



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 11, 2023 – 08:55 am GMT

PDB ID : 4C5R
Title : Structural Investigations into the Stereochemistry and Activity of a Phenylalanine-2,3-Aminomutase from *Taxus chinensis*
Authors : Wybenga, G.G.; Szymanski, W.; Wu, B.; Feringa, B.L.; Janssen, D.B.; Dijkstra, B.W.
Deposited on : 2013-09-16
Resolution : 2.14 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

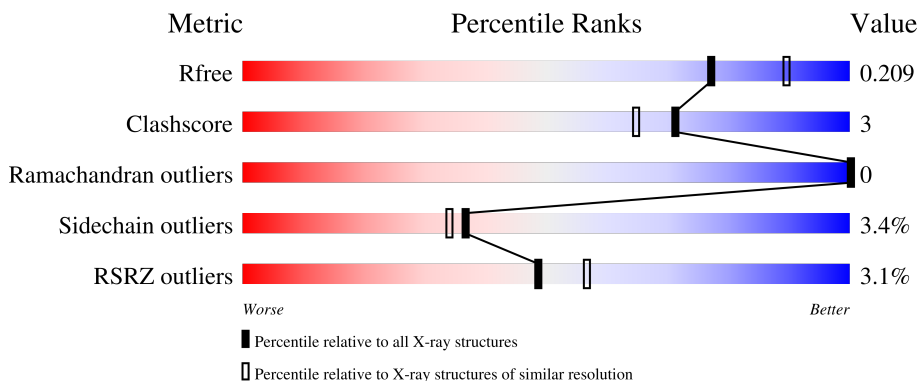
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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}	130704	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)
RSRZ outliers	127900	2485 (2.16-2.12)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	705	 4% 81% 8% • 10%
1	B	705	 2% 81% 9% • 9%
1	C	705	 3% 80% 10% • 9%
1	D	705	 2% 81% 8% • 10%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 20505 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 PHENYLALANINE AMMONIA-LYASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	635	4926	3129	847	927	23	0	0	0
1	B	640	4967	3152	855	937	23	0	0	0
1	C	640	4968	3153	855	937	23	0	0	0
1	D	636	4935	3132	848	932	23	0	0	0

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	175	MDO	ALA	chromophore	UNP Q68G84
A	175	MDO	SER	chromophore	UNP Q68G84
A	175	MDO	GLY	chromophore	UNP Q68G84
B	175	MDO	ALA	chromophore	UNP Q68G84
B	175	MDO	SER	chromophore	UNP Q68G84
B	175	MDO	GLY	chromophore	UNP Q68G84
C	175	MDO	ALA	chromophore	UNP Q68G84
C	175	MDO	SER	chromophore	UNP Q68G84
C	175	MDO	GLY	chromophore	UNP Q68G84
D	175	MDO	ALA	chromophore	UNP Q68G84
D	175	MDO	SER	chromophore	UNP Q68G84
D	175	MDO	GLY	chromophore	UNP Q68G84
A	-19	MET	-	expression tag	UNP Q68G84
A	-18	GLY	-	expression tag	UNP Q68G84
A	-17	SER	-	expression tag	UNP Q68G84
A	-16	SER	-	expression tag	UNP Q68G84
A	-15	HIS	-	expression tag	UNP Q68G84
A	-14	HIS	-	expression tag	UNP Q68G84
A	-13	HIS	-	expression tag	UNP Q68G84
A	-12	HIS	-	expression tag	UNP Q68G84
A	-11	HIS	-	expression tag	UNP Q68G84

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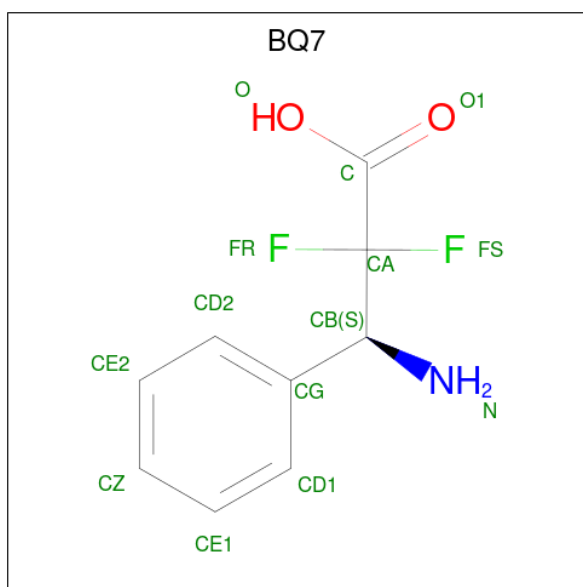
Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	HIS	-	expression tag	UNP Q68G84
A	-9	SER	-	expression tag	UNP Q68G84
A	-8	SER	-	expression tag	UNP Q68G84
A	-7	GLY	-	expression tag	UNP Q68G84
A	-6	LEU	-	expression tag	UNP Q68G84
A	-5	VAL	-	expression tag	UNP Q68G84
A	-4	PRO	-	expression tag	UNP Q68G84
A	-3	ARG	-	expression tag	UNP Q68G84
A	-2	GLY	-	expression tag	UNP Q68G84
A	-1	SER	-	expression tag	UNP Q68G84
A	0	HIS	-	expression tag	UNP Q68G84
B	-19	MET	-	expression tag	UNP Q68G84
B	-18	GLY	-	expression tag	UNP Q68G84
B	-17	SER	-	expression tag	UNP Q68G84
B	-16	SER	-	expression tag	UNP Q68G84
B	-15	HIS	-	expression tag	UNP Q68G84
B	-14	HIS	-	expression tag	UNP Q68G84
B	-13	HIS	-	expression tag	UNP Q68G84
B	-12	HIS	-	expression tag	UNP Q68G84
B	-11	HIS	-	expression tag	UNP Q68G84
B	-10	HIS	-	expression tag	UNP Q68G84
B	-9	SER	-	expression tag	UNP Q68G84
B	-8	SER	-	expression tag	UNP Q68G84
B	-7	GLY	-	expression tag	UNP Q68G84
B	-6	LEU	-	expression tag	UNP Q68G84
B	-5	VAL	-	expression tag	UNP Q68G84
B	-4	PRO	-	expression tag	UNP Q68G84
B	-3	ARG	-	expression tag	UNP Q68G84
B	-2	GLY	-	expression tag	UNP Q68G84
B	-1	SER	-	expression tag	UNP Q68G84
B	0	HIS	-	expression tag	UNP Q68G84
C	-19	MET	-	expression tag	UNP Q68G84
C	-18	GLY	-	expression tag	UNP Q68G84
C	-17	SER	-	expression tag	UNP Q68G84
C	-16	SER	-	expression tag	UNP Q68G84
C	-15	HIS	-	expression tag	UNP Q68G84
C	-14	HIS	-	expression tag	UNP Q68G84
C	-13	HIS	-	expression tag	UNP Q68G84
C	-12	HIS	-	expression tag	UNP Q68G84
C	-11	HIS	-	expression tag	UNP Q68G84
C	-10	HIS	-	expression tag	UNP Q68G84
C	-9	SER	-	expression tag	UNP Q68G84

