



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:07 PM GMT

PDB ID : 3SWW
Title : Crystal structure of human dpp-iv in complex with sa-(+)-3-(aminomethyl)-4-(2,4-dichlorophenyl)-6-(2-methoxyphenyl)-2-methyl-5h-pyrrolo[3,4-b]pyridin-7(6h)-one
Authors : Klei, H.E.
Deposited on : 2011-07-14
Resolution : 2.00 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

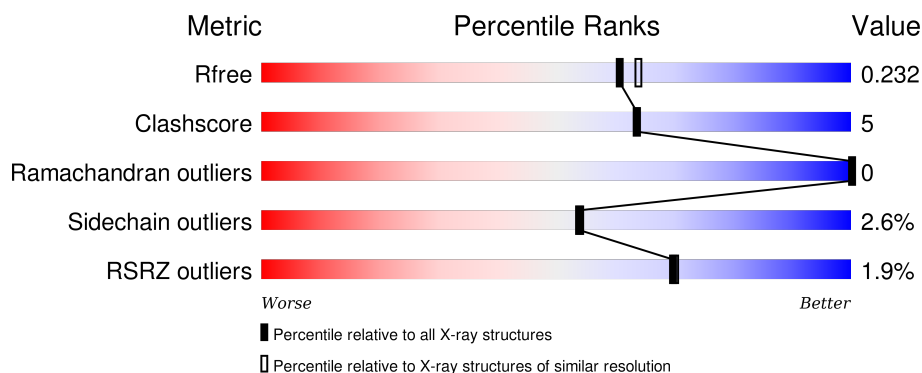
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

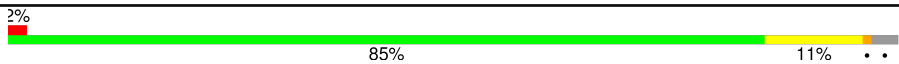

The reported resolution of this entry is 2.00 Å.

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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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 ≥ 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	753	
1	B	753	

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
2	NAG	A	1501	-	-	-	X
2	NAG	A	2191	-	-	-	X
2	NAG	A	5201	-	-	-	X
2	NAG	B	1501	-	-	-	X
2	NAG	B	2191	-	-	-	X
2	NAG	B	5201	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12465 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 Dipeptidyl peptidase 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	727	Total	C	N	O	S	0	0	0
			5896	3796	958	1116	26			
1	B	727	Total	C	N	O	S	0	0	0
			5892	3792	956	1118	26			

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	37	GLU	-	EXPRESSION TAG	UNP P27487
A	38	PHE	-	EXPRESSION TAG	UNP P27487
A	767	PRO	-	EXPRESSION TAG	UNP P27487
A	768	LEU	-	EXPRESSION TAG	UNP P27487
A	769	GLU	-	EXPRESSION TAG	UNP P27487
A	770	GLN	-	EXPRESSION TAG	UNP P27487
A	771	LYS	-	EXPRESSION TAG	UNP P27487
A	772	LEU	-	EXPRESSION TAG	UNP P27487
A	773	ILE	-	EXPRESSION TAG	UNP P27487
A	774	SER	-	EXPRESSION TAG	UNP P27487
A	775	GLU	-	EXPRESSION TAG	UNP P27487
A	776	GLU	-	EXPRESSION TAG	UNP P27487
A	777	ASP	-	EXPRESSION TAG	UNP P27487
A	778	LEU	-	EXPRESSION TAG	UNP P27487
A	779	ASN	-	EXPRESSION TAG	UNP P27487
A	780	SER	-	EXPRESSION TAG	UNP P27487
A	781	ALA	-	EXPRESSION TAG	UNP P27487
A	782	VAL	-	EXPRESSION TAG	UNP P27487
A	783	ASP	-	EXPRESSION TAG	UNP P27487
A	784	HIS	-	EXPRESSION TAG	UNP P27487
A	785	HIS	-	EXPRESSION TAG	UNP P27487
A	786	HIS	-	EXPRESSION TAG	UNP P27487
A	787	HIS	-	EXPRESSION TAG	UNP P27487
A	788	HIS	-	EXPRESSION TAG	UNP P27487
A	789	HIS	-	EXPRESSION TAG	UNP P27487

