



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:45 PM GMT

PDB ID : 4G1F
Title : Crystal Structure of human Dipeptidyl Peptidase IV in complex with a pyridopyrimidinedione analogue
Authors : Skene, R.J.; Gwaltney, S.L.
Deposited on : 2012-07-10
Resolution : 2.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

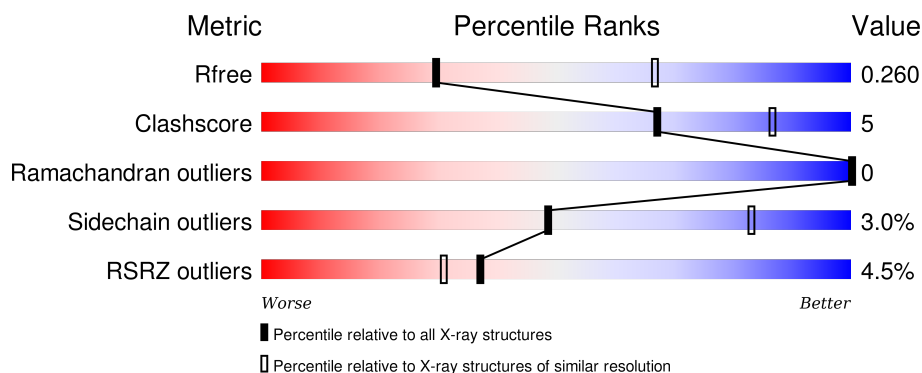
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (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 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	740	<div> <div>4%</div> <div>85% 12% ..</div> </div>
1	B	740	<div> <div>2%</div> <div>81% 16% ..</div> </div>
1	C	740	<div> <div>6%</div> <div>83% 14% ..</div> </div>
1	D	740	<div> <div>5%</div> <div>83% 12% ..</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 24443 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	724	Total	C	N	O	S	0	1	0
			5935	3812	977	1120	26			
1	B	727	Total	C	N	O	S	0	0	0
			5945	3818	977	1124	26			
1	C	722	Total	C	N	O	S	0	0	0
			5913	3798	972	1117	26			
1	D	715	Total	C	N	O	S	0	0	0
			5855	3762	964	1103	26			

There are 48 discrepancies between the modelled and reference sequences:

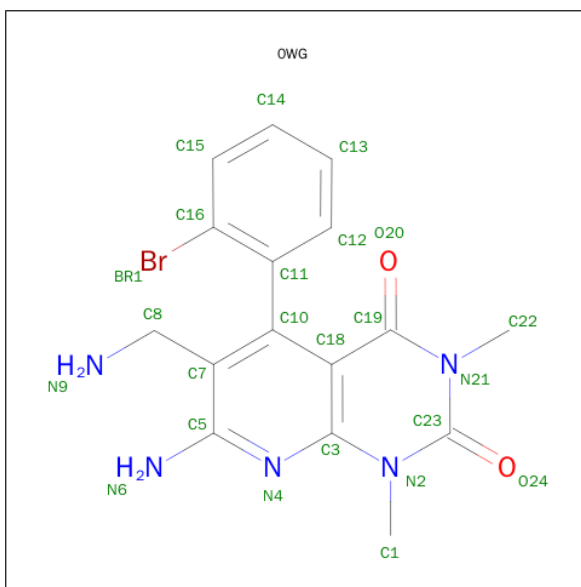
Chain	Residue	Modelled	Actual	Comment	Reference
A	27	ALA	-	EXPRESSION TAG	UNP P27487
A	28	ASP	-	EXPRESSION TAG	UNP P27487
A	29	PRO	-	EXPRESSION TAG	UNP P27487
A	30	GLY	-	EXPRESSION TAG	UNP P27487
A	31	GLY	-	EXPRESSION TAG	UNP P27487
A	32	SER	-	EXPRESSION TAG	UNP P27487
A	33	HIS	-	EXPRESSION TAG	UNP P27487
A	34	HIS	-	EXPRESSION TAG	UNP P27487
A	35	HIS	-	EXPRESSION TAG	UNP P27487
A	36	HIS	-	EXPRESSION TAG	UNP P27487
A	37	HIS	-	EXPRESSION TAG	UNP P27487
A	38	HIS	-	EXPRESSION TAG	UNP P27487
B	27	ALA	-	EXPRESSION TAG	UNP P27487
B	28	ASP	-	EXPRESSION TAG	UNP P27487
B	29	PRO	-	EXPRESSION TAG	UNP P27487
B	30	GLY	-	EXPRESSION TAG	UNP P27487
B	31	GLY	-	EXPRESSION TAG	UNP P27487
B	32	SER	-	EXPRESSION TAG	UNP P27487
B	33	HIS	-	EXPRESSION TAG	UNP P27487
B	34	HIS	-	EXPRESSION TAG	UNP P27487
B	35	HIS	-	EXPRESSION TAG	UNP P27487

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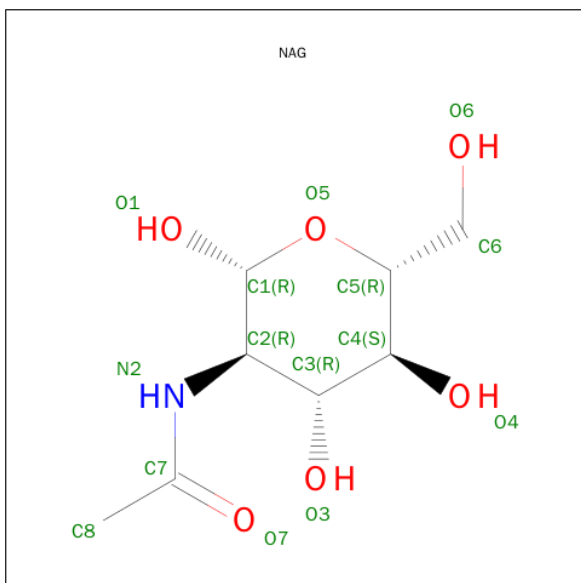
Chain	Residue	Modelled	Actual	Comment	Reference
B	36	HIS	-	EXPRESSION TAG	UNP P27487
B	37	HIS	-	EXPRESSION TAG	UNP P27487
B	38	HIS	-	EXPRESSION TAG	UNP P27487
C	27	ALA	-	EXPRESSION TAG	UNP P27487
C	28	ASP	-	EXPRESSION TAG	UNP P27487
C	29	PRO	-	EXPRESSION TAG	UNP P27487
C	30	GLY	-	EXPRESSION TAG	UNP P27487
C	31	GLY	-	EXPRESSION TAG	UNP P27487
C	32	SER	-	EXPRESSION TAG	UNP P27487
C	33	HIS	-	EXPRESSION TAG	UNP P27487
C	34	HIS	-	EXPRESSION TAG	UNP P27487
C	35	HIS	-	EXPRESSION TAG	UNP P27487
C	36	HIS	-	EXPRESSION TAG	UNP P27487
C	37	HIS	-	EXPRESSION TAG	UNP P27487
C	38	HIS	-	EXPRESSION TAG	UNP P27487
D	27	ALA	-	EXPRESSION TAG	UNP P27487
D	28	ASP	-	EXPRESSION TAG	UNP P27487
D	29	PRO	-	EXPRESSION TAG	UNP P27487
D	30	GLY	-	EXPRESSION TAG	UNP P27487
D	31	GLY	-	EXPRESSION TAG	UNP P27487
D	32	SER	-	EXPRESSION TAG	UNP P27487
D	33	HIS	-	EXPRESSION TAG	UNP P27487
D	34	HIS	-	EXPRESSION TAG	UNP P27487
D	35	HIS	-	EXPRESSION TAG	UNP P27487
D	36	HIS	-	EXPRESSION TAG	UNP P27487
D	37	HIS	-	EXPRESSION TAG	UNP P27487
D	38	HIS	-	EXPRESSION TAG	UNP P27487