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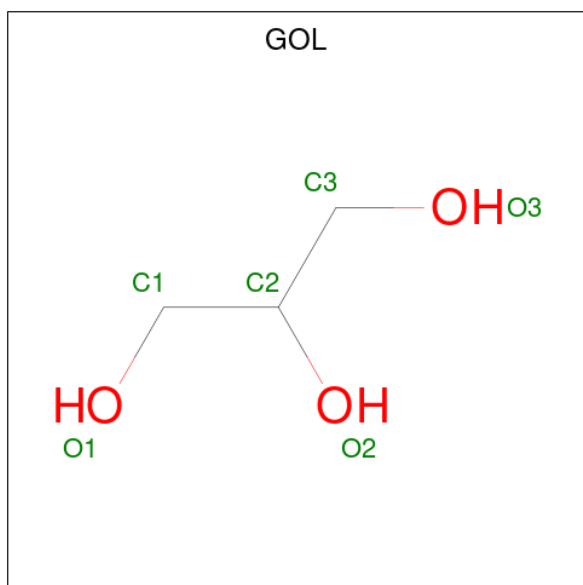
Chain	Residue	Modelled	Actual	Comment	Reference
C	-8	SER	-	expression tag	UNP Q68G84
C	-7	GLY	-	expression tag	UNP Q68G84
C	-6	LEU	-	expression tag	UNP Q68G84
C	-5	VAL	-	expression tag	UNP Q68G84
C	-4	PRO	-	expression tag	UNP Q68G84
C	-3	ARG	-	expression tag	UNP Q68G84
C	-2	GLY	-	expression tag	UNP Q68G84
C	-1	SER	-	expression tag	UNP Q68G84
C	0	HIS	-	expression tag	UNP Q68G84
D	-19	MET	-	expression tag	UNP Q68G84
D	-18	GLY	-	expression tag	UNP Q68G84
D	-17	SER	-	expression tag	UNP Q68G84
D	-16	SER	-	expression tag	UNP Q68G84
D	-15	HIS	-	expression tag	UNP Q68G84
D	-14	HIS	-	expression tag	UNP Q68G84
D	-13	HIS	-	expression tag	UNP Q68G84
D	-12	HIS	-	expression tag	UNP Q68G84
D	-11	HIS	-	expression tag	UNP Q68G84
D	-10	HIS	-	expression tag	UNP Q68G84
D	-9	SER	-	expression tag	UNP Q68G84
D	-8	SER	-	expression tag	UNP Q68G84
D	-7	GLY	-	expression tag	UNP Q68G84
D	-6	LEU	-	expression tag	UNP Q68G84
D	-5	VAL	-	expression tag	UNP Q68G84
D	-4	PRO	-	expression tag	UNP Q68G84
D	-3	ARG	-	expression tag	UNP Q68G84
D	-2	GLY	-	expression tag	UNP Q68G84
D	-1	SER	-	expression tag	UNP Q68G84
D	0	HIS	-	expression tag	UNP Q68G84

- Molecule 2 is (3S)-3-amino-2,2-difluoro-3-phenylpropanoic acid (three-letter code: BQ7) (formula: C₉H₉F₂NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	F	N			O
2	A	1	Total 14	C 9	F 2	N 1	O 2	0	0
2	B	1	Total 14	C 9	F 2	N 1	O 2	0	0
2	C	1	Total 14	C 9	F 2	N 1	O 2	0	0
2	D	1	Total 14	C 9	F 2	N 1	O 2	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