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Chain	Residue	Modelled	Actual	Comment	Reference
B	37	GLU	-	EXPRESSION TAG	UNP P27487
B	38	PHE	-	EXPRESSION TAG	UNP P27487
B	767	PRO	-	EXPRESSION TAG	UNP P27487
B	768	LEU	-	EXPRESSION TAG	UNP P27487
B	769	GLU	-	EXPRESSION TAG	UNP P27487
B	770	GLN	-	EXPRESSION TAG	UNP P27487
B	771	LYS	-	EXPRESSION TAG	UNP P27487
B	772	LEU	-	EXPRESSION TAG	UNP P27487
B	773	ILE	-	EXPRESSION TAG	UNP P27487
B	774	SER	-	EXPRESSION TAG	UNP P27487
B	775	GLU	-	EXPRESSION TAG	UNP P27487
B	776	GLU	-	EXPRESSION TAG	UNP P27487
B	777	ASP	-	EXPRESSION TAG	UNP P27487
B	778	LEU	-	EXPRESSION TAG	UNP P27487
B	779	ASN	-	EXPRESSION TAG	UNP P27487
B	780	SER	-	EXPRESSION TAG	UNP P27487
B	781	ALA	-	EXPRESSION TAG	UNP P27487
B	782	VAL	-	EXPRESSION TAG	UNP P27487
B	783	ASP	-	EXPRESSION TAG	UNP P27487
B	784	HIS	-	EXPRESSION TAG	UNP P27487
B	785	HIS	-	EXPRESSION TAG	UNP P27487
B	786	HIS	-	EXPRESSION TAG	UNP P27487
B	787	HIS	-	EXPRESSION TAG	UNP P27487
B	788	HIS	-	EXPRESSION TAG	UNP P27487
B	789	HIS	-	EXPRESSION TAG	UNP P27487

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C₈H₁₅NO₆).

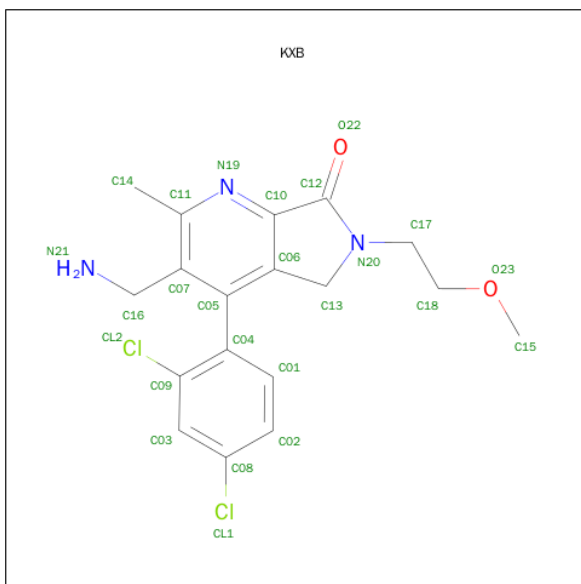


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1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

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

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

- Molecule 4 is 3-(AMINOMETHYL)-4-(2,4-DICHLOROPHENYL)-6-(2-METHOXYETHYL)-2-METHYL-5,6-DIHYDRO-7H-PYRROLO[3,4-B]PYRIDIN-7-ONE (three-letter code: KXB) (formula: C₁₈H₁₉Cl₂N₃O₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Cl	N	O	0	0
			25	18	2	3	2		
4	B	1	Total	C	Cl	N	O	0	0
			25	18	2	3	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	218	Total	O	0	0
			218	218		
5	B	213	Total	O	0	0
			213	213		

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.

- Chain A:
-
- 2% 85% 11%
- GLU
PHE
SER
R40
N51
L60
D65
H66
E73
V78
L90
E91
N92
S93
T94
F95
D96
E97
F98
G99
Y105
P109
I114
S127
Y135
L142
E145
E146
R147
W154
G161
H162
K163
N196
E206
Y211
S212
N219
G220
T221
- A224
Q227
P234
F268
T273
S278
T279
T280
N281
W305
Q308
I311
Q314
I319
Q320
N325
D326
I327
S333
S334
G335
R336
T341
A342
R343
T350
R358
F371
Y372
K373
Y381
R382
C385
I389
D390
T401
E452
V463
- E464
R471
C472
Y480
V486
D501
Q505
Q508
I517
E521
H533
F534
D535
K538
Y566
E571
I594
F601
Q612
K615
N621
K622
L640
G650
R658
W659
E660
Y661
Y662
D663
R669
E677
V726
G727
V728
Q731
- G741
I742
I751
W755
K760
L765
P766
PRU
LEU
GLU
GLN
LYS
LEU
ILE
SER
GLU
GLU
ASP
LEU
ASN
SER
ALA
VAL
ASP
HIS
HIS
HIS
HIS
HIS
HIS

