



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:44 PM GMT

PDB ID : 4JBS  
Title : Crystal structure of the human Endoplasmic Reticulum Aminopeptidase 2 in complex with PHOSPHINIC PSEUDOTRIPEPTIDE inhibitor.  
Authors : Saridakis, E.; Birtley, J.; Stratikos, E.; Mavridis, I.M.  
Deposited on : 2013-02-20  
Resolution : 2.79 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  
<http://wwpdb.org/validation/2016/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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

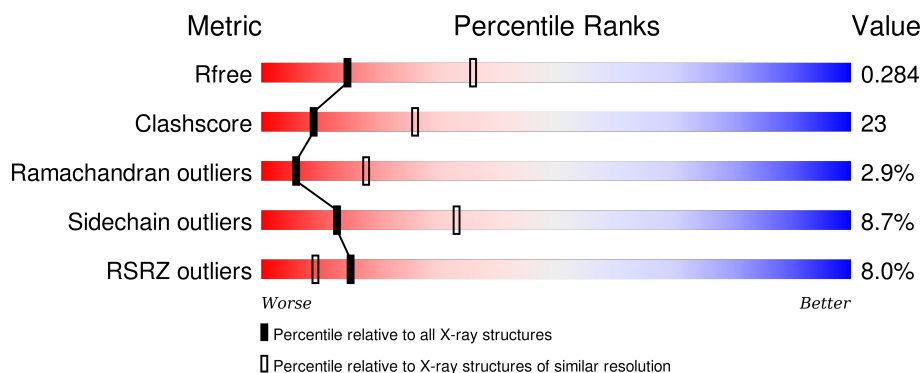
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.79 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))
$R_{free}$	91344	3004 (2.80-2.76)
Clashscore	102246	3480 (2.80-2.76)
Ramachandran outliers	100387	3423 (2.80-2.76)
Sidechain outliers	100360	3425 (2.80-2.76)
RSRZ outliers	91569	3016 (2.80-2.76)

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.

Mol	Chain	Length	Quality of chain
1	A	967	
1	B	967	

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
6	P52	A	1009	-	-	-	X
6	P52	B	1010	-	-	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 14457 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 Endoplasmic reticulum aminopeptidase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	869	Total	C	N	O	S	2	2	0
			7045	4547	1170	1301	27			
1	B	854	Total	C	N	O	S	0	0	0
			6831	4416	1130	1259	26			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	CLONING ARTIFACT	UNP Q6P179
A	2	VAL	-	CLONING ARTIFACT	UNP Q6P179
A	961	ARG	-	EXPRESSION TAG	UNP Q6P179
A	962	HIS	-	EXPRESSION TAG	UNP Q6P179
A	963	HIS	-	EXPRESSION TAG	UNP Q6P179
A	964	HIS	-	EXPRESSION TAG	UNP Q6P179
A	965	HIS	-	EXPRESSION TAG	UNP Q6P179
A	966	HIS	-	EXPRESSION TAG	UNP Q6P179
A	967	HIS	-	EXPRESSION TAG	UNP Q6P179
B	1	MET	-	CLONING ARTIFACT	UNP Q6P179
B	2	VAL	-	CLONING ARTIFACT	UNP Q6P179
B	961	ARG	-	EXPRESSION TAG	UNP Q6P179
B	962	HIS	-	EXPRESSION TAG	UNP Q6P179
B	963	HIS	-	EXPRESSION TAG	UNP Q6P179
B	964	HIS	-	EXPRESSION TAG	UNP Q6P179
B	965	HIS	-	EXPRESSION TAG	UNP Q6P179
B	966	HIS	-	EXPRESSION TAG	UNP Q6P179
B	967	HIS	-	EXPRESSION TAG	UNP Q6P179

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

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

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

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	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		