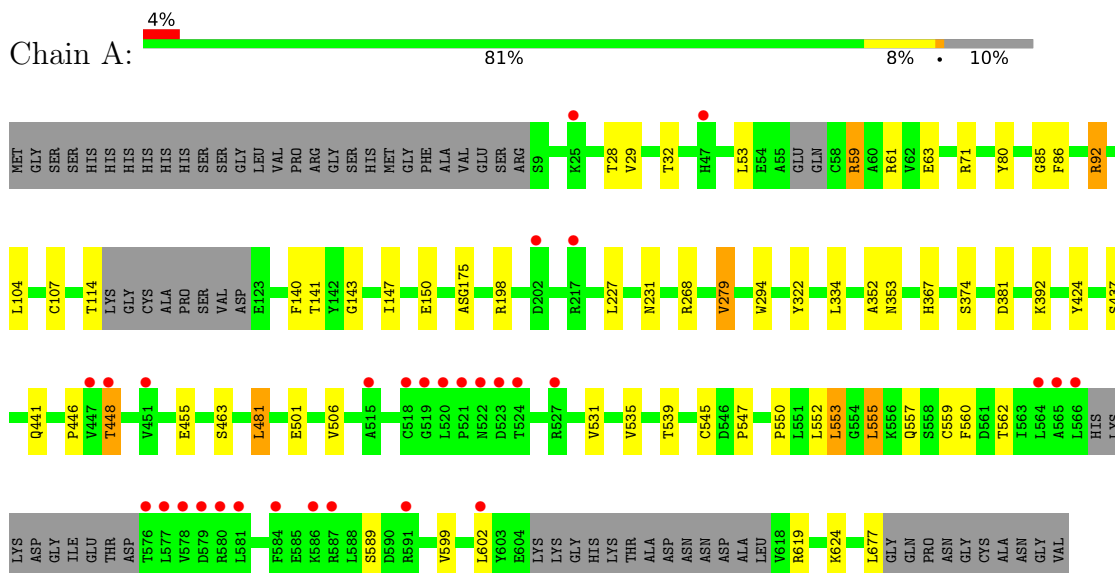
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	181	Total	O	0	0
			181	181		
4	B	154	Total	O	0	0
			154	154		
4	C	161	Total	O	0	0
			161	161		
4	D	145	Total	O	0	0
			145	145		

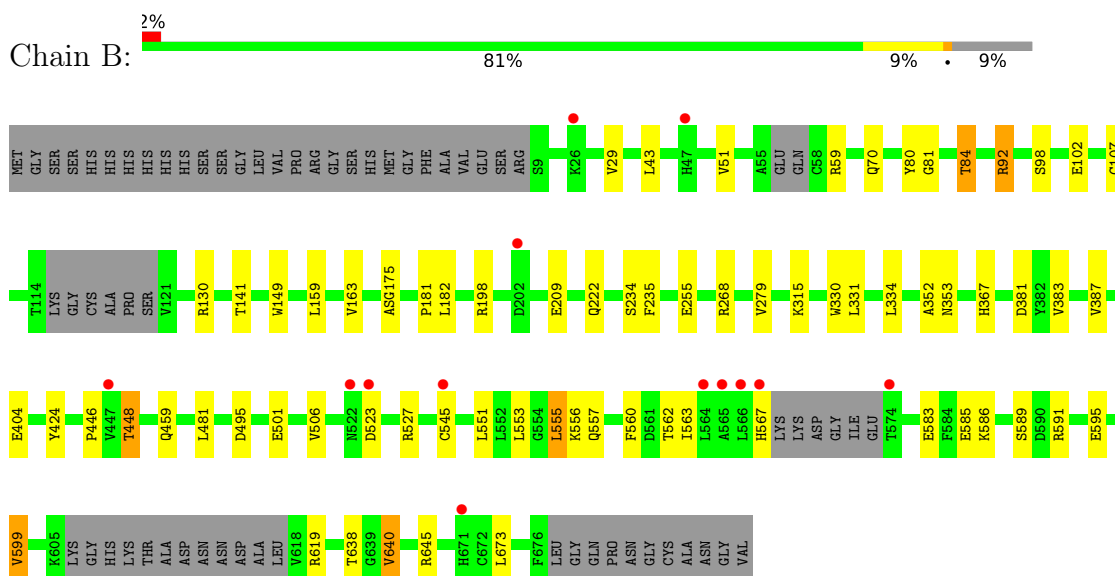
3 Residue-property plots i

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

- Molecule 1: PHENYLALANINE AMMONIA-LYASE



- Molecule 1: PHENYLALANINE AMMONIA-LYASE



- Molecule 1: PHENYLALANINE AMMONIA-LYASE

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	99.39Å 145.48Å 99.56Å 90.00° 99.54° 90.00°	Depositor
Resolution (Å)	49.09 – 2.14 49.09 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.4 (49.09-2.14) 99.4 (49.09-2.15)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 2.14Å)	Xtrriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.172 , 0.210 0.173 , 0.209	Depositor DCC
R_{free} test set	7602 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	21.0	Xtrriage
Anisotropy	0.030	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 40.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.019 for l,-k,h	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	20505	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MDO, BQ7

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	0.53	2/4996 (0.0%)	0.61	2/6778 (0.0%)
1	B	0.53	2/5038 (0.0%)	0.61	0/6835
1	C	0.53	3/5039 (0.1%)	0.61	0/6836
1	D	0.53	2/5005 (0.0%)	0.63	3/6790 (0.0%)
All	All	0.53	9/20078 (0.0%)	0.62	5/27239 (0.0%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	455	GLU	CD-OE2	-6.06	1.19	1.25
1	A	455	GLU	CD-OE1	-5.75	1.19	1.25
1	C	68	TRP	CD2-CE2	5.32	1.47	1.41
1	C	330	TRP	CD2-CE2	5.28	1.47	1.41
1	D	294	TRP	CD2-CE2	5.28	1.47	1.41
1	B	149	TRP	CD2-CE2	5.11	1.47	1.41
1	C	149	TRP	CD2-CE2	5.11	1.47	1.41
1	B	330	TRP	CD2-CE2	5.07	1.47	1.41
1	D	368	GLY	C-O	-5.01	1.15	1.23