- Chain B:
-
- 85% 11%
- GLU PHE SER R40 N81 L55 W62 I63 S64 D65 L69 E73 L77 V78 V88 F89 T94 D96 E97 F98 Y105 S108 I114 I148 G161 H162 K163 L164 E177 L180 L214 N219 G220 T221 A224 E237 D243 Y248
- R253 F268 T273 V279 T280 T288 A289 D302 Q308 Q314 Q320 D326 D331 E332 S333 S334 G335 R336 T350 I384 I389 D390 D393 V404 L415 R429 T443 V459 S460 F461 S462 K463 E464 K465 K466 Y467 L500 L504
- M509 L519 K523 K538 V546 V558 F559 R560 I594 Q612 F618 I626 W627 T636 L640 G650 I651 D663 R669 R684 E693 K696 V726 G727 V728 G741 I742 S756 K760 L765 F766 P766 L770 C771

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.53Å 67.93Å 423.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.16 – 2.00 47.16 – 2.00	Depositor EDS
% Data completeness (in resolution range)	84.8 (47.16-2.00) 84.8 (47.16-2.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.19 (at 2.00Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: DEV_613)	Depositor
R, R_{free}	0.197 , 0.234 0.197 , 0.232	Depositor DCC
R_{free} test set	5538 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	32.8	Xtriage
Anisotropy	0.392	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 37.9	EDS
Estimated twinning fraction	0.029 for k,h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 109958 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12465	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.75% 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, 0.375 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: KXB, 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	0.38	0/6068	0.54	0/8266
1	B	0.38	0/6064	0.55	0/8259
All	All	0.38	0/12132	0.54	0/16525

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	5896	0	5536	66	0
1	B	5892	0	5514	54	0
2	A	70	0	65	5	0
2	B	70	0	65	1	0
3	A	28	0	25	1	0
3	B	28	0	25	1	0
4	A	25	0	19	0	0
4	B	25	0	19	0	0
5	A	218	0	0	8	0
5	B	213	0	0	10	0
All	All	12465	0	11268	121	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 5.

The worst 5 of 121 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:B:162:HIS:HB3	5:B:800:HOH:O	1.58	1.00
1:A:508:GLN:HE21	1:A:533:HIS:CE1	1.85	0.95
1:A:319:ILE:HD12	1:A:319:ILE:H	1.32	0.93
1:A:508:GLN:HE21	1:A:533:HIS:HE1	1.15	0.92
1:B:219:ASN:HB2	1:B:308:GLN:OE1	1.80	0.81

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	725/753 (96%)	694 (96%)	31 (4%)	0	100	100
1	B	725/753 (96%)	698 (96%)	27 (4%)	0	100	100
All	All	1450/1506 (96%)	1392 (96%)	58 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	631/677 (93%)	612 (97%)	19 (3%)	48	47
1	B	629/677 (93%)	615 (98%)	14 (2%)	60	62
All	All	1260/1354 (93%)	1227 (97%)	33 (3%)	54	54

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	621	ASN
1	A	731	GLN
1	B	612	GLN
1	A	622	LYS
1	A	677	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	592	HIS
1	A	748	HIS
1	B	169	ASN
1	A	586	GLN
1	B	383	HIS

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 ⓘ

4 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	$\# Z > 2$
3	NAG	A	2291	1,3	14,14,15	0.53	0	15,19,21	0.90	1 (6%)
3	NAG	A	2292	3	14,14,15	0.45	0	15,19,21	1.16	1 (6%)
3	NAG	B	2291	1,3	14,14,15	0.50	0	15,19,21	0.89	0
3	NAG	B	2292	3	14,14,15	0.49	0	15,19,21	1.13	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
3	NAG	A	2291	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	2292	3	-	0/6/23/26	0/1/1/1
3	NAG	B	2291	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	2292	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2291	NAG	C2-N2-C7	-2.32	120.06	123.04
3	B	2292	NAG	C1-O5-C5	2.74	115.73	112.25
3	A	2292	NAG	C1-O5-C5	3.53	116.73	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2291	NAG	1	0
3	A	2292	NAG	1	0
3	B	2291	NAG	1	0
3	B	2292	NAG	1	0