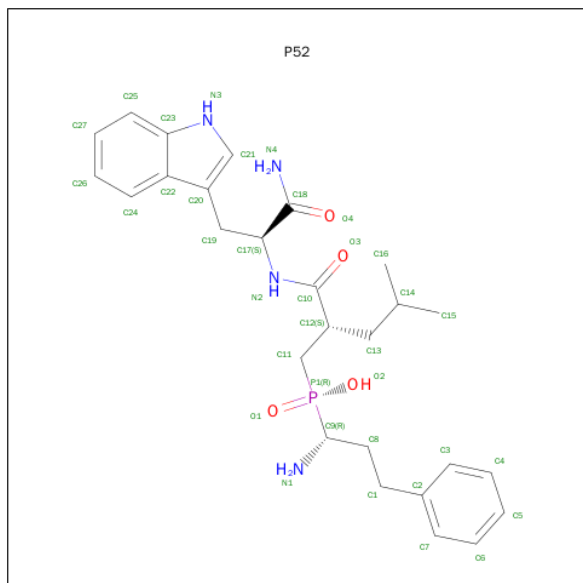
- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Zn	0	0
			1	1		
4	A	1	Total	Zn	0	0
			1	1		

- Molecule 5 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 6 is NALPHA-[(2S)-2-{[[(1R)-1-AMINO-3-PHENYLPROPYL](HYDROXY)PHOSPHORYL]METHYL}-4-METHYLPENTANOYL]-L-TRYPTOPHANAMIDE (three-letter code: P52) (formula: C<sub>27</sub>H<sub>37</sub>N<sub>4</sub>O<sub>4</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	P	1	0
			36	27	4	4	1		
6	B	1	Total	C	N	O	P	1	0
			36	27	4	4	1		

- Molecule 7 is IMIDAZOLE (three-letter code: IMD) (formula: C<sub>3</sub>H<sub>5</sub>N<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	N	0	0
			5	3	2		
7	A	1	Total	C	N	0	0
			5	3	2		

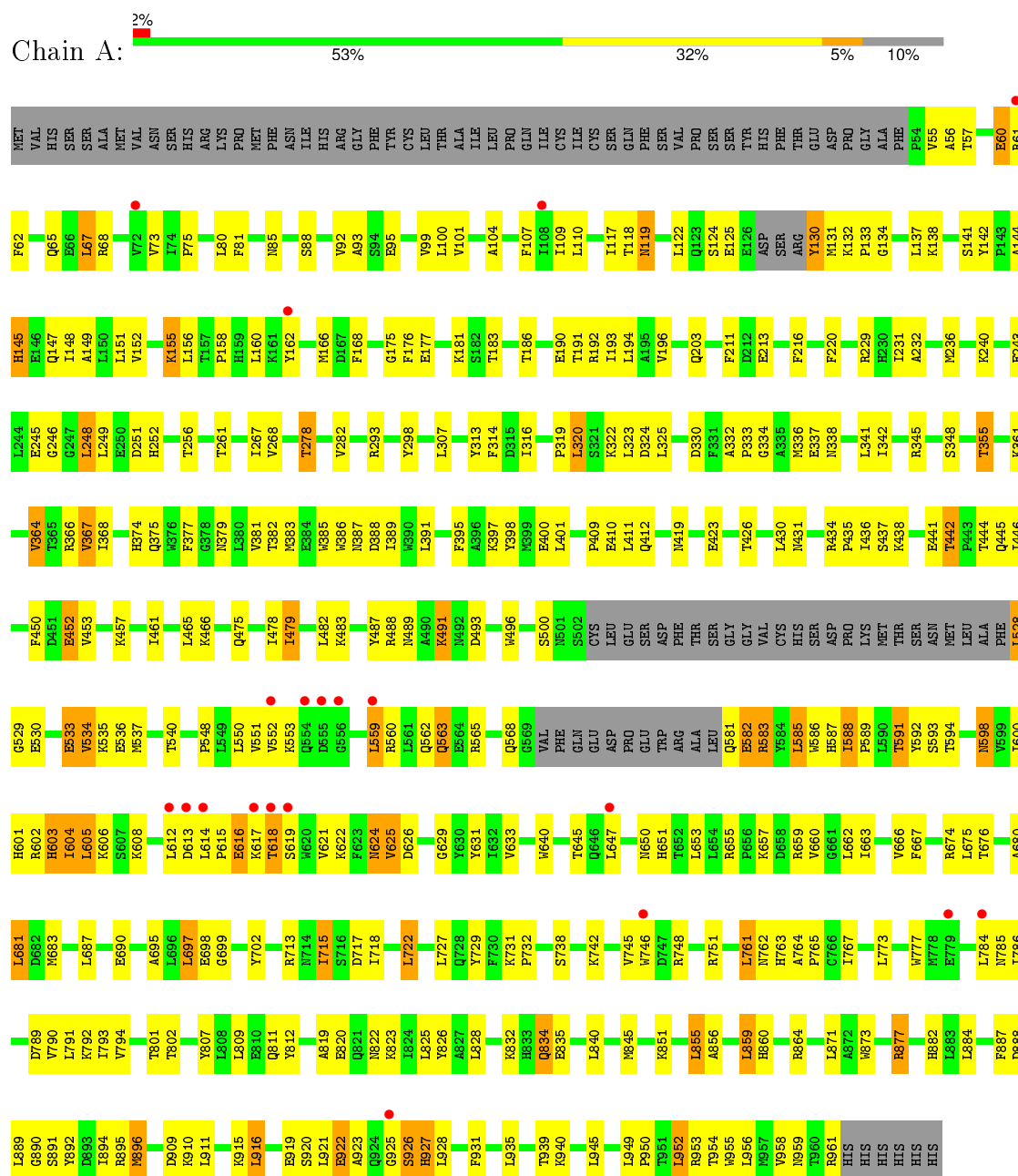
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	207	Total	O	0	0
			207	207		
8	B	86	Total	O	0	0
			86	86		

