	4/4950 (0.1%)	0.76	5/6741 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	529	GLU	CD-OE1	-8.78	1.16	1.25
2	B	529	GLU	CD-OE1	-8.01	1.16	1.25
2	B	529	GLU	CD-OE2	-7.74	1.17	1.25
2	D	529	GLU	CD-OE2	-7.45	1.17	1.25

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	529	GLU	OE1-CD-OE2	-16.97	102.93	123.30
2	D	529	GLU	OE1-CD-OE2	-16.73	103.23	123.30
2	D	529	GLU	CG-CD-OE2	5.70	129.70	118.30
2	B	529	GLU	CG-CD-OE2	5.29	128.87	118.30
1	A	27	ASN	N-CA-C	5.24	125.15	111.00

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	1406	0	1322	76	0
2	B	1711	0	1687	131	1
2	D	1704	0	1679	126	1
3	A	84	0	71	3	0
3	B	28	0	24	1	0
3	D	28	0	24	0	0
4	A	44	0	38	1	0
4	B	44	0	37	8	0
4	D	11	0	10	0	0
5	A	20	0	20	0	0
6	A	5	0	0	1	0
6	B	15	0	0	2	0
6	D	5	0	0	0	0
7	A	68	0	91	13	0
7	D	78	0	105	12	0
All	All	5251	0	5108	356	2

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 34.

The worst 5 of 356 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)
7:A:371:CPS:C5	7:A:371:CPS:C10	1.75	1.65
7:D:105:CPS:C10	7:D:105:CPS:C5	1.75	1.58
7:A:371:CPS:N1	7:A:371:CPS:C25	1.67	1.50
4:B:696:MAN:H61	4:B:697:MAN:H3	1.41	1.00
1:A:115:VAL:HG22	1:A:155:VAL:HG22	1.49	0.92

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:518:GLN:OE1	2:D:518:GLN:OE1[11_566]	1.79	0.41
2:B:351:ARG:NH2	2:B:351:ARG:NH2[4_556]	2.12	0.08

## 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	171/176 (97%)	147 (86%)	20 (12%)	4 (2%)	7	39
2	B	215/222 (97%)	177 (82%)	29 (14%)	9 (4%)	3	26
2	D	214/222 (96%)	175 (82%)	30 (14%)	9 (4%)	3	26
All	All	600/620 (97%)	499 (83%)	79 (13%)	22 (4%)	4	29

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	27	ASN
2	B	334	ARG
2	B	531	ALA
2	D	426	PRO
2	D	531	ALA

### 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	154/157 (98%)	147 (96%)	7 (4%)	30	65
2	B	192/195 (98%)	176 (92%)	16 (8%)	12	43
2	D	191/195 (98%)	175 (92%)	16 (8%)	12	42
All	All	537/547 (98%)	498 (93%)	39 (7%)	15	49

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	429	LEU
2	B	506	PHE
2	D	481	ASN
2	B	431	ARG
2	B	475	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	528	HIS
2	B	538	GLN
2	D	481	ASN
2	B	481	ASN
2	B	518	GLN

### 5.3.3 RNA [i](#)

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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