- Molecule 2 is 7-AMINO-6-(AMINOMETHYL)-5-(2-BROMOPHENYL)-1,3-DIMETHYLPYRIDO[2,3-D]PYRIMIDINE-2,4(1H,3H)-DIONE (three-letter code: 0WG) (formula: C₁₆H₁₆BrN₅O₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	Br	C	N	O	0	0
			24	1	16	5	2		
2	B	1	Total	Br	C	N	O	0	0
			24	1	16	5	2		
2	C	1	Total	Br	C	N	O	0	0
			24	1	16	5	2		
2	D	1	Total	Br	C	N	O	0	0
			24	1	16	5	2		

- 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	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	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	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	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 a polymer of unknown type called SUGAR (2-MER).

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	115	Total	O	0	0
			115	115		

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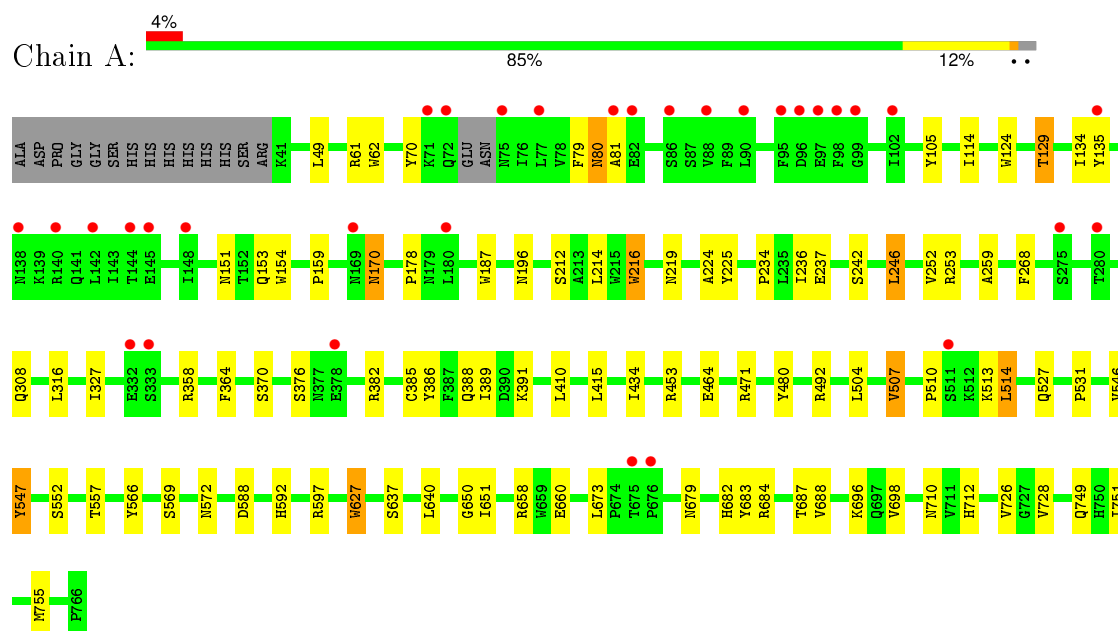
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	112	Total 112	O 112	0	0
5	C	91	Total 91	O 91	0	0
5	D	73	Total 73	O 73	0	0

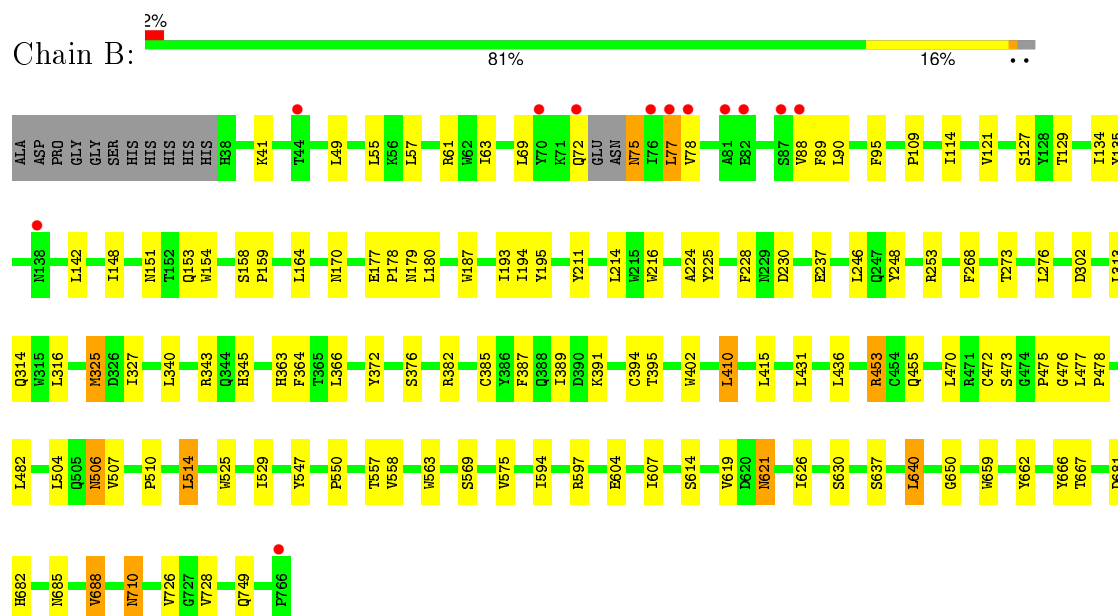
3 Residue-property plots [i](#)