### 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 errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

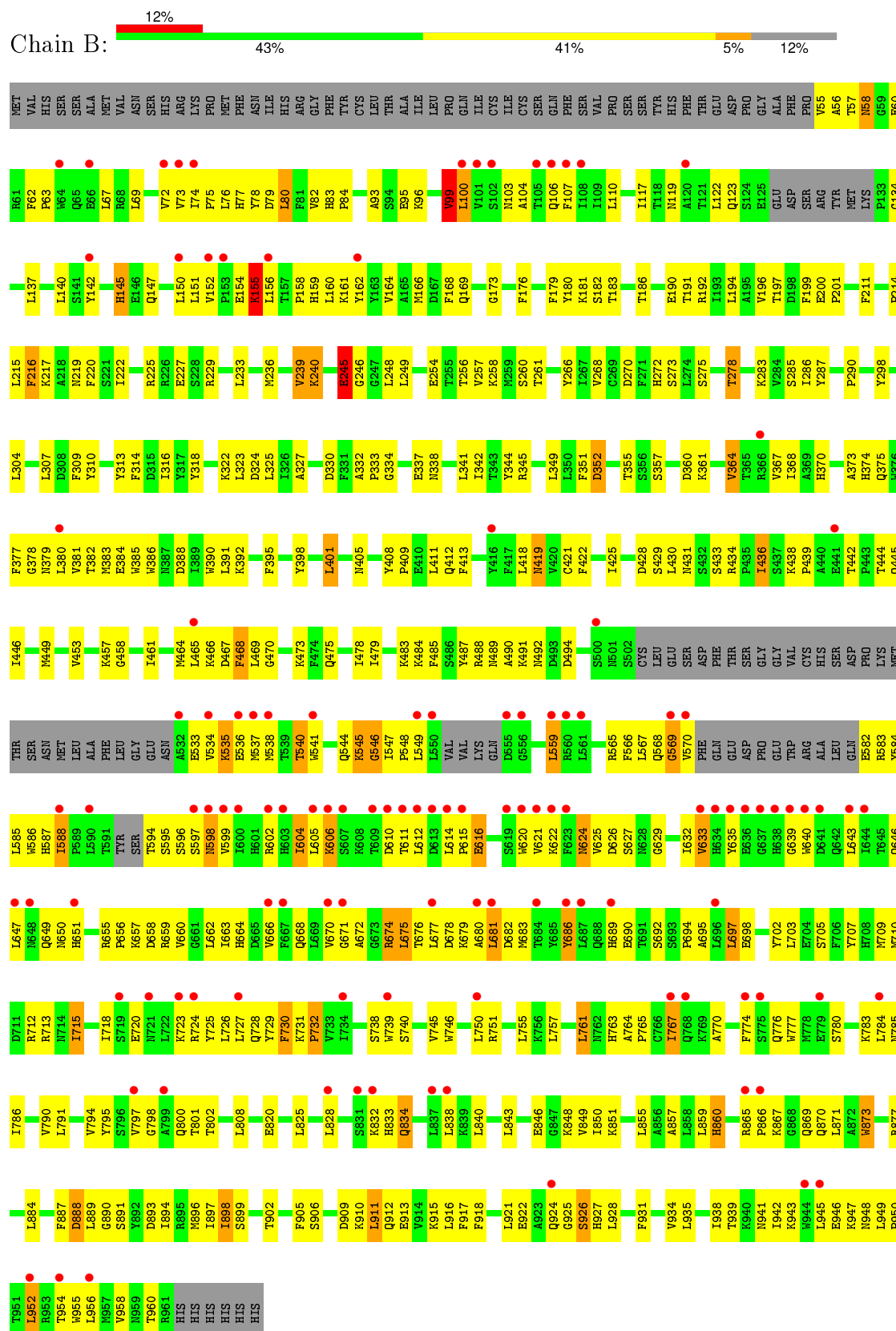
#### • Molecule 1: Endoplasmic reticulum aminopeptidase 2