31 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
6	SO4	A	203	-	4,4,4	0.60	0	6,6,6	0.25	0
3	NAG	A	221	1,3,5	14,14,15	0.49	0	17,19,21	0.92	1 (5%)
3	NAG	A	222	3,4	14,14,15	0.52	0	17,19,21	0.76	0
4	MAN	A	223	3	11,11,12	0.47	0	15,15,17	0.24	0
5	FUC	A	224	3	9,10,11	0.47	0	13,14,16	0.50	0
3	NAG	A	242	1,3	14,14,15	0.54	0	17,19,21	0.93	1 (5%)
3	NAG	A	243	3,4	14,14,15	0.53	0	17,19,21	0.86	1 (5%)
4	MAN	A	244	3,4	11,11,12	0.70	0	15,15,17	0.42	0
4	MAN	A	245	4	11,11,12	0.66	0	15,15,17	0.65	0
4	MAN	A	246	4	11,11,12	0.51	0	15,15,17	0.60	0
3	NAG	A	366	1,3,5	14,14,15	0.61	0	17,19,21	0.85	1 (5%)
3	NAG	A	367	3	14,14,15	0.47	0	17,19,21	0.67	0
5	FUC	A	369	3	9,10,11	0.42	0	13,14,16	0.48	0
7	CPS	A	370	-	29,29,45	4.61	16 (55%)	47,47,70	4.06	27 (57%)
7	CPS	A	371	-	45,45,45	4.91	23 (51%)	68,70,70	3.38	33 (48%)
6	SO4	B	201	-	4,4,4	0.51	0	6,6,6	0.12	0
6	SO4	B	202	-	4,4,4	0.34	0	6,6,6	0.28	0
6	SO4	B	204	-	4,4,4	0.64	0	6,6,6	0.43	0
3	NAG	B	694	3,2	14,14,15	0.39	0	17,19,21	0.80	0
3	NAG	B	695	3,4	14,14,15	0.70	0	17,19,21	0.70	0
4	MAN	B	696	3,4	11,11,12	0.62	0	15,15,17	0.91	0
4	MAN	B	697	4	11,11,12	0.74	0	15,15,17	1.18	0
4	MAN	B	698	4	11,11,12	0.60	0	15,15,17	0.55	0
4	MAN	B	699	4	11,11,12	1.05	1 (9%)	15,15,17	0.84	1 (6%)
7	CPS	D	103	-	29,29,45	4.76	18 (62%)	47,47,70	3.91	28 (59%)
7	CPS	D	104	-	29,29,45	4.79	17 (58%)	47,47,70	3.91	28 (59%)
7	CPS	D	105	-	29,29,45	4.97	17 (58%)	47,47,70	3.83	27 (57%)
6	SO4	D	205	-	4,4,4	0.60	0	6,6,6	0.28	0
3	NAG	D	694	3,2	14,14,15	0.64	0	17,19,21	0.70	0
3	NAG	D	695	3,4	14,14,15	0.72	0	17,19,21	0.79	1 (5%)
4	MAN	D	696	3	11,11,12	0.55	0	15,15,17	0.30	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
6	SO4	A	203	-	-	0/0/0/0	0/0/0/0
3	NAG	A	221	1,3,5	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	222	3,4	-	0/6/23/26	0/1/1/1
4	MAN	A	223	3	1/1/4/5	0/2/19/22	0/1/1/1
5	FUC	A	224	3	-	0/0/17/20	0/1/1/1
3	NAG	A	242	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	243	3,4	-	0/6/23/26	0/1/1/1
4	MAN	A	244	3,4	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	A	245	4	-	0/2/19/22	0/1/1/1
4	MAN	A	246	4	-	0/2/19/22	0/1/1/1
3	NAG	A	366	1,3,5	-	0/6/23/26	0/1/1/1
3	NAG	A	367	3	-	0/6/23/26	0/1/1/1
5	FUC	A	369	3	-	0/0/17/20	0/1/1/1
7	CPS	A	370	-	-	0/6/71/90	0/4/4/4
7	CPS	A	371	-	-	1/25/90/90	0/4/4/4
6	SO4	B	201	-	-	0/0/0/0	0/0/0/0
6	SO4	B	202	-	-	0/0/0/0	0/0/0/0
6	SO4	B	204	-	-	0/0/0/0	0/0/0/0
3	NAG	B	694	3,2	-	0/6/23/26	0/1/1/1
3	NAG	B	695	3,4	-	1/6/23/26	0/1/1/1
4	MAN	B	696	3,4	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	B	697	4	-	0/2/19/22	0/1/1/1
4	MAN	B	698	4	-	0/2/19/22	0/1/1/1
4	MAN	B	699	4	-	0/2/19/22	0/1/1/1
7	CPS	D	103	-	-	0/6/71/90	0/4/4/4
7	CPS	D	104	-	-	0/6/71/90	0/4/4/4
7	CPS	D	105	-	-	0/6/71/90	0/4/4/4
6	SO4	D	205	-	-	0/0/0/0	0/0/0/0
3	NAG	D	694	3,2	-	0/6/23/26	0/1/1/1
3	NAG	D	695	3,4	-	0/6/23/26	0/1/1/1
4	MAN	D	696	3	1/1/4/5	0/2/19/22	0/1/1/1

The worst 5 of 92 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	371	CPS	C32-S	-16.17	1.54	1.77
7	D	103	CPS	O4-C4	-13.32	1.21	1.43
7	A	370	CPS	O4-C4	-13.13	1.21	1.43
7	D	104	CPS	O4-C4	-12.99	1.21	1.43
7	D	105	CPS	O4-C4	-12.88	1.21	1.43

The worst 5 of 149 bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	370	CPS	C19-C18-C17	-9.52	100.75	111.92
7	D	104	CPS	C19-C18-C17	-9.10	101.23	111.92
7	D	105	CPS	C19-C18-C17	-8.57	101.85	111.92
7	D	103	CPS	C19-C18-C17	-8.41	102.04	111.92
7	A	371	CPS	C19-C18-C17	-8.32	102.15	111.92

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	223	MAN	C1
4	A	244	MAN	C1
4	D	696	MAN	C1
4	B	696	MAN	C1

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	695	NAG	O7-C7-N2-C2
7	A	371	CPS	C25-C26-C27-N2

There are no ring outliers.

16 monomers are involved in 41 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	203	SO4	1	0
3	A	242	NAG	3	0
3	A	243	NAG	3	0
4	A	244	MAN	1	0
4	A	245	MAN	1	0
7	A	370	CPS	1	0
7	A	371	CPS	13	0
6	B	202	SO4	1	0
6	B	204	SO4	1	0
3	B	694	NAG	1	0
3	B	695	NAG	1	0
4	B	696	MAN	7	0
4	B	697	MAN	8	0
4	B	699	MAN	1	0
7	D	103	CPS	1	0
7	D	105	CPS	11	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 [i](#)

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.