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	130	ARG	NE-CZ-NH2	-5.61	117.50	120.30
1	A	71	ARG	NE-CZ-NH2	-5.57	117.52	120.30
1	A	481	LEU	CA-CB-CG	5.22	127.30	115.30
1	D	381	ASP	CB-CG-OD1	5.21	122.99	118.30
1	D	481	LEU	CA-CB-CG	5.04	126.90	115.30

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	4926	0	4988	40	0
1	B	4967	0	5021	41	0
1	C	4968	0	5023	48	0
1	D	4935	0	4987	34	0
2	A	14	0	7	0	0
2	B	14	0	7	0	0
2	C	14	0	7	0	0
2	D	14	0	7	1	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0
4	A	181	0	0	7	0
4	B	154	0	0	0	0
4	C	161	0	0	4	0
4	D	145	0	0	3	0
All	All	20505	0	20063	139	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 3.

All (139) 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:506:VAL:HG21	1:B:599:VAL:HG11	1.45	0.96
1:A:352:ALA:HB3	1:B:279:VAL:CG1	2.03	0.87
1:C:381:ASP:OD2	1:C:448:THR:HB	1.74	0.86
1:A:279:VAL:HG13	1:B:352:ALA:HB3	1.57	0.84
1:C:279:VAL:HG13	1:D:352:ALA:HB3	1.60	0.83
1:A:381:ASP:OD2	1:A:448:THR:HB	1.79	0.82
1:D:145:SER:O	1:D:224:LYS:HE3	1.80	0.81
1:C:294:TRP:CH2	1:C:624:LYS:HE2	2.17	0.79
1:C:352:ALA:HB3	1:D:279:VAL:HG13	1.65	0.78
1:B:381:ASP:OD2	1:B:448:THR:HB	1.88	0.74
1:B:501:GLU:OE1	1:B:619:ARG:HD2	1.90	0.71
1:A:352:ALA:HB3	1:B:279:VAL:HG13	1.71	0.71
1:C:29:VAL:HG23	1:C:141:THR:HG21	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:VAL:HG22	1:A:141:THR:HG21	1.76	0.67
1:A:501:GLU:OE1	1:A:619:ARG:HD2	1.95	0.66
1:A:557:GLN:OE1	1:D:557:GLN:NE2	2.28	0.65
1:A:294:TRP:CH2	1:A:624:LYS:HE2	2.32	0.65
1:A:92:ARG:HB3	1:A:92:ARG:NH1	2.13	0.63
1:C:546:ASP:OD1	1:C:548:THR:HB	2.00	0.62
1:A:279:VAL:CG1	1:B:352:ALA:HB3	2.28	0.61
1:A:92:ARG:HB3	1:A:92:ARG:HH11	1.65	0.60
1:D:130:ARG:HD2	4:D:2037:HOH:O	2.01	0.60
4:A:2103:HOH:O	1:B:448:THR:HG23	2.01	0.58
1:C:446:PRO:HD3	1:D:446:PRO:HD3	1.85	0.58
1:C:501:GLU:OE1	1:C:619:ARG:HD2	2.04	0.58
1:C:279:VAL:CG1	1:D:352:ALA:HB3	2.33	0.57
1:A:446:PRO:HD3	1:B:446:PRO:HD3	1.87	0.56
1:C:84:THR:HG22	1:C:85:GLY:O	2.04	0.56
1:B:557:GLN:NE2	1:C:557:GLN:OE1	2.27	0.56
1:C:352:ALA:HB3	1:D:279:VAL:CG1	2.36	0.56
1:C:591:ARG:HB2	1:C:591:ARG:HH11	1.70	0.56
1:A:437:SER:O	1:A:441:GLN:HG2	2.06	0.55
1:C:516:ASP:OD1	1:C:525:LYS:HE3	2.06	0.55
1:C:131:SER:HB2	1:C:238:ALA:HB1	1.89	0.54
1:C:531:VAL:O	1:C:535:VAL:HG13	2.08	0.54
1:A:61:ARG:HG3	1:A:143:GLY:HA3	1.88	0.54
1:D:43:LEU:O	1:D:130:ARG:NH2	2.42	0.53
1:D:227:LEU:O	1:D:231:ASN:HB2	2.09	0.53
1:D:29:VAL:HG23	1:D:141:THR:HG21	1.91	0.52
1:B:181:PRO:HB2	1:B:235:PHE:CD2	2.44	0.52
1:C:70:GLN:OE1	1:C:222:GLN:HB3	2.10	0.52
1:D:437:SER:O	1:D:441:GLN:HG2	2.09	0.52
1:C:548:THR:HG22	1:C:549:LEU:HD23	1.92	0.52
1:A:545:CYS:HA	1:A:552:LEU:HD23	1.92	0.51
1:A:322:TYR:CZ	1:B:459:GLN:HG2	2.45	0.51
1:A:59:ARG:HD2	1:A:63:GLU:CD	2.31	0.51
1:C:43:LEU:HD22	1:C:134:LEU:HD22	1.93	0.50
1:C:459:GLN:HG2	1:D:322:TYR:CZ	2.45	0.50
1:B:424:TYR:OH	1:D:85:GLY:HA2	2.12	0.50
1:A:85:GLY:HA2	1:C:424:TYR:OH	2.12	0.50
1:C:546:ASP:HB3	1:C:549:LEU:HG	1.94	0.50
1:C:437:SER:O	1:C:441:GLN:HG2	2.13	0.49
1:B:315:LYS:NZ	1:C:548:THR:HG21	2.28	0.49
1:B:545:CYS:SG	1:B:589:SER:HA	2.52	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:506:VAL:HG21	1:A:599:VAL:HG11	1.94	0.49
1:A:150:GLU:HB2	4:A:2042:HOH:O	2.11	0.48
1:C:80:TYR:HB3	1:C:367:HIS:CD2	2.48	0.48
1:B:51:VAL:HG21	1:B:159:LEU:HD13	1.95	0.48
1:B:495:ASP:CB	1:B:640:VAL:HG13	2.44	0.48
1:C:374:SER:HA	1:C:463:SER:HB2	1.95	0.48
4:A:2103:HOH:O	1:B:448:THR:CG2	2.61	0.47
1:D:495:ASP:CB	1:D:640:VAL:HG13	2.44	0.47
1:B:551:LEU:HG	1:B:555:LEU:HD22	1.96	0.47
1:A:531:VAL:HG11	1:A:555:LEU:HD13	1.96	0.47
1:B:560:PHE:HB2	1:C:560:PHE:HB2	1.96	0.47
1:A:545:CYS:SG	1:A:589:SER:HA	2.54	0.47
1:C:178:ASP:HB3	1:C:181:PRO:HG2	1.95	0.47
1:B:506:VAL:HG21	1:B:599:VAL:CG1	2.31	0.46
