Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 03:02 PM GMT

PDB ID	:	4BAA
Title	:	Redesign of a Phenylalanine Aminomutase into a beta-Phenylalanine Ammonia Lyase
Authors	:	Bartsch, S.; Wybenga, G.G.; Jansen, M.; Heberling, M.M.; Wu, B.; Dijkstra, B.W.; Janssen, D.B.
Deposited on	:	2012-09-12
Resolution	:	2.50 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

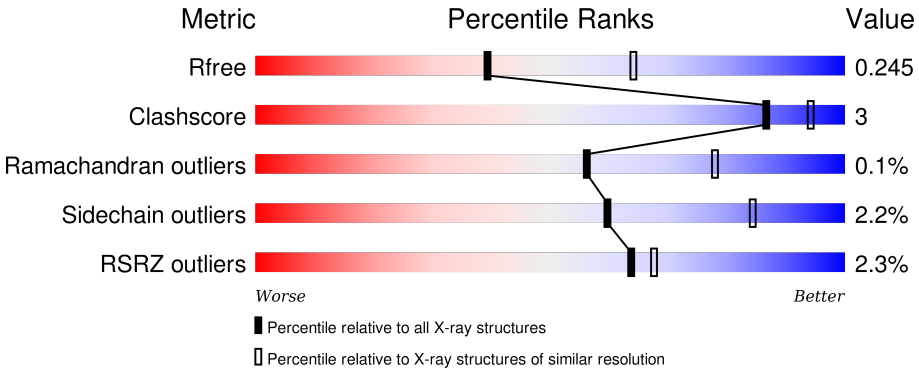
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 <=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	2% 82% 8% 10%
1	B	705	2% 83% 8% 9%
1	C	705	% 79% 8% 12%
1	D	705	3% 83% 7% • 9%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 19964 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
1	A	636	Total	C	N	O	S	0	0	0
			4933	3129	847	934	23			
1	B	644	Total	C	N	O	S	0	0	0
			4998	3171	857	947	23			
1	C	618	Total	C	N	O	S	0	0	0
			4812	3062	825	903	22			
1	D	642	Total	C	N	O	S	0	0	0
			4981	3160	855	943	23			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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
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
A	92	SER	ARG	ENGINEERED MUTATION	UNP Q68G84

Continued on next page...

Continued from previous page...

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	-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
B	92	SER	ARG	ENGINEERED MUTATION	UNP Q68G84
B	175	MDO	ALA	CHROMOPHORE	UNP Q68G84
B	175	MDO	SER	CHROMOPHORE	UNP Q68G84
B	175	MDO	GLY	CHROMOPHORE	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
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

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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
C	92	SER	ARG	ENGINEERED MUTATION	UNP Q68G84
C	175	MDO	ALA	CHROMOPHORE	UNP Q68G84
C	175	MDO	SER	CHROMOPHORE	UNP Q68G84
C	175	MDO	GLY	CHROMOPHORE	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
D	92	SER	ARG	ENGINEERED MUTATION	UNP Q68G84
D	175	MDO	ALA	CHROMOPHORE	UNP Q68G84
D	175	MDO	SER	CHROMOPHORE	UNP Q68G84
D	175	MDO	GLY	CHROMOPHORE	UNP Q68G84

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	67	Total O 67 67	0	0
2	B	59	Total O 59 59	0	0
2	C	61	Total O 61 61	0	0

Continued on next page...

Continued from previous page...

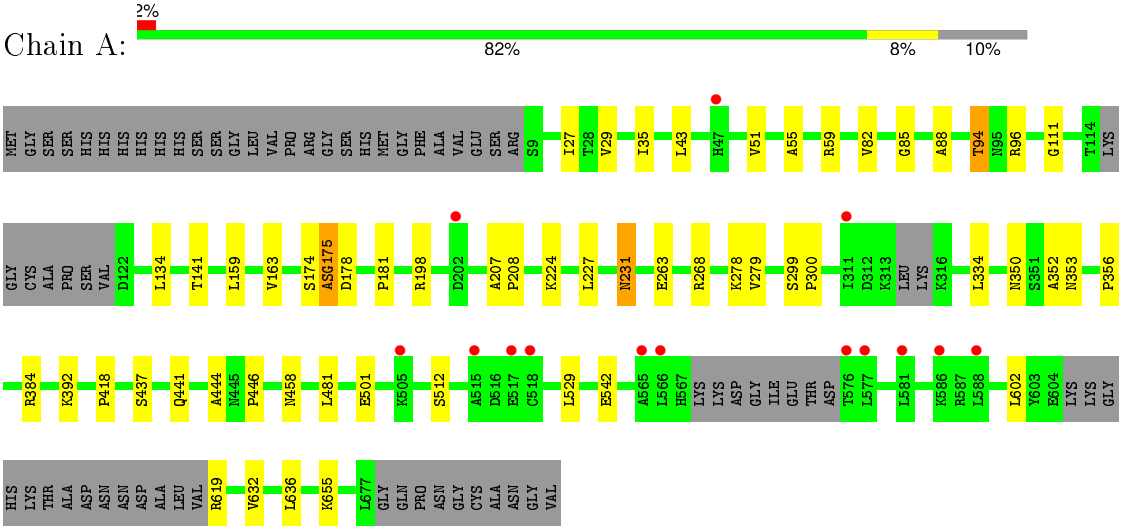
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	53	Total O 53 53	0	0

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.