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: Dipeptidyl peptidase 4



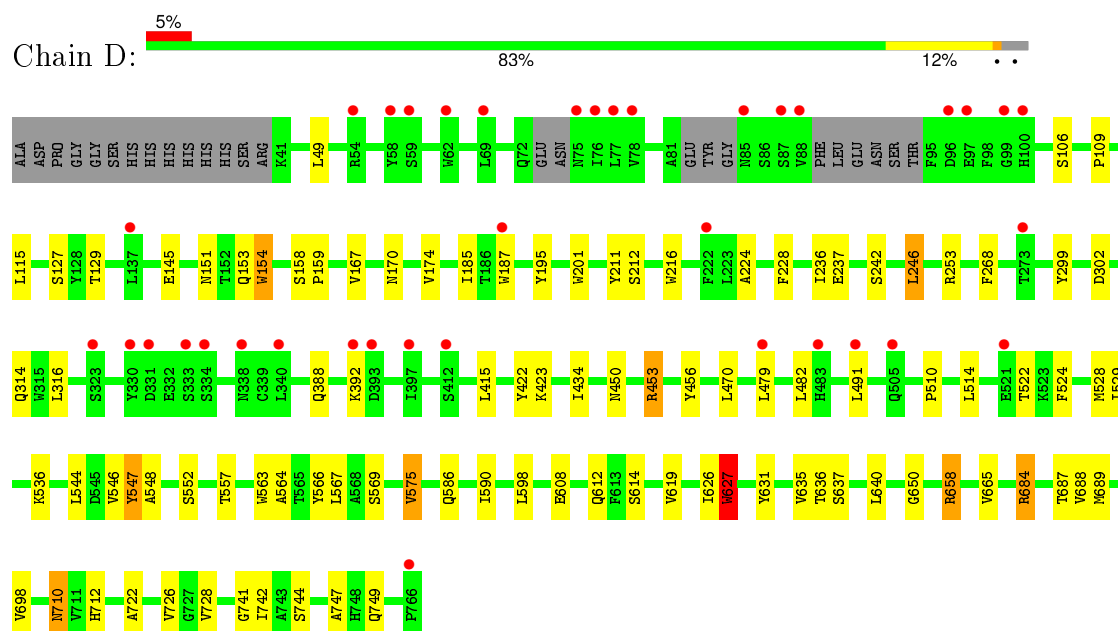
- Molecule 1: Dipeptidyl peptidase 4



- Molecule 1: Dipeptidyl peptidase 4



- Molecule 1: Dipeptidyl peptidase 4



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	121.62Å 121.36Å 143.26Å 90.00° 114.63° 90.00°	Depositor
Resolution (Å)	40.00 – 2.90 40.01 – 2.90	Depositor EDS
% Data completeness (in resolution range)	96.4 (40.00-2.90) 96.5 (40.01-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.60 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.7.0025	Depositor
R, R_{free}	0.207 , 0.259 0.207 , 0.260	Depositor DCC
R_{free} test set	4185 reflections (5.42%)	DCC
Wilson B-factor (Å ²)	39.4	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 37.7	EDS
Estimated twinning fraction	0.011 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 81297 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	24443	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.01% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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: 0WG, 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	0.50	5/6111 (0.1%)	0.54	0/8311
1	B	0.50	4/6116 (0.1%)	0.55	1/8318 (0.0%)
1	C	0.51	6/6082 (0.1%)	0.55	0/8270
1	D	0.51	4/6022 (0.1%)	0.54	0/8187
All	All	0.51	19/24331 (0.1%)	0.54	1/33086 (0.0%)

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	124	TRP	CD2-CE2	5.22	1.47	1.41
1	C	629	TRP	CD2-CE2	5.16	1.47	1.41
1	D	627	TRP	CD2-CE2	5.16	1.47	1.41
1	C	187	TRP	CD2-CE2	5.15	1.47	1.41
1	C	154	TRP	CD2-CE2	5.13	1.47	1.41
1	B	563	TRP	CD2-CE2	5.12	1.47	1.41
1	D	563	TRP	CD2-CE2	5.11	1.47	1.41
1	C	315	TRP	CD2-CE2	5.09	1.47	1.41
1	A	62	TRP	CD2-CE2	5.09	1.47	1.41
1	B	187	TRP	CD2-CE2	5.06	1.47	1.41
1	C	168	TRP	CD2-CE2	5.05	1.47	1.41
1	D	187	TRP	CD2-CE2	5.05	1.47	1.41
1	C	305	TRP	CD2-CE2	5.03	1.47	1.41
1	B	402	TRP	CD2-CE2	5.02	1.47	1.41
1	A	627	TRP	CD2-CE2	5.02	1.47	1.41
1	B	154	TRP	CD2-CE2	5.02	1.47	1.41
1	D	154	TRP	CD2-CE2	5.02	1.47	1.41
1	A	187	TRP	CD2-CE2	5.01	1.47	1.41
1	A	216	TRP	CD2-CE2	5.00	1.47	1.41

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	415	LEU	CA-CB-CG	5.72	128.46	115.30

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	5935	0	5657	52	0
1	B	5945	0	5658	69	0
1	C	5913	0	5638	57	0
1	D	5855	0	5587	51	0
2	A	24	0	16	0	0
2	B	24	0	16	1	0
2	C	24	0	16	1	0
2	D	24	0	16	0	0
3	A	56	0	52	0	0
3	B	56	0	52	0	0
3	C	28	0	26	0	0
3	D	28	0	26	0	0
4	A	56	0	50	0	0
4	B	28	0	25	0	0
4	C	28	0	25	0	0
4	D	28	0	25	0	0
5	A	115	0	0	1	0
5	B	112	0	0	0	0
5	C	91	0	0	0	0
5	D	73	0	0	0	0
All	All	24443	0	22885	226	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.