1:B:556:LYS:HE2	1:B:585:GLU:OE2	2.15	0.46
1:D:392:LYS:HD3	1:D:392:LYS:HA	1.64	0.46
1:D:492:GLN:HB2	1:D:641:MET:HE3	1.98	0.46
1:A:227:LEU:O	1:A:231:ASN:HB2	2.15	0.46
1:A:352:ALA:CB	1:B:279:VAL:HG13	2.45	0.46
1:C:51:VAL:HG21	1:C:159:LEU:HD13	1.98	0.45
1:A:560:PHE:HB2	1:D:560:PHE:HB2	1.97	0.45
1:B:495:ASP:HB3	1:B:640:VAL:HG13	1.97	0.45
1:D:518:CYS:O	1:D:580:ARG:HD3	2.16	0.45
1:A:80:TYR:HB3	1:A:367:HIS:CD2	2.51	0.45
1:B:98:SER:O	1:B:102:GLU:HG2	2.16	0.45
1:A:448:THR:HG23	4:A:2139:HOH:O	2.17	0.45
1:B:70:GLN:OE1	1:B:222:GLN:HB3	2.17	0.45
1:C:322:TYR:CZ	1:D:459:GLN:HG2	2.52	0.44
1:B:81:GLY:H	1:B:84:THR:HG22	1.82	0.44
1:D:531:VAL:O	1:D:535:VAL:HG12	2.16	0.44
1:B:29:VAL:HG12	1:B:141:THR:HG21	1.99	0.44
1:A:392:LYS:HE3	4:A:2105:HOH:O	2.17	0.44
1:A:424:TYR:OH	1:C:85:GLY:HA2	2.18	0.44
1:D:641:MET:HE2	4:D:2121:HOH:O	2.18	0.44
1:B:583:GLU:HA	1:B:586:LYS:HE3	1.99	0.44
1:B:595:GLU:O	1:B:599:VAL:HG13	2.18	0.44
1:A:374:SER:HA	1:A:463:SER:HB2	2.00	0.43
1:B:523:ASP:O	1:B:527:ARG:HG3	2.18	0.43
1:D:426:LEU:HD21	1:D:641:MET:HE1	1.99	0.43
1:C:545:CYS:SG	1:C:589:SER:HA	2.58	0.43
1:C:547:PRO:O	1:C:553:LEU:HD13	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:70:GLN:OE1	1:D:222:GLN:HB3	2.18	0.43
1:B:80:TYR:HB3	1:B:367:HIS:CD2	2.53	0.43
1:B:255:GLU:HG2	1:B:331:LEU:HD13	2.01	0.43
1:A:392:LYS:HD3	1:A:392:LYS:HA	1.77	0.43
1:A:392:LYS:CE	4:A:2105:HOH:O	2.66	0.43
1:B:557:GLN:HG3	1:C:557:GLN:HG3	2.01	0.42
1:A:539:THR:HB	1:A:550:PRO:HG2	2.01	0.42
1:C:392:LYS:HE2	4:C:2105:HOH:O	2.18	0.42
1:C:559:CYS:O	1:C:562:THR:HG22	2.19	0.42
1:B:563:ILE:O	1:B:567:HIS:HB2	2.19	0.42
1:C:227:LEU:O	1:C:231:ASN:HB2	2.18	0.42
1:D:89:CYS:O	1:D:92:ARG:HG3	2.18	0.42
1:D:545:CYS:HA	1:D:552:LEU:HD13	2.02	0.42
1:C:43:LEU:O	1:C:130:ARG:NH2	2.52	0.42
1:C:86:PHE:CE2	1:C:104:LEU:HB2	2.55	0.42
2:D:1678:BQ7:HD2	2:D:1678:BQ7:O	2.19	0.42
1:A:114:THR:HG22	1:C:657:PHE:CZ	2.55	0.42
1:C:640:VAL:HG23	4:C:2153:HOH:O	2.19	0.41
1:B:182:LEU:HD21	1:B:234:SER:HB2	2.02	0.41
1:D:80:TYR:HB3	1:D:367:HIS:CD2	2.55	0.41
1:D:92:ARG:HB3	1:D:92:ARG:NH1	2.35	0.41
1:C:182:LEU:HD23	1:C:185:ILE:HD12	2.02	0.41
1:C:448:THR:CG2	4:C:2126:HOH:O	2.67	0.41
1:D:12:LYS:HE3	1:D:677:LEU:HB3	2.03	0.41
1:B:43:LEU:O	1:B:130:ARG:NH2	2.53	0.41
1:D:92:ARG:HB3	1:D:92:ARG:HH11	1.84	0.41
1:A:86:PHE:CE2	1:A:104:LEU:HB2	2.55	0.41
1:D:270:GLU:HB2	4:D:2059:HOH:O	2.21	0.41
1:A:29:VAL:HG13	1:A:53:LEU:HA	2.02	0.41
1:B:92:ARG:HH22	1:D:542:GLU:CD	2.24	0.41
1:C:88:ALA:HB2	1:C:458:ASN:HB2	2.01	0.41
1:C:392:LYS:CE	4:C:2105:HOH:O	2.68	0.41
1:D:384:ARG:HG2	1:D:444:ALA:HA	2.02	0.41
1:A:559:CYS:O	1:A:562:THR:HG22	2.21	0.41
1:B:638:THR:HA	1:B:645:ARG:HH22	1.86	0.41
1:A:198:ARG:NH2	4:A:2031:HOH:O	2.55	0.40
1:C:392:LYS:HD3	1:C:392:LYS:HA	1.75	0.40
1:D:551:LEU:HG	1:D:555:LEU:HD22	2.03	0.40
1:C:378:PHE:CE2	1:C:448:THR:HG21	2.56	0.40
1:C:552:LEU:O	1:C:556:LYS:HG3	2.21	0.40
1:A:140:PHE:CG	1:A:147:ILE:HG21	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:163:VAL:HA	1:B:198:ARG:O	2.21	0.40
1:A:547:PRO:O	1:A:553:LEU:HD13	2.21	0.40
1:B:383:VAL:O	1:B:387:VAL:HG23	2.21	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	622/705 (88%)	613 (99%)	9 (1%)	0	100	100
1	B	627/705 (89%)	615 (98%)	12 (2%)	0	100	100
1	C	627/705 (89%)	616 (98%)	11 (2%)	0	100	100
1	D	623/705 (88%)	610 (98%)	13 (2%)	0	100	100
All	All	2499/2820 (89%)	2454 (98%)	45 (2%)	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	537/592 (91%)	521 (97%)	16 (3%)	41	39
1	B	542/592 (92%)	524 (97%)	18 (3%)	38	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	542/592 (92%)	522 (96%)	20 (4%)	34	31
1	D	538/592 (91%)	518 (96%)	20 (4%)	34	31
All	All	2159/2368 (91%)	2085 (97%)	74 (3%)	37	34