● Molecule 1: Endoplasmic reticulum aminopeptidase 2

Chain B:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.15Å 134.77Å 128.73Å 90.00° 90.28° 90.00°	Depositor
Resolution (Å)	10.99 – 2.79 48.77 – 2.79	Depositor EDS
% Data completeness (in resolution range)	94.7 (10.99-2.79) 99.8 (48.77-2.79)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.47 (at 2.77Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, $R_{free}$	0.206 , 0.278 0.211 , 0.284	Depositor DCC
$R_{free}$ test set	3171 reflections (5.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	59.4	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 65.4	EDS
Estimated twinning fraction	0.015 for -h,-l,-k 0.006 for -h,l,k 0.025 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 63682 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	14457	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.06% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN, MAN, NAG, P52, IMD

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	0.27	0/7222	0.46	0/9787
1	B	0.26	0/6995	0.45	0/9488
All	All	0.27	0/14217	0.46	0/19275

There are no bond length outliers.

There are no bond angle outliers.

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	7045	0	6981	282	0
1	B	6831	0	6698	374	0
2	A	56	0	50	0	0
2	B	28	0	25	3	0
3	A	42	0	39	0	0
3	B	28	0	26	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	B	50	0	43	4	0
6	A	36	0	36	3	0
6	B	36	0	35	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	10	0	10	0	0
8	A	207	0	0	6	0
8	B	86	0	0	0	0
All	All	14457	0	13943	658	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 23.