All (226) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:684:ARG:HG3	1:D:684:ARG:HH21	1.25	0.97
1:B:63:ILE:HD11	1:B:69:LEU:HG	1.43	0.97
1:C:343:ARG:HD2	1:C:389:ILE:HG22	1.47	0.96
1:C:153:GLN:HE22	1:C:170:ASN:H	1.16	0.89
1:A:153:GLN:HE22	1:A:170:ASN:H	1.25	0.82
1:A:637:SER:HB3	1:A:688:VAL:HG21	1.65	0.79
1:B:327:ILE:HD13	1:B:389:ILE:HG13	1.65	0.79
1:B:153:GLN:HE22	1:B:170:ASN:H	1.30	0.78
1:B:114:ILE:HG23	1:B:135:TYR:HB3	1.68	0.76
1:D:153:GLN:HE22	1:D:170:ASN:H	1.34	0.75
1:A:410:LEU:HD13	1:A:415:LEU:HD23	1.68	0.75
1:A:242:SER:HB3	1:A:246:LEU:HD12	1.70	0.74
1:B:640:LEU:HD21	1:B:650:GLY:HA3	1.71	0.71
1:A:61:ARG:HG3	1:A:61:ARG:HH11	1.55	0.68
1:C:343:ARG:HD2	1:C:389:ILE:CG2	2.22	0.68
1:A:114:ILE:HG23	1:A:135:TYR:HB3	1.76	0.67
1:D:658:ARG:HB2	1:D:687:THR:HG22	1.75	0.67
1:D:237:GLU:HG2	1:D:253:ARG:HG2	1.77	0.67
1:C:129:THR:HG23	1:C:151:ASN:HA	1.75	0.66
1:A:253:ARG:HH21	1:B:253:ARG:HH21	1.44	0.65
1:D:684:ARG:HG3	1:D:684:ARG:NH2	2.01	0.65
1:A:531:PRO:HB3	1:A:572:ASN:HD22	1.63	0.63
1:A:726:VAL:HG23	1:A:728:VAL:HG23	1.80	0.63
1:A:640:LEU:HD11	1:A:650:GLY:HA3	1.81	0.63
1:B:237:GLU:HG2	1:B:253:ARG:HG2	1.81	0.63
1:C:201:TRP:HZ2	1:C:710:ASN:HA	1.64	0.62
1:A:170:ASN:N	1:A:170:ASN:HD22	1.98	0.61
1:D:726:VAL:HG23	1:D:728:VAL:HG23	1.83	0.61
1:D:529:ILE:HB	1:D:575:VAL:HG13	1.83	0.60
1:C:109:PRO:HG2	1:C:158:SER:O	2.02	0.59
1:D:453:ARG:HH21	1:D:479:LEU:HB2	1.69	0.58
1:D:129:THR:HG23	1:D:151:ASN:HA	1.86	0.58
1:C:696:LYS:HG3	1:C:728:VAL:HG22	1.85	0.58
1:C:114:ILE:HG23	1:C:135:TYR:HB3	1.83	0.58
1:B:637:SER:HB3	1:B:688:VAL:HG21	1.84	0.58
1:D:640:LEU:HB3	1:D:698:VAL:HG21	1.87	0.57
1:C:201:TRP:CZ2	1:C:710:ASN:HA	2.38	0.57
1:D:510:PRO:HD3	1:D:569:SER:HB2	1.87	0.57
1:D:302:ASP:HB3	1:D:314:GLN:HB2	1.86	0.57
1:A:49:LEU:HD22	1:A:749:GLN:HA	1.87	0.57
1:C:49:LEU:HD22	1:C:749:GLN:HA	1.87	0.57
1:C:510:PRO:HD3	1:C:569:SER:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:364:PHE:HE2	1:B:389:ILE:HD11	1.70	0.56
1:B:109:PRO:HG2	1:B:158:SER:O	2.05	0.56
1:B:614:SER:HA	1:B:619:VAL:HB	1.87	0.56
1:A:658:ARG:HB2	1:A:687:THR:HG22	1.88	0.56
1:B:681:ASP:O	1:B:685:ASN:HB2	2.07	0.55
1:D:174:VAL:HG23	1:D:185:ILE:HD11	1.88	0.55
1:D:640:LEU:HD11	1:D:650:GLY:HA3	1.90	0.54
1:B:630:SER:HB2	2:B:800:OWG:O20	2.06	0.54
1:B:504:LEU:HA	1:B:507:VAL:HG12	1.89	0.54
1:D:201:TRP:CZ2	1:D:710:ASN:HA	2.42	0.54
1:B:314:GLN:HG2	1:B:325:MET:HB2	1.90	0.54
1:C:726:VAL:HG23	1:C:728:VAL:HG23	1.90	0.54
1:B:302:ASP:HB3	1:B:314:GLN:HB2	1.90	0.54
1:A:224:ALA:HB1	1:A:268:PHE:CZ	2.43	0.53
1:C:129:THR:HG21	1:C:151:ASN:HD22	1.72	0.53
1:D:637:SER:HB3	1:D:688:VAL:HG21	1.90	0.53
1:A:80:ASN:HD22	1:A:81:ALA:N	2.06	0.53
1:B:177:GLU:HB2	1:B:180:LEU:HD12	1.90	0.53
1:C:640:LEU:HD11	1:C:650:GLY:HA3	1.91	0.53
1:A:129:THR:HG21	1:A:151:ASN:HD22	1.73	0.52
1:B:129:THR:HG23	1:B:151:ASN:HA	1.92	0.52
1:C:327:ILE:HD13	1:C:389:ILE:HD12	1.92	0.52
1:D:456:TYR:HB2	1:D:557:THR:OG1	2.08	0.52
1:B:325:MET:HG2	1:B:345:HIS:HB2	1.92	0.52
1:D:614:SER:HA	1:D:619:VAL:HB	1.92	0.52
1:D:109:PRO:HG2	1:D:158:SER:O	2.09	0.52
1:A:640:LEU:HB3	1:A:698:VAL:HG21	1.92	0.52
1:D:224:ALA:HB1	1:D:268:PHE:CZ	2.45	0.52
1:D:564:ALA:HA	1:D:567:LEU:HD12	1.92	0.52
1:A:388:GLN:HB2	1:A:391:LYS:HB2	1.91	0.51
1:B:340:LEU:HD13	1:B:343:ARG:HE	1.74	0.51
1:C:237:GLU:HG2	1:C:253:ARG:HG2	1.92	0.51
1:D:159:PRO:HD3	1:D:216:TRP:HB3	1.92	0.51
1:B:506:ASN:HB2	1:C:440:THR:HG23	1.93	0.51
1:A:219:ASN:HB3	1:A:308:GLN:HE22	1.75	0.51
1:C:164:LEU:HB3	1:C:175:LYS:HB2	1.93	0.51
1:D:546:VAL:HG12	1:D:627:TRP:O	2.11	0.51
1:B:510:PRO:HD3	1:B:569:SER:HB2	1.92	0.51
1:D:684:ARG:CG	1:D:684:ARG:HH21	2.11	0.50
1:C:176:ILE:HD11	1:C:276:LEU:HD12	1.93	0.50
1:A:684:ARG:NH1	5:A:968:HOH:O	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:49:LEU:HB3	1:B:749:GLN:HG2	1.93	0.50
1:C:529:ILE:HB	1:C:575:VAL:HG13	1.94	0.50
1:B:597:ARG:HH11	1:B:682:HIS:HB2	1.77	0.50
1:B:193:ILE:HG22	1:B:194:ILE:HG12	1.95	0.49
1:D:242:SER:HB3	1:D:246:LEU:HD12	1.93	0.49
1:C:498:SER:O	1:C:502:LYS:HG2	2.11	0.49
1:C:429:ARG:HB2	1:C:457:TYR:H	1.78	0.49
1:C:115:LEU:HD11	1:C:132:TYR:HB3	1.95	0.49
1:D:159:PRO:HD3	1:D:216:TRP:CB	2.42	0.48
1:C:106:SER:HB3	1:C:115:LEU:HB3	1.95	0.48
1:D:586:GLN:HB3	1:D:590:ILE:HD12	1.94	0.48
1:B:159:PRO:HD3	1:B:216:TRP:HB3	1.95	0.48
1:C:236:ILE:HG12	1:C:712:HIS:CD2	2.48	0.48
1:D:626:ILE:HG23	1:D:636:THR:HG23	1.95	0.48
1:A:159:PRO:HD3	1:A:216:TRP:CB	2.44	0.48
1:D:453:ARG:NH2	1:D:479:LEU:HB2	2.29	0.48
1:B:529:ILE:HB	1:B:575:VAL:HG13	1.95	0.48
1:C:626:ILE:O	1:C:650:GLY:HA2	2.14	0.47
1:C:554:LYS:HB3	1:C:577:SER:HB3	1.96	0.47
1:C:526:TYR:HB3	1:C:578:PHE:HD1	1.78	0.47
1:C:242:SER:HB3	1:C:246:LEU:HD12	1.97	0.47
1:B:726:VAL:HG23	1:B:728:VAL:HG23	1.96	0.47
1:C:148:ILE:HD11	1:C:164:LEU:HD21	1.96	0.47
1:D:415:LEU:HB3	1:D:434:ILE:HG23	1.97	0.47
1:B:453:ARG:HB2	1:B:476:GLY:HA3	1.96	0.47
1:D:684:ARG:CG	1:D:684:ARG:NH2	2.74	0.47
1:A:514:LEU:HD12	1:A:557:THR:HG22	1.97	0.47
1:D:236:ILE:HG12	1:D:712:HIS:CD2	2.50	0.47
1:A:214:LEU:HD23	1:A:225:TYR:HB3	1.97	0.47