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	THR
1	A	32	THR
1	A	59	ARG
1	A	92	ARG
1	A	107	CYS
1	A	268	ARG
1	A	279	VAL
1	A	334	LEU
1	A	353	ASN
1	A	448	THR
1	A	481	LEU
1	A	535	VAL
1	A	553	LEU
1	A	555	LEU
1	A	602	LEU
1	A	677	LEU
1	B	59	ARG
1	B	84	THR
1	B	92	ARG
1	B	107	CYS
1	B	209	GLU
1	B	268	ARG
1	B	334	LEU
1	B	353	ASN
1	B	404	GLU
1	B	448	THR
1	B	481	LEU
1	B	553	LEU
1	B	555	LEU
1	B	562	THR
1	B	591	ARG
1	B	599	VAL
1	B	640	VAL
1	B	673	LEU

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Mol	Chain	Res	Type
1	C	29	VAL
1	C	59	ARG
1	C	82	VAL
1	C	92	ARG
1	C	162	ASN
1	C	209	GLU
1	C	268	ARG
1	C	279	VAL
1	C	334	LEU
1	C	353	ASN
1	C	392	LYS
1	C	448	THR
1	C	535	VAL
1	C	548	THR
1	C	553	LEU
1	C	555	LEU
1	C	591	ARG
1	C	602	LEU
1	C	640	VAL
1	C	673	LEU
1	D	26	LYS
1	D	59	ARG
1	D	92	ARG
1	D	107	CYS
1	D	164	SER
1	D	202	ASP
1	D	268	ARG
1	D	279	VAL
1	D	334	LEU
1	D	353	ASN
1	D	392	LYS
1	D	404	GLU
1	D	481	LEU
1	D	548	THR
1	D	555	LEU
1	D	587	ARG
1	D	589	SER
1	D	602	LEU
1	D	640	VAL
1	D	673	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	360	HIS
1	B	362	ASN
1	D	47	HIS
1	D	162	ASN
1	D	671	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MDO	B	175	2,1	12,13,14	2.77	6 (50%)	15,18,20	3.05	5 (33%)
1	MDO	A	175	2,1	12,13,14	2.84	5 (41%)	15,18,20	2.90	4 (26%)
1	MDO	C	175	2,1	12,13,14	2.70	6 (50%)	15,18,20	3.07	3 (20%)
1	MDO	D	175	2,1	12,13,14	2.84	5 (41%)	15,18,20	2.69	5 (33%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MDO	B	175	2,1	-	2/4/23/24	0/1/1/1
1	MDO	A	175	2,1	-	3/4/23/24	0/1/1/1
1	MDO	C	175	2,1	-	2/4/23/24	0/1/1/1
1	MDO	D	175	2,1	-	2/4/23/24	0/1/1/1