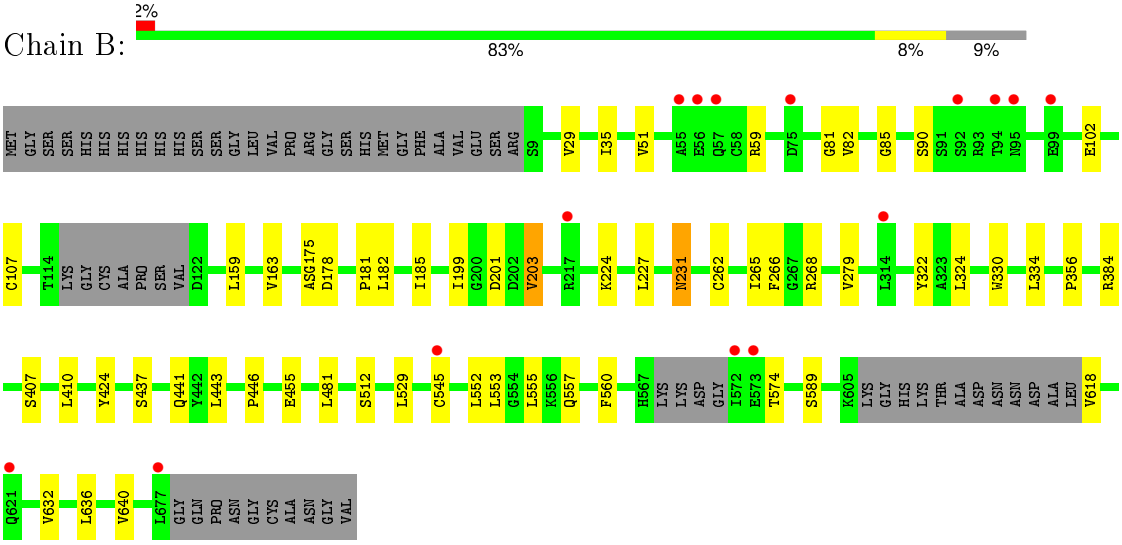
- Molecule 1: PHENYLALANINE AMMONIA-LYASE

Chain A:



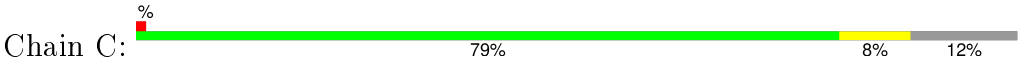
- Molecule 1: PHENYLALANINE AMMONIA-LYASE

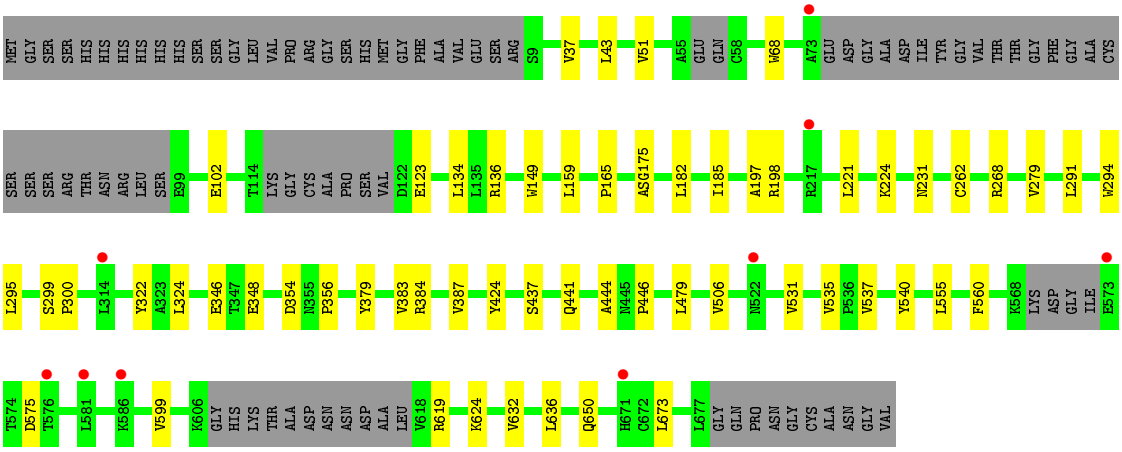
Chain B:



- Molecule 1: PHENYLALANINE AMMONIA-LYASE

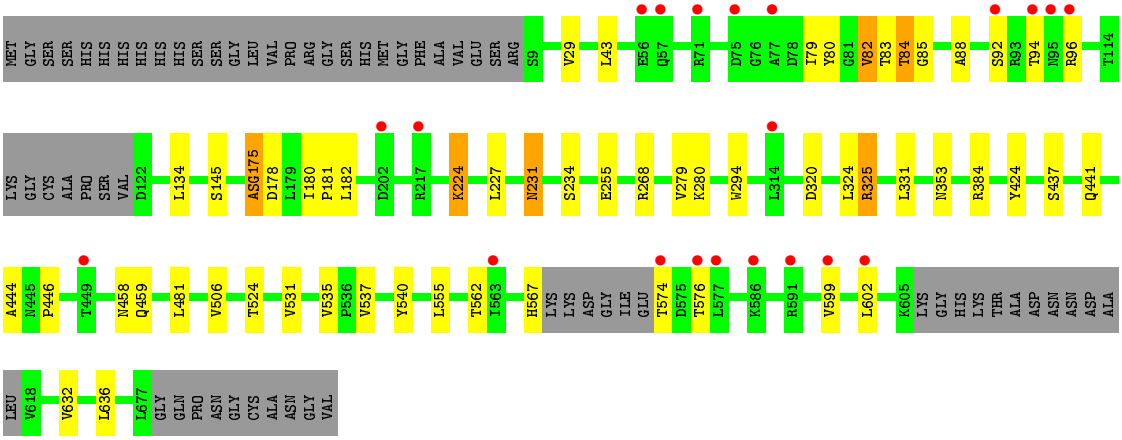
Chain C:





- Molecule 1: PHENYLALANINE AMMONIA-LYASE

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	99.30Å 145.84Å 99.41Å 90.00° 99.96° 90.00°	Depositor
Resolution (Å)	48.90 – 2.50 48.05 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.0 (48.90-2.50) 98.0 (48.05-2.50)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.39 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.209 , 0.246 0.208 , 0.245	Depositor DCC
R_{free} test set	4821 reflections (5.38%)	DCC
Wilson B-factor (Å^2)	31.5	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 25.8	EDS
Estimated twinning fraction	0.022 for l,-k,h	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	0 of 94332 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	19964	wwPDB-VP
Average B, all atoms (Å^2)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: MDO

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	0.39	0/5004	0.49	0/6790
1	B	0.40	1/5070 (0.0%)	0.49	0/6880
1	C	0.41	3/4880 (0.1%)	0.48	0/6618
1	D	0.45	1/5053 (0.0%)	0.50	0/6857
All	All	0.41	5/20007 (0.0%)	0.49	0/27145

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	2
1	C	0	2
1	D	0	2
All	All	0	9

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	330	TRP	CD2-CE2	5.10	1.47	1.41
1	C	68	TRP	CD2-CE2	5.05	1.47	1.41
1	D	294	TRP	CD2-CE2	5.03	1.47	1.41
1	C	149	TRP	CD2-CE2	5.03	1.47	1.41
1	C	294	TRP	CD2-CE2	5.02	1.47	1.41

There are no bond angle outliers.

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	174	SER	Mainchain
1	A	175	MDO	Mainchain,Peptide
1	B	175	MDO	Mainchain,Peptide
1	C	175	MDO	Mainchain,Peptide
1	D	175	MDO	Mainchain,Peptide