1:A:513:LYS:O	1:A:527:GLN:HA	2.15	0.47
1:D:689:MET:HG3	1:D:722:ALA:HB2	1.97	0.47
1:C:314:GLN:HG2	1:C:325:MET:HB2	1.95	0.46
1:C:167:VAL:HG11	1:C:198:ILE:HG12	1.98	0.46
1:A:376:SER:HA	1:A:382:ARG:HA	1.96	0.46
1:C:640:LEU:HB3	1:C:698:VAL:HG21	1.96	0.46
1:B:49:LEU:HD22	1:B:749:GLN:HA	1.97	0.46
1:A:134:ILE:HG21	1:A:178:PRO:HB3	1.98	0.46
1:B:273:THR:HA	1:B:276:LEU:HG	1.98	0.46
1:B:364:PHE:CE2	1:B:389:ILE:HD11	2.49	0.46
1:B:127:SER:HB3	1:B:211:TYR:CD2	2.50	0.46
1:D:201:TRP:HZ2	1:D:710:ASN:HA	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:715:GLN:O	1:C:719:ILE:HG13	2.16	0.46
1:C:224:ALA:HB1	1:C:268:PHE:CZ	2.51	0.45
1:A:415:LEU:HB3	1:A:434:ILE:HG23	1.98	0.45
1:C:314:GLN:NE2	1:C:362:PRO:HD3	2.32	0.45
1:C:658:ARG:HH12	1:C:684:ARG:HE	1.63	0.45
1:A:129:THR:HG23	1:A:151:ASN:HA	1.97	0.45
1:C:630:SER:HB2	2:C:800:OWG:O20	2.16	0.45
1:D:127:SER:HB3	1:D:211:TYR:CD2	2.51	0.45
1:A:546:VAL:HG12	1:A:627:TRP:O	2.16	0.45
1:B:550:PRO:HD2	1:B:666:TYR:OH	2.16	0.45
1:B:78:VAL:HG23	1:B:89:PHE:HB2	1.99	0.45
1:B:376:SER:HA	1:B:382:ARG:HA	1.98	0.44
1:A:627:TRP:HB2	1:A:651:ILE:HB	1.99	0.44
1:C:134:ILE:HD13	1:C:178:PRO:HB3	1.99	0.44
1:B:659:TRP:HB3	1:B:667:THR:HG21	1.99	0.44
1:C:710:ASN:HD22	1:C:710:ASN:C	2.21	0.44
1:C:388:GLN:HB2	1:C:391:LYS:HG2	1.98	0.44
1:A:61:ARG:CG	1:A:61:ARG:HH11	2.28	0.44
1:A:327:ILE:HG12	1:A:389:ILE:HD12	2.00	0.44
1:D:49:LEU:HD22	1:D:749:GLN:HA	1.98	0.44
1:B:514:LEU:HD22	1:B:525:TRP:HE3	1.82	0.44
1:C:256:TYR:CZ	1:C:663:ASP:HB3	2.53	0.44
1:B:472:CYS:O	1:B:478:PRO:HA	2.18	0.44
1:C:154:TRP:CE2	1:C:212:SER:HB3	2.53	0.44
1:D:482:LEU:HD22	1:D:491:LEU:HD12	1.98	0.44
1:B:504:LEU:HA	1:B:507:VAL:CG1	2.48	0.44
1:A:364:PHE:HE2	1:A:389:ILE:HD11	1.82	0.44
1:D:106:SER:HB3	1:D:115:LEU:HB3	2.00	0.44
1:B:90:LEU:HD21	1:B:95:PHE:HE2	1.83	0.44
1:A:751:ILE:O	1:A:755:MET:HG3	2.18	0.43
1:B:77:LEU:HD12	1:B:88:VAL:HG22	1.99	0.43
1:C:293:MET:CE	1:C:324:VAL:HG12	2.48	0.43
1:B:614:SER:HB2	1:B:621:ASN:HD22	1.83	0.43
1:C:48:TYR:CE1	1:C:562:ASN:HA	2.53	0.43
1:B:148:ILE:HD11	1:B:164:LEU:HD21	2.01	0.43
1:B:135:TYR:HD1	1:B:142:LEU:HD13	1.84	0.43
1:C:162:HIS:NE2	1:C:177:GLU:OE1	2.51	0.43
1:A:236:ILE:HG12	1:A:712:HIS:CD2	2.54	0.43
1:C:49:LEU:HB3	1:C:749:GLN:HG2	2.00	0.43
1:D:154:TRP:CE2	1:D:212:SER:HB3	2.54	0.43
1:A:696:LYS:HG3	1:A:728:VAL:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:134:ILE:HD13	1:B:178:PRO:HB3	2.01	0.42
1:D:547:TYR:CD2	1:D:552:SER:HB2	2.54	0.42
1:B:55:LEU:HD22	1:B:478:PRO:HG2	2.00	0.42
1:B:455:GLN:HB2	1:B:475:PRO:HD3	2.00	0.42
1:B:431:LEU:HD22	1:B:470:LEU:HD21	2.01	0.42
1:A:259:ALA:HB3	1:A:660:GLU:HA	2.02	0.42
1:D:195:TYR:HB2	1:D:228:PHE:HB2	2.01	0.42
1:B:387:PHE:CD1	1:B:394:CYS:HB3	2.55	0.42
1:A:679:ASN:O	1:A:683:TYR:HD2	2.02	0.42
1:B:473:SER:HB3	1:B:558:VAL:HG13	2.00	0.42
1:B:224:ALA:HB1	1:B:268:PHE:CZ	2.55	0.42
1:A:170:ASN:O	1:A:196:ASN:HB2	2.19	0.42
1:A:370:SER:HB3	1:A:386:TYR:CE2	2.54	0.42
1:B:626:ILE:O	1:B:650:GLY:HA2	2.19	0.42
1:A:234:PRO:HB2	1:B:248:TYR:CZ	2.55	0.42
1:B:134:ILE:HG21	1:B:178:PRO:HB3	2.00	0.42
1:D:598:LEU:HG	1:D:631:TYR:OH	2.20	0.42
1:B:604:GLU:HA	1:B:607:ILE:HD12	2.02	0.41
1:C:170:ASN:N	1:C:170:ASN:HD22	2.18	0.41
1:C:172:ILE:HG22	1:C:185:ILE:HD12	2.02	0.41
1:B:72:GLN:HB2	1:B:75:ASN:HB2	2.01	0.41
1:B:195:TYR:HB2	1:B:228:PHE:HB2	2.02	0.41
1:C:285:ILE:HG21	1:C:336:ARG:HA	2.01	0.41
1:C:123:GLN:HB3	1:C:127:SER:OG	2.21	0.41
1:B:121:VAL:HB	1:B:129:THR:HB	2.00	0.41
1:D:608:GLU:O	1:D:612:GLN:HG2	2.19	0.41
1:C:669:ARG:HD2	1:C:670:TYR:CZ	2.54	0.41
1:D:153:GLN:NE2	1:D:167:VAL:HG12	2.35	0.41
1:A:471:ARG:HG3	1:A:480:TYR:CE1	2.55	0.41
1:B:363:HIS:HB3	1:B:410:LEU:HD22	2.03	0.41
1:B:214:LEU:HD23	1:B:225:TYR:HB3	2.03	0.41
1:B:372:TYR:OH	1:B:436:LEU:HG	2.20	0.41
1:A:597:ARG:HH11	1:A:682:HIS:HB2	1.83	0.41
1:B:313:LEU:O	1:B:325:MET:HA	2.21	0.41
1:D:522:THR:HB	1:D:524:PHE:CE2	2.56	0.41
1:C:70:TYR:HB3	1:C:79:PHE:CE1	2.55	0.41
1:C:410:LEU:HD22	1:C:411:THR:O	2.21	0.41
1:D:544:LEU:HD23	1:D:626:ILE:HD12	2.02	0.41
1:B:453:ARG:NH2	1:B:477:LEU:O	2.53	0.41
1:A:70:TYR:HB3	1:A:79:PHE:HE1	1.83	0.41
1:A:154:TRP:CE2	1:A:212:SER:HB3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:369:ASN:O	1:C:389:ILE:HG12	2.21	0.41
1:B:614:SER:HB2	1:B:621:ASN:ND2	2.36	0.41
1:A:588:ASP:HB3	1:A:592:HIS:CD2	2.56	0.41
1:B:662:TYR:HE1	1:B:710:ASN:HD22	1.69	0.41
1:D:744:SER:HB2	1:D:747:ALA:HB3	2.03	0.40
1:A:237:GLU:HA	1:A:252:VAL:O	2.21	0.40
1:B:153:GLN:HB3	1:B:211:TYR:CE1	2.57	0.40
1:B:475:PRO:HA	1:B:557:THR:O	2.20	0.40
1:A:547:TYR:CD2	1:A:552:SER:HB2	2.56	0.40
1:A:170:ASN:ND2	1:A:170:ASN:N	2.69	0.40
1:B:343:ARG:HH21	1:B:389:ILE:HG21	1.87	0.40
1:A:105:TYR:HB2	1:A:114:ILE:HD11	2.04	0.40
1:C:423:LYS:HE2	1:C:423:LYS:HB3	1.91	0.40
1:D:548:ALA:HB3	1:D:635:VAL:HG21	2.02	0.40
1:D:299:TYR:CE1	1:D:665:VAL:HG22	2.57	0.40
1:D:422:TYR:CE1	1:D:423:LYS:HE2	2.56	0.40
1:A:504:LEU:HA	1:A:507:VAL:HG13	2.04	0.40
1:C:405:ILE:HG12	1:C:419:SER:HA	2.02	0.40
1:D:741:GLY:O	1:D:742:ILE:C	2.59	0.40
1:A:510:PRO:HD3	1:A:569:SER:HB2	2.02	0.40