The worst 5 of 658 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:ALA:HB1	1:A:57:THR:HA	1.31	1.09
1:B:374:HIS:HE1	1:B:392:LYS:HG2	1.29	0.96
1:B:565:ARG:HD2	1:B:584:TYR:HE2	1.28	0.94
1:B:582:GLU:N	1:B:583:ARG:HB2	1.85	0.92
1:B:104:ALA:HB2	1:B:158:PRO:HD3	1.50	0.91

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	863/967 (89%)	771 (89%)	76 (9%)	16 (2%)	10	30
1	B	842/967 (87%)	701 (83%)	107 (13%)	34 (4%)	4	11
All	All	1705/1934 (88%)	1472 (86%)	183 (11%)	50 (3%)	6	18

5 of 50 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	119	ASN

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Mol	Chain	Res	Type
1	A	583	ARG
1	A	616	GLU
1	A	617	LYS
1	A	922	GLU

### 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	772/870 (89%)	699 (90%)	73 (10%)	11	28
1	B	733/870 (84%)	675 (92%)	58 (8%)	15	38
All	All	1505/1740 (86%)	1374 (91%)	131 (9%)	13	33

5 of 131 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	801	THR
1	B	58	ASN
1	B	767	ILE
1	A	825	LEU
1	A	877	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	927	HIS
1	B	203	GLN
1	B	860	HIS
1	B	58	ASN
1	B	301	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 ⓘ

10 carbohydrates are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
2	NAG	A	1001	1,2	14,14,15	0.55	0	15,19,21	0.86	1 (6%)
2	NAG	A	1002	2	14,14,15	0.46	0	15,19,21	1.00	2 (13%)
2	NAG	A	1003	1,2	14,14,15	0.54	0	15,19,21	0.88	1 (6%)
2	NAG	A	1004	2	14,14,15	0.50	0	15,19,21	0.95	1 (6%)
5	MAN	B	1001	5	11,11,12	0.56	0	14,15,17	2.14	4 (28%)
5	MAN	B	1002	5	11,11,12	0.53	0	14,15,17	2.11	3 (21%)
5	NAG	B	1003	1,5	14,14,15	0.47	0	15,19,21	1.99	3 (20%)
5	NAG	B	1004	5	14,14,15	0.52	0	15,19,21	1.50	1 (6%)
2	NAG	B	1005	1,2	14,14,15	0.51	0	15,19,21	0.75	0
2	NAG	B	1006	2	14,14,15	0.57	0	15,19,21	1.14	1 (6%)

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
2	NAG	A	1001	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1002	2	-	0/6/23/26	0/1/1/1
2	NAG	A	1003	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1004	2	-	0/6/23/26	0/1/1/1
5	MAN	B	1001	5	-	0/2/19/22	0/1/1/1
5	MAN	B	1002	5	-	0/2/19/22	0/1/1/1
5	NAG	B	1003	1,5	-	0/6/23/26	0/1/1/1
5	NAG	B	1004	5	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	1005	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	1006	2	-	0/6/23/26	0/1/1/1

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(°)
5	B	1003	NAG	C4-C3-C2	-3.90	105.16	111.23
5	B	1002	MAN	C2-C3-C4	-2.67	106.50	111.04
5	B	1002	MAN	C6-C5-C4	-2.51	106.82	113.02
2	A	1002	NAG	C2-N2-C7	-2.02	120.44	123.04
2	A	1003	NAG	C1-O5-C5	2.06	114.86	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1001	MAN	3	0
5	B	1002	MAN	2	0
5	B	1003	NAG	1	0
2	B	1005	NAG	3	0
2	B	1006	NAG	1	0