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	175	MDO	O2-C2	6.48	1.36	1.23
1	A	175	MDO	O2-C2	6.42	1.36	1.23
1	B	175	MDO	O2-C2	5.98	1.35	1.23
1	C	175	MDO	O2-C2	5.44	1.34	1.23
1	B	175	MDO	O3-C3	4.41	1.44	1.19
1	A	175	MDO	O3-C3	4.17	1.43	1.19
1	C	175	MDO	O3-C3	4.02	1.42	1.19
1	D	175	MDO	O3-C3	3.90	1.42	1.19
1	C	175	MDO	C2-N3	-3.75	1.31	1.39
1	A	175	MDO	C2-N3	-3.25	1.32	1.39
1	A	175	MDO	CA1-C1	3.25	1.55	1.51
1	B	175	MDO	CA2-N2	-3.18	1.33	1.39
1	B	175	MDO	C2-N3	-3.17	1.32	1.39
1	D	175	MDO	CA2-N2	-3.14	1.33	1.39
1	D	175	MDO	C2-N3	-3.07	1.32	1.39
1	D	175	MDO	CA1-C1	3.05	1.55	1.51
1	C	175	MDO	C1-N2	2.77	1.36	1.32
1	C	175	MDO	CA2-N2	-2.74	1.34	1.39
1	A	175	MDO	CA2-N2	-2.69	1.34	1.39
1	C	175	MDO	CA1-C1	2.28	1.54	1.51
1	B	175	MDO	CA1-C1	2.14	1.54	1.51
1	B	175	MDO	CA2-C2	-2.06	1.39	1.43

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	175	MDO	CA2-C2-N3	9.58	107.90	103.37
1	B	175	MDO	CA2-C2-N3	8.24	107.27	103.37
1	A	175	MDO	CA2-C2-N3	7.40	106.87	103.37
1	D	175	MDO	CA2-C2-N3	6.75	106.56	103.37
1	A	175	MDO	O3-C3-CA3	-5.49	109.81	126.39
1	D	175	MDO	O3-C3-CA3	-5.40	110.07	126.39
1	B	175	MDO	O2-C2-CA2	-5.20	128.04	130.96
1	C	175	MDO	O3-C3-CA3	-5.17	110.77	126.39
1	B	175	MDO	O3-C3-CA3	-5.13	110.90	126.39
1	A	175	MDO	O2-C2-CA2	-4.90	128.21	130.96
1	D	175	MDO	O2-C2-CA2	-4.01	128.71	130.96
1	C	175	MDO	O2-C2-CA2	-3.37	129.07	130.96
1	D	175	MDO	N3-C1-N2	-2.85	109.48	111.45
1	A	175	MDO	N3-C1-N2	-2.81	109.51	111.45
1	B	175	MDO	N3-C1-N2	-2.33	109.84	111.45
1	B	175	MDO	CB2-CA2-C2	2.20	126.78	122.76
1	D	175	MDO	CB2-CA2-C2	2.16	126.71	122.76

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	175	MDO	N2-C1-CA1-CB
1	B	175	MDO	N2-C1-CA1-CB
1	C	175	MDO	N2-C1-CA1-CB
1	D	175	MDO	N2-C1-CA1-CB
1	A	175	MDO	C3-CA3-N3-C2
1	A	175	MDO	N3-C1-CA1-CB
1	B	175	MDO	N3-C1-CA1-CB
1	C	175	MDO	N3-C1-CA1-CB
1	D	175	MDO	N3-C1-CA1-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 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	$\# Z > 2$
3	GOL	B	1679	-	5,5,5	0.31	0	5,5,5	0.75	0
3	GOL	A	1679	-	5,5,5	0.13	0	5,5,5	0.46	0
2	BQ7	B	1678	1	12,14,14	1.39	1 (8%)	17,20,20	0.98	1 (5%)
2	BQ7	D	1678	1	12,14,14	1.32	1 (8%)	17,20,20	1.39	2 (11%)
2	BQ7	C	1678	1	12,14,14	1.35	2 (16%)	17,20,20	0.90	1 (5%)
2	BQ7	A	1678	1	12,14,14	1.36	1 (8%)	17,20,20	0.97	1 (5%)

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	GOL	B	1679	-	-	2/4/4/4	-
3	GOL	A	1679	-	-	3/4/4/4	-
2	BQ7	B	1678	1	-	5/14/16/16	0/1/1/1
2	BQ7	D	1678	1	-	4/14/16/16	0/1/1/1
2	BQ7	C	1678	1	-	5/14/16/16	0/1/1/1
2	BQ7	A	1678	1	-	5/14/16/16	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1678	BQ7	CG-CB	3.44	1.56	1.52
2	B	1678	BQ7	CG-CB	3.38	1.56	1.52
2	A	1678	BQ7	CG-CB	2.90	1.55	1.52
2	C	1678	BQ7	CG-CB	2.78	1.55	1.52
2	C	1678	BQ7	FS-CA	-2.15	1.32	1.36

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1678	BQ7	FS-CA-CB	3.43	113.44	109.43
2	A	1678	BQ7	FS-CA-CB	2.78	112.69	109.43
2	D	1678	BQ7	O-C-CA	2.45	118.32	112.69
2	C	1678	BQ7	O-C-CA	2.22	117.80	112.69
2	B	1678	BQ7	O-C-CA	2.01	117.32	112.69