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	721/740 (97%)	679 (94%)	42 (6%)	0	100	100
1	B	723/740 (98%)	682 (94%)	41 (6%)	0	100	100
1	C	716/740 (97%)	677 (95%)	39 (5%)	0	100	100
1	D	707/740 (96%)	665 (94%)	42 (6%)	0	100	100
All	All	2867/2960 (97%)	2703 (94%)	164 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	650/662 (98%)	633 (97%)	17 (3%)	54	85
1	B	650/662 (98%)	625 (96%)	25 (4%)	40	76
1	C	648/662 (98%)	629 (97%)	19 (3%)	50	83
1	D	641/662 (97%)	623 (97%)	18 (3%)	51	84
All	All	2589/2648 (98%)	2510 (97%)	79 (3%)	48	82

All (79) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	80	ASN
1	A	129	THR
1	A	170	ASN
1	A	246	LEU
1	A	316	LEU
1	A	358[A]	ARG
1	A	358[B]	ARG
1	A	385	CYS
1	A	453	ARG
1	A	464	GLU
1	A	492	ARG
1	A	507	VAL
1	A	514	LEU
1	A	547	TYR
1	A	566	TYR
1	A	673	LEU
1	A	710	ASN
1	B	41	LYS
1	B	57	LEU
1	B	61	ARG
1	B	75	ASN
1	B	77	LEU

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Mol	Chain	Res	Type
1	B	179	ASN
1	B	230	ASP
1	B	246	LEU
1	B	316	LEU
1	B	325	MET
1	B	366	LEU
1	B	385	CYS
1	B	391	LYS
1	B	395	THR
1	B	410	LEU
1	B	453	ARG
1	B	482	LEU
1	B	506	ASN
1	B	514	LEU
1	B	547	TYR
1	B	594	ILE
1	B	621	ASN
1	B	640	LEU
1	B	688	VAL
1	B	710	ASN
1	C	129	THR
1	C	243	ASP
1	C	246	LEU
1	C	316	LEU
1	C	326	ASP
1	C	329	ASP
1	C	385	CYS
1	C	410	LEU
1	C	441	LYS
1	C	453	ARG
1	C	463	LYS
1	C	470	LEU
1	C	504	LEU
1	C	547	TYR
1	C	575	VAL
1	C	597	ARG
1	C	615	LYS
1	C	627	TRP
1	C	710	ASN
1	D	145	GLU
1	D	246	LEU
1	D	316	LEU

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Mol	Chain	Res	Type
1	D	388	GLN
1	D	392	LYS
1	D	450	ASN
1	D	453	ARG
1	D	470	LEU
1	D	514	LEU
1	D	528	MET
1	D	536	LYS
1	D	547	TYR
1	D	566	TYR
1	D	575	VAL
1	D	627	TRP
1	D	658	ARG
1	D	684	ARG
1	D	710	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	ASN
1	A	72	GLN
1	A	80	ASN
1	A	151	ASN
1	A	153	GLN
1	A	170	ASN
1	A	196	ASN
1	A	227	GLN
1	A	344	GLN
1	A	455	GLN
1	A	505	GLN
1	A	572	ASN
1	A	685	ASN
1	A	710	ASN
1	B	72	GLN
1	B	75	ASN
1	B	80	ASN
1	B	141	GLN
1	B	151	ASN
1	B	153	GLN
1	B	169	ASN
1	B	170	ASN
1	B	179	ASN

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Mol	Chain	Res	Type
1	B	227	GLN
1	B	505	GLN
1	B	572	ASN
1	B	592	HIS
1	B	710	ASN
1	C	85	ASN
1	C	112	GLN
1	C	151	ASN
1	C	153	GLN
1	C	170	ASN
1	C	344	GLN
1	C	455	GLN
1	C	505	GLN
1	C	572	ASN
1	C	586	GLN
1	C	697	GLN
1	C	710	ASN
1	D	85	ASN
1	D	153	GLN
1	D	169	ASN
1	D	170	ASN
1	D	179	ASN
1	D	450	ASN
1	D	455	GLN
1	D	572	ASN
1	D	710	ASN