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	4933	0	4980	29	0
1	B	4998	0	5055	25	0
1	C	4812	0	4892	32	0
1	D	4981	0	5038	33	0
2	A	67	0	0	0	0
2	B	59	0	0	1	0
2	C	61	0	0	0	0
2	D	53	0	0	0	0
All	All	19964	0	19965	106	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 (106) 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:83:THR:HG23	1:D:94:THR:O	1.63	0.96
1:D:145:SER:O	1:D:224:LYS:HE3	1.70	0.92
1:D:320:ASP:O	1:D:325:ARG:NH1	2.03	0.89
1:D:83:THR:CG2	1:D:94:THR:O	2.20	0.88
1:A:35:ILE:H	1:A:350:ASN:HD21	1.26	0.81
1:D:506:VAL:HG21	1:D:599:VAL:HG21	1.71	0.72
1:D:29:VAL:O	1:D:29:VAL:HG23	1.87	0.71
1:A:224:LYS:HE2	1:A:356:PRO:HD2	1.71	0.71
1:B:407:SER:HB3	1:B:410:LEU:HB2	1.74	0.69
1:B:224:LYS:HE2	1:B:356:PRO:HD2	1.76	0.66
1:A:352:ALA:HB3	1:B:279:VAL:CG1	2.27	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:29:VAL:O	1:D:29:VAL:CG2	2.46	0.63
1:C:506:VAL:HG21	1:C:599:VAL:HG21	1.80	0.62
1:D:227:LEU:O	1:D:231:ASN:HB2	2.02	0.59
1:B:29:VAL:HG12	1:B:35:ILE:HD11	1.83	0.59
1:B:424:TYR:OH	1:D:85:GLY:HA2	2.02	0.58
1:A:29:VAL:HG12	1:A:141:THR:HG21	1.85	0.58
1:A:35:ILE:H	1:A:350:ASN:ND2	2.00	0.58
1:C:446:PRO:HD3	1:D:446:PRO:HD3	1.86	0.58
1:D:224:LYS:O	1:D:224:LYS:HG3	2.04	0.57
1:B:512:SER:HB2	1:B:529:LEU:HD21	1.87	0.57
1:D:437:SER:O	1:D:441:GLN:HG2	2.05	0.57
1:D:80:TYR:HA	1:D:84:THR:HG23	1.87	0.56
1:A:227:LEU:O	1:A:231:ASN:HB2	2.07	0.55
1:C:43:LEU:HD13	1:C:134:LEU:HD22	1.89	0.54
1:B:632:VAL:HA	1:B:636:LEU:HD12	1.89	0.53
1:A:446:PRO:HD3	1:B:446:PRO:HD3	1.90	0.52
1:B:384:ARG:HD2	1:B:443:LEU:O	2.10	0.52
1:A:352:ALA:HB3	1:B:279:VAL:HG12	1.92	0.51
1:C:632:VAL:HA	1:C:636:LEU:HD12	1.93	0.50
1:D:531:VAL:O	1:D:535:VAL:HG22	2.12	0.50
1:C:384:ARG:HG2	1:C:444:ALA:HA	1.93	0.50
1:C:51:VAL:HG21	1:C:159:LEU:HD13	1.94	0.50
1:B:178:ASP:HB3	1:B:181:PRO:HG2	1.93	0.49
1:D:632:VAL:HA	1:D:636:LEU:HD12	1.93	0.49
1:B:227:LEU:O	1:B:231:ASN:HB2	2.12	0.49
1:A:111:GLY:O	1:C:650:GLN:HG3	2.13	0.48
1:C:300:PRO:HB2	1:C:619:ARG:HG3	1.94	0.48
1:A:94:THR:HG22	1:A:96:ARG:H	1.79	0.48
1:A:384:ARG:HG2	1:A:444:ALA:HA	1.96	0.48
1:A:632:VAL:HA	1:A:636:LEU:HD12	1.96	0.48
1:A:85:GLY:HA2	1:C:424:TYR:OH	2.14	0.48
1:D:80:TYR:HA	1:D:84:THR:CG2	2.43	0.47
1:C:182:LEU:HD23	1:C:185:ILE:HD12	1.96	0.47
1:B:437:SER:O	1:B:441:GLN:HG2	2.14	0.47
1:B:85:GLY:HA2	1:D:424:TYR:OH	2.14	0.47
1:C:506:VAL:CG2	1:C:599:VAL:HG21	2.43	0.47
1:B:51:VAL:HG21	1:B:159:LEU:HD13	1.95	0.47
1:C:291:LEU:HD11	1:C:673:LEU:HD22	1.98	0.46
1:A:178:ASP:HB3	1:A:181:PRO:HG2	1.96	0.46
1:C:387:VAL:HG13	1:C:479:LEU:HD22	1.97	0.46
1:B:182:LEU:HD23	1:B:185:ILE:HD12	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:136:ARG:HD3	1:C:182:LEU:HD22	1.97	0.46
1:A:299:SER:HA	1:A:300:PRO:HD3	1.81	0.46
1:D:255:GLU:HG2	1:D:331:LEU:HD13	1.98	0.46
1:A:43:LEU:HD22	1:A:134:LEU:HD22	1.99	0.45
1:B:265:ILE:O	1:B:266:PHE:HB2	2.14	0.45
1:C:322:TYR:HE2	1:D:175:MDO:HB1	1.81	0.45
1:D:384:ARG:HG2	1:D:444:ALA:HA	1.98	0.45
1:A:88:ALA:HB2	1:A:458:ASN:HB2	1.98	0.45
1:B:557:GLN:HB3	2:B:2054:HOH:O	2.17	0.45
1:C:537:VAL:HA	1:C:540:TYR:CE2	2.51	0.45
1:A:207:ALA:N	1:A:208:PRO:HD2	2.32	0.45
1:A:636:LEU:HD22	1:A:655:LYS:HB3	1.98	0.45
1:C:437:SER:O	