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1678	BQ7	O-C-CA-FS
2	A	1678	BQ7	C-CA-CB-CG
2	A	1678	BQ7	FR-CA-CB-CG
2	B	1678	BQ7	C-CA-CB-CG
2	B	1678	BQ7	FR-CA-CB-CG
2	C	1678	BQ7	C-CA-CB-CG
2	C	1678	BQ7	FR-CA-CB-CG

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Mol	Chain	Res	Type	Atoms
2	D	1678	BQ7	O-C-CA-FS
2	D	1678	BQ7	C-CA-CB-CG
3	B	1679	GOL	O1-C1-C2-O2
3	A	1679	GOL	O1-C1-C2-C3
3	A	1679	GOL	C1-C2-C3-O3
3	B	1679	GOL	O1-C1-C2-C3
2	B	1678	BQ7	O-C-CA-FS
2	C	1678	BQ7	O-C-CA-FS
2	B	1678	BQ7	O1-C-CA-FS
2	C	1678	BQ7	O1-C-CA-FS
2	B	1678	BQ7	O1-C-CA-CB
2	C	1678	BQ7	O1-C-CA-CB
2	D	1678	BQ7	O1-C-CA-CB
3	A	1679	GOL	O1-C1-C2-O2
2	A	1678	BQ7	O1-C-CA-FS
2	D	1678	BQ7	O1-C-CA-FS
2	A	1678	BQ7	FR-CA-CB-N

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1678	BQ7	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

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	634/705 (89%)	0.08	30 (4%) 31 38	11, 24, 49, 60	0
1	B	639/705 (90%)	0.02	13 (2%) 65 71	12, 24, 40, 54	0
1	C	639/705 (90%)	-0.01	23 (3%) 42 50	12, 22, 42, 54	0
1	D	635/705 (90%)	-0.01	14 (2%) 62 68	11, 22, 45, 57	0
All	All	2547/2820 (90%)	0.02	80 (3%) 49 57	11, 23, 44, 60	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	576	THR	4.6
1	A	576	THR	4.0
1	A	580	ARG	3.7
1	C	591	ARG	3.6
1	A	515	ALA	3.5
1	A	522	ASN	3.5
1	C	576	THR	3.4
1	A	47	HIS	3.4
1	A	577	LEU	3.4
1	A	586	LYS	3.4
1	D	602	LEU	3.3
1	B	202	ASP	3.2
1	D	591	ARG	3.2
1	A	602	LEU	3.1
1	D	577	LEU	3.1
1	C	584	PHE	3.1
1	B	567	HIS	3.1
1	A	579	ASP	3.1
1	A	564	LEU	3.1
1	B	523	ASP	3.0
1	A	518	CYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	586	LYS	2.9
1	C	589	SER	2.9
1	C	566	LEU	2.9
1	A	521	PRO	2.9
1	A	584	PHE	2.9
1	C	518	CYS	2.8
1	C	586	LYS	2.7
1	D	564	LEU	2.7
1	C	599	VAL	2.7
1	A	520	LEU	2.7
1	A	523	ASP	2.7
1	D	578	VAL	2.7
1	B	565	ALA	2.7
1	C	590	ASP	2.6
1	A	451	VAL	2.6
1	D	579	ASP	2.6
1	A	581	LEU	2.6
1	A	566	LEU	2.6
1	D	521	PRO	2.6
1	A	578	VAL	2.5
1	C	579	ASP	2.5
1	C	581	LEU	2.5
1	A	447	VAL	2.5
1	B	545	CYS	2.5
1	C	605	LYS	2.5
1	C	575	ASP	2.5
1	C	580	ARG	2.5
1	A	217	ARG	2.4
1	A	591	ARG	2.4
1	A	202	ASP	2.4
1	A	565	ALA	2.4
1	C	574	THR	2.4
1	A	519	GLY	2.3
1	B	574	THR	2.3
1	C	522	ASN	2.3
1	A	587	ARG	2.3
1	B	47	HIS	2.3
1	B	564	LEU	2.3
1	A	527	ARG	2.3
1	A	524	THR	2.2
1	D	201	ASP	2.2
1	D	47	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	587	ARG	2.2
1	D	581	LEU	2.2
1	C	677	LEU	2.2
1	B	26	LYS	2.2
1	C	583	GLU	2.2
1	D	202	ASP	2.2
1	D	443	LEU	2.1
1	B	447	VAL	2.1
1	C	513	THR	2.1
1	B	566	LEU	2.1
1	C	577	LEU	2.1
1	B	522	ASN	2.1
1	C	565	ALA	2.1
1	A	448	THR	2.1
1	C	516	ASP	2.0
1	B	671	HIS	2.0
1	A	25	LYS	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	MDO	B	175	13/14	0.95	0.10	18,21,23,25	0
1	MDO	A	175	13/14	0.96	0.11	18,19,20,22	0
1	MDO	D	175	13/14	0.96	0.12	16,18,19,21	0
1	MDO	C	175	13/14	0.97	0.11	15,16,18,19	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	BQ7	A	1678	14/14	0.86	0.16	26,28,36,37	0
2	BQ7	B	1678	14/14	0.90	0.13	27,31,37,40	0
3	GOL	A	1679	6/6	0.90	0.17	28,30,32,36	0
3	GOL	B	1679	6/6	0.90	0.13	28,32,32,35	0
2	BQ7	C	1678	14/14	0.93	0.12	24,25,30,31	0
2	BQ7	D	1678	14/14	0.94	0.11	27,29,34,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.