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	$\# Z > 2$
4	NAG	A	804	1,4	14,14,15	0.52	0	15,19,21	0.74	0
4	NAG	A	805	4	14,14,15	0.47	0	15,19,21	0.86	1 (6%)
4	NAG	A	806	1,4	14,14,15	0.52	0	15,19,21	1.01	1 (6%)
4	NAG	A	807	4	14,14,15	0.51	0	15,19,21	0.68	0
4	NAG	B	804	1,4	14,14,15	0.54	0	15,19,21	0.90	1 (6%)
4	NAG	B	805	4	14,14,15	0.46	0	15,19,21	0.70	0
4	NAG	C	803	1,4	14,14,15	0.60	0	15,19,21	0.82	1 (6%)
4	NAG	C	804	4	14,14,15	0.46	0	15,19,21	0.84	1 (6%)
4	NAG	D	802	1,4	14,14,15	0.49	0	15,19,21	1.15	1 (6%)
4	NAG	D	803	4	14,14,15	0.47	0	15,19,21	1.07	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
4	NAG	A	804	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	805	4	-	0/6/23/26	0/1/1/1
4	NAG	A	806	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	807	4	-	2/6/23/26	0/1/1/1
4	NAG	B	804	1,4	-	0/6/23/26	0/1/1/1
4	NAG	B	805	4	-	0/6/23/26	0/1/1/1
4	NAG	C	803	1,4	-	0/6/23/26	0/1/1/1
4	NAG	C	804	4	-	0/6/23/26	0/1/1/1
4	NAG	D	802	1,4	-	0/6/23/26	0/1/1/1
4	NAG	D	803	4	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	803	NAG	C4-C3-C2	2.13	114.55	111.23
4	B	804	NAG	C1-O5-C5	2.16	114.99	112.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	805	NAG	C1-O5-C5	2.42	115.32	112.25
4	C	804	NAG	C1-O5-C5	2.59	115.54	112.25
4	D	803	NAG	C1-O5-C5	3.08	116.16	112.25
4	D	802	NAG	C1-O5-C5	3.12	116.20	112.25
4	A	806	NAG	C1-O5-C5	3.14	116.23	112.25

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	807	NAG	C8-C7-N2-C2
4	A	807	NAG	O7-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry [i](#)

16 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$
2	0WG	A	800	-	22,26,26	1.25	3 (13%)	20,39,39	1.38	2 (10%)
3	NAG	A	801	1	14,14,15	0.43	0	15,19,21	1.04	1 (6%)
3	NAG	A	802	1	14,14,15	0.45	0	15,19,21	1.08	1 (6%)
3	NAG	A	803	1	14,14,15	0.56	0	15,19,21	1.23	2 (13%)
3	NAG	A	808	1	14,14,15	0.44	0	15,19,21	1.18	1 (6%)
2	0WG	B	800	-	22,26,26	1.21	1 (4%)	20,39,39	1.43	3 (15%)
3	NAG	B	801	1	14,14,15	0.60	0	15,19,21	1.23	2 (13%)
3	NAG	B	802	1	14,14,15	0.46	0	15,19,21	0.95	1 (6%)
3	NAG	B	803	1	14,14,15	0.45	0	15,19,21	0.62	0
3	NAG	B	806	1	14,14,15	0.43	0	15,19,21	1.24	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	0WG	C	800	-	22,26,26	1.27	1 (4%)	20,39,39	1.27	2 (10%)
3	NAG	C	801	1	14,14,15	0.44	0	15,19,21	1.65	1 (6%)
3	NAG	C	802	1	14,14,15	0.52	0	15,19,21	0.62	0
2	0WG	D	800	-	22,26,26	1.21	1 (4%)	20,39,39	1.32	4 (20%)
3	NAG	D	801	1	14,14,15	0.50	0	15,19,21	1.08	1 (6%)
3	NAG	D	804	1	14,14,15	0.60	0	15,19,21	1.22	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
2	0WG	A	800	-	-	0/5/6/6	0/3/3/3
3	NAG	A	801	1	-	0/6/23/26	0/1/1/1
3	NAG	A	802	1	-	0/6/23/26	0/1/1/1
3	NAG	A	803	1	-	0/6/23/26	0/1/1/1
3	NAG	A	808	1	-	0/6/23/26	0/1/1/1
2	0WG	B	800	-	-	0/5/6/6	0/3/3/3
3	NAG	B	801	1	-	0/6/23/26	0/1/1/1
3	NAG	B	802	1	-	0/6/23/26	0/1/1/1
3	NAG	B	803	1	-	0/6/23/26	0/1/1/1
3	NAG	B	806	1	-	1/6/23/26	0/1/1/1
2	0WG	C	800	-	-	0/5/6/6	0/3/3/3
3	NAG	C	801	1	-	0/6/23/26	0/1/1/1
3	NAG	C	802	1	-	0/6/23/26	0/1/1/1
2	0WG	D	800	-	-	0/5/6/6	0/3/3/3
3	NAG	D	801	1	-	0/6/23/26	0/1/1/1
3	NAG	D	804	1	-	0/6/23/26	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	800	0WG	C5-N6	2.01	1.39	1.34
2	A	800	0WG	C10-C7	2.13	1.41	1.38
2	A	800	0WG	C19-C18	3.78	1.47	1.41
2	B	800	0WG	C19-C18	3.89	1.48	1.41
2	D	800	0WG	C19-C18	3.89	1.48	1.41
2	C	800	0WG	C19-C18	4.02	1.48	1.41

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	800	0WG	C10-C11-C16	-3.92	118.35	122.65
2	B	800	0WG	C10-C11-C16	-3.13	119.21	122.65
2	B	800	0WG	C18-C3-N4	-3.09	119.86	123.52
2	C	800	0WG	C18-C3-N4	-3.01	119.95	123.52
2	D	800	0WG	C18-C3-N4	-2.97	120.00	123.52
2	C	800	0WG	C10-C11-C16	-2.96	119.40	122.65
2	D	800	0WG	C10-C11-C16	-2.76	119.62	122.65
2	A	800	0WG	C18-C3-N4	-2.75	120.26	123.52
2	D	800	0WG	C19-C18-C3	-2.16	117.11	119.99
3	A	803	NAG	C3-C4-C5	2.04	113.75	110.20
2	B	800	0WG	C11-C10-C18	2.09	123.68	119.69
2	D	800	0WG	C11-C10-C18	2.20	123.90	119.69
3	D	804	NAG	C1-O5-C5	2.33	115.20	112.25
3	B	801	NAG	C4-C3-C2	2.53	115.17	111.23
3	B	802	NAG	C1-O5-C5	2.73	115.72	112.25
3	D	804	NAG	C2-N2-C7	2.80	126.63	123.04
3	B	801	NAG	C1-O5-C5	2.94	115.98	112.25
3	D	801	NAG	C1-O5-C5	3.03	116.10	112.25
3	A	801	NAG	C1-O5-C5	3.09	116.17	112.25
3	A	803	NAG	C4-C3-C2	3.26	116.29	111.23
3	B	806	NAG	C1-O5-C5	3.41	116.58	112.25
3	A	802	NAG	C1-O5-C5	3.50	116.69	112.25
3	A	808	NAG	C1-O5-C5	4.05	117.39	112.25
3	C	801	NAG	C1-O5-C5	5.83	119.64	112.25