## 5.6 Ligand geometry

Of 11 ligands modelled in this entry, 2 are monoatomic - leaving 9 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	$\# Z  > 2$
3	NAG	A	1005	1	14,14,15	0.48	0	15,19,21	1.00	1 (6%)
3	NAG	A	1006	1	14,14,15	0.74	0	15,19,21	0.88	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAG	A	1007	1	14,14,15	0.46	0	15,19,21	0.91	1 (6%)
6	P52	A	1009	4	33,38,38	4.00	5 (15%)	31,53,53	2.46	8 (25%)
7	IMD	A	1010	-	3,5,5	0.53	0	4,5,5	0.72	0
7	IMD	A	1011	-	3,5,5	0.52	0	4,5,5	0.49	0
3	NAG	B	1007	1	14,14,15	0.54	0	15,19,21	0.77	0
3	NAG	B	1008	1	14,14,15	0.46	0	15,19,21	0.86	1 (6%)
6	P52	B	1010	4	33,38,38	4.00	5 (15%)	31,53,53	3.13	5 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	1005	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1006	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1007	1	-	0/6/23/26	0/1/1/1
6	P52	A	1009	4	-	0/28/36/36	0/3/3/3
7	IMD	A	1010	-	-	0/0/0/0	0/1/1/1
7	IMD	A	1011	-	-	0/0/0/0	0/1/1/1
3	NAG	B	1007	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1008	1	-	0/6/23/26	0/1/1/1
6	P52	B	1010	4	-	0/28/36/36	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1009	P52	P1-C11	-20.69	1.60	1.79
6	B	1010	P52	P1-C11	-20.61	1.60	1.79
6	B	1010	P52	C9-N1	-6.37	1.29	1.47
6	A	1009	P52	C9-N1	-6.32	1.29	1.47
6	B	1010	P52	P1-O1	-2.02	1.46	1.49

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	1010	P52	O4-C18-N4	-3.10	118.49	123.08
6	A	1009	P52	O4-C18-N4	-2.83	118.88	123.08
6	A	1009	P52	O3-C10-N2	-2.51	118.02	122.93
6	B	1010	P52	O3-C10-N2	-2.23	118.56	122.93
6	A	1009	P52	O2-P1-O1	-2.12	110.46	113.72



There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1009	P52	3	0
6	B	1010	P52	2	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](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	869/967 (89%)	0.02	20 (2%) 64 56	21, 48, 86, 115	2 (0%)
1	B	854/967 (88%)	0.80	118 (13%) 4 2	29, 84, 120, 144	0
All	All	1723/1934 (89%)	0.41	138 (8%) 15 9	21, 62, 112, 144	2 (0%)

The worst 5 of 138 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	640	TRP	12.1
1	B	570	VAL	8.9
1	B	559	LEU	8.4
1	B	687	LEU	7.5
1	B	603	HIS	6.6

### 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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	NAG	A	1002	14/15	0.88	0.21	1.32	62,80,91,93	0
2	NAG	A	1001	14/15	0.95	0.19	0.18	39,61,68,68	0
5	NAG	B	1004	14/15	0.90	0.15	0.01	48,71,91,97	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	B	1005	14/15	0.91	0.16	-0.34	67,85,101,103	0
5	NAG	B	1003	14/15	0.94	0.14	-0.43	36,53,63,63	0
2	NAG	A	1003	14/15	0.97	0.15	-0.62	40,47,62,64	0
2	NAG	A	1004	14/15	0.94	0.14	-	50,63,70,72	0
5	MAN	B	1002	11/12	0.70	0.33	-	91,109,129,132	0
2	NAG	B	1006	14/15	0.86	0.20	-	62,94,102,102	0
5	MAN	B	1001	11/12	0.83	0.17	-	70,86,98,107	0

## 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
6	P52	B	1010	36/36	0.95	0.32	2.43	33,57,88,90	4
6	P52	A	1009	36/36	0.95	0.31	2.24	25,38,60,66	3
7	IMD	A	1010	5/5	0.79	0.24	1.61	64,68,69,80	0
3	NAG	A	1005	14/15	0.94	0.17	0.26	65,78,82,84	0
4	ZN	B	1009	1/1	0.98	0.23	-0.11	47,47,47,47	0
4	ZN	A	1008	1/1	1.00	0.22	-0.12	25,25,25,25	0
7	IMD	A	1011	5/5	0.91	0.22	-0.24	57,60,69,70	0
3	NAG	B	1007	14/15	0.77	0.27	-	85,112,123,137	0
3	NAG	B	1008	14/15	0.83	0.29	-	79,109,118,122	0
3	NAG	A	1007	14/15	0.85	0.18	-	80,105,111,113	0
3	NAG	A	1006	14/15	0.88	0.27	-	76,88,106,106	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.