5.6 Ligand geometry ⓘ

12 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	KXB	A	1	-	27,27,27	1.15	2 (7%)	26,39,39	0.99	2 (7%)
2	NAG	A	1501	1	14,14,15	0.50	0	15,19,21	1.01	1 (6%)
2	NAG	A	2191	1	14,14,15	0.66	1 (7%)	15,19,21	1.40	1 (6%)
2	NAG	A	2811	-	14,14,15	0.52	0	15,19,21	0.88	0
2	NAG	A	5201	1	14,14,15	0.36	0	15,19,21	1.76	3 (20%)
2	NAG	A	851	1	14,14,15	0.62	0	15,19,21	0.84	0
2	NAG	B	1501	1	14,14,15	0.61	0	15,19,21	0.83	1 (6%)
4	KXB	B	2	-	27,27,27	1.30	4 (14%)	26,39,39	0.92	1 (3%)
2	NAG	B	2191	1	14,14,15	0.59	0	15,19,21	1.01	1 (6%)
2	NAG	B	5201	1	14,14,15	0.55	0	15,19,21	1.15	1 (6%)
2	NAG	B	851	1	14,14,15	0.69	0	15,19,21	1.20	2 (13%)
2	NAG	B	921	1	14,14,15	0.42	0	15,19,21	1.28	2 (13%)

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	KXB	A	1	-	-	0/9/22/22	0/3/3/3
2	NAG	A	1501	1	-	0/6/23/26	0/1/1/1
2	NAG	A	2191	1	-	0/6/23/26	0/1/1/1
2	NAG	A	2811	-	-	0/6/23/26	0/1/1/1
2	NAG	A	5201	1	-	0/6/23/26	0/1/1/1
2	NAG	A	851	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1501	1	-	0/6/23/26	0/1/1/1
4	KXB	B	2	-	-	0/9/22/22	0/3/3/3
2	NAG	B	2191	1	-	0/6/23/26	0/1/1/1
2	NAG	B	5201	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	851	1	-	0/6/23/26	0/1/1/1
2	NAG	B	921	1	-	0/6/23/26	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	2	KXB	C04-C05	-2.91	1.46	1.50
2	A	2191	NAG	C1-C2	2.02	1.55	1.52
4	A	1	KXB	C11-N19	2.22	1.37	1.34
4	B	2	KXB	C17-C18	2.47	1.58	1.50
4	B	2	KXB	C11-N19	2.80	1.38	1.34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	921	NAG	C2-N2-C7	-2.69	119.59	123.04
2	B	851	NAG	C2-N2-C7	-2.30	120.09	123.04
4	A	1	KXB	C09-C03-C08	-2.28	116.16	118.69
2	A	5201	NAG	C6-C5-C4	-2.14	107.74	113.02
4	A	1	KXB	C14-C11-N19	-2.12	112.99	116.34

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1501	NAG	1	0
2	A	2811	NAG	4	0
2	B	5201	NAG	1	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, 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	727/753 (96%)	0.03	17 (2%) 64 64	23, 33, 56, 78	0
1	B	727/753 (96%)	0.01	11 (1%) 76 77	23, 34, 55, 77	0
All	All	1454/1506 (96%)	0.02	28 (1%) 70 70	23, 33, 56, 78	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	765	LEU	5.8
1	B	766	PRO	4.3
1	B	765	LEU	4.1
1	A	766	PRO	4.0
1	A	280	THR	3.6

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, 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	LLDF	B-factors(Å ²)	Q<0.9
3	NAG	B	2291	14/15	0.93	0.14	0.95	37,44,52,56	0
3	NAG	A	2291	14/15	0.92	0.13	0.58	37,45,53,57	0
3	NAG	A	2292	14/15	0.76	0.26	-	54,61,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	B	2292	14/15	0.84	0.33	-	53,66,72,75	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, 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	LLDF	B-factors(\AA^2)	Q<0.9
2	NAG	A	2191	14/15	0.71	0.40	8.30	49,61,67,68	0
2	NAG	B	2191	14/15	0.62	0.41	7.64	58,66,70,70	0
2	NAG	B	5201	14/15	0.72	0.29	5.87	49,65,71,71	0
2	NAG	B	1501	14/15	0.78	0.23	4.88	40,65,77,82	0
2	NAG	A	5201	14/15	0.82	0.29	3.61	47,64,69,69	0
2	NAG	A	1501	14/15	0.89	0.21	3.46	55,58,62,63	0
4	KXB	B	2	25/25	0.94	0.18	1.78	23,33,43,50	0
4	KXB	A	1	25/25	0.94	0.17	1.30	25,31,40,44	0
2	NAG	B	851	14/15	0.96	0.09	-0.57	31,35,40,41	0
2	NAG	A	851	14/15	0.96	0.08	-1.02	30,34,36,38	0
2	NAG	A	2811	14/15	0.85	0.28	-	61,66,69,73	0
2	NAG	B	921	14/15	0.88	0.24	-	60,62,66,68	0

6.5 Other polymers [i](#)

There are no such residues in this entry.