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	806	NAG	O7-C7-N2-C2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	800	0WG	1	0
2	C	800	0WG	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	724/740 (97%)	0.19	32 (4%) 38 32	16, 38, 82, 108	0
1	B	727/740 (98%)	0.03	12 (1%) 73 70	17, 37, 67, 117	0
1	C	722/740 (97%)	0.28	48 (6%) 22 16	18, 43, 86, 118	0
1	D	715/740 (96%)	0.29	37 (5%) 31 24	18, 49, 90, 128	0
All	All	2888/2960 (97%)	0.20	129 (4%) 37 31	16, 41, 84, 128	0

All (129) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	81	ALA	6.4
1	C	93	SER	4.9
1	A	96	ASP	4.9
1	B	87	SER	4.7
1	C	98	PHE	4.6
1	C	87	SER	4.6
1	B	766	PRO	4.4
1	C	100	HIS	4.4
1	A	98	PHE	4.3
1	D	77	LEU	4.3
1	C	79	PHE	4.1
1	C	99	GLY	4.0
1	B	70	TYR	3.9
1	A	138	ASN	3.9
1	D	505	GLN	3.8
1	C	96	ASP	3.8
1	A	97	GLU	3.7
1	C	89	PHE	3.7
1	C	92	ASN	3.6
1	C	80	ASN	3.5
1	C	95	PHE	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	77	LEU	3.5
1	D	87	SER	3.5
1	B	72	GLN	3.4
1	C	101	SER	3.4
1	D	59	SER	3.4
1	C	78	VAL	3.4
1	A	145	GLU	3.4
1	B	82	GLU	3.4
1	C	86	SER	3.3
1	C	102	ILE	3.3
1	C	72	GLN	3.3
1	D	99	GLY	3.3
1	C	88	VAL	3.3
1	D	333	SER	3.2
1	D	392	LYS	3.2
1	A	144	THR	3.2
1	D	97	GLU	3.1
1	C	490	GLY	3.1
1	C	41	LYS	3.1
1	A	142	LEU	3.1
1	A	332	GLU	3.0
1	C	91	GLU	3.0
1	A	86	SER	3.0
1	C	766	PRO	3.0
1	D	78	VAL	3.0
1	A	676	PRO	3.0
1	D	58	TYR	2.9
1	D	331	ASP	2.8
1	A	81	ALA	2.8
1	C	131	SER	2.8
1	D	100	HIS	2.8
1	C	179	ASN	2.8
1	A	99	GLY	2.8
1	D	330	TYR	2.7
1	D	69	LEU	2.7
1	C	97	GLU	2.7
1	D	75	ASN	2.7
1	C	63	ILE	2.7
1	D	340	LEU	2.7
1	B	76	ILE	2.7
1	B	78	VAL	2.7
1	C	144	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	412	SER	2.7
1	C	138	ASN	2.6
1	A	511	SER	2.6
1	A	75	ASN	2.6
1	C	132	TYR	2.6
1	B	88	VAL	2.6
1	C	118	TYR	2.6
1	D	323	SER	2.6
1	A	275	SER	2.5
1	C	81	ALA	2.5
1	A	71	LYS	2.5
1	B	138	ASN	2.5
1	A	135	TYR	2.5
1	D	766	PRO	2.5
1	C	139	LYS	2.5
1	D	62	TRP	2.5
1	C	331	ASP	2.5
1	A	280	THR	2.5
1	C	116	LEU	2.5
1	C	394	CYS	2.5
1	D	88	VAL	2.5
1	C	82	GLU	2.4
1	A	72	GLN	2.4
1	D	96	ASP	2.4
1	A	333	SER	2.4
1	C	342	ALA	2.4
1	A	378	GLU	2.4
1	D	338	ASN	2.4
1	C	90	LEU	2.4
1	C	335	GLY	2.4
1	C	491	LEU	2.3
1	A	169	ASN	2.3
1	A	90	LEU	2.3
1	A	95	PHE	2.3
1	C	333	SER	2.3
1	C	533	HIS	2.3
1	C	42	THR	2.3
1	A	102	ILE	2.2
1	D	85	ASN	2.2
1	D	483	HIS	2.2
1	C	277	SER	2.2
1	D	54	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	77	LEU	2.2
1	C	105	TYR	2.2
1	C	140	ARG	2.2
1	A	88	VAL	2.2
1	C	392	LYS	2.2
1	D	137	LEU	2.2
1	D	273	THR	2.1
1	A	180	LEU	2.1
1	A	140	ARG	2.1
1	A	148	ILE	2.1
1	D	76	ILE	2.1
1	D	397	ILE	2.1
1	D	479	LEU	2.1
1	D	222	PHE	2.1
1	B	44	THR	2.1
1	D	393	ASP	2.1
1	D	521	GLU	2.1
1	C	52	THR	2.1
1	D	334	SER	2.1
1	A	82	GLU	2.0
1	D	491	LEU	2.0
1	D	187	TRP	2.0
1	A	675	THR	2.0
1	C	309	GLU	2.0

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
4	NAG	C	803	14/15	0.88	0.25	0.79	42,50,61,68	0
4	NAG	A	804	14/15	0.92	0.19	-0.08	46,52,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	NAG	B	804	14/15	0.92	0.20	-0.09	47,54,62,66	0
4	NAG	D	802	14/15	0.95	0.17	-0.61	37,41,42,49	0
4	NAG	A	806	14/15	0.80	0.18	-1.08	67,75,80,82	0
4	NAG	A	807	14/15	0.84	0.27	-	78,82,92,97	0
4	NAG	D	803	14/15	0.79	0.24	-	53,56,60,60	0
4	NAG	A	805	14/15	0.82	0.24	-	53,61,64,66	0
4	NAG	B	805	14/15	0.65	0.29	-	74,83,88,88	0
4	NAG	C	804	14/15	0.72	0.39	-	76,85,86,87	0

6.4 Ligands ⓘ

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	A	808	14/15	0.87	0.32	1.97	46,53,56,61	0
3	NAG	C	802	14/15	0.72	0.32	0.66	66,73,77,81	0
2	0WG	B	800	24/24	0.94	0.18	0.34	26,32,35,46	0
2	0WG	A	800	24/24	0.96	0.20	0.32	25,29,32,39	0
2	0WG	D	800	24/24	0.94	0.18	0.10	29,31,35,45	0
3	NAG	A	801	14/15	0.68	0.28	-0.25	58,62,64,64	0
2	0WG	C	800	24/24	0.95	0.15	-1.81	26,31,32,41	0
3	NAG	B	801	14/15	0.74	0.21	-	51,55,58,60	0
3	NAG	D	804	14/15	0.88	0.21	-	62,66,70,70	0
3	NAG	B	806	14/15	0.84	0.17	-	52,56,57,60	0
3	NAG	B	802	14/15	0.82	0.28	-	51,55,57,60	0
3	NAG	B	803	14/15	0.84	0.27	-	51,56,58,59	0
3	NAG	A	802	14/15	0.71	0.34	-	73,81,83,84	0
3	NAG	C	801	14/15	0.76	0.35	-	24,26,26,26	0
3	NAG	D	801	14/15	0.72	0.29	-	34,36,36,37	0
3	NAG	A	803	14/15	0.83	0.52	-	61,68,78,79	0

6.5 Other polymers ⓘ

There are no such residues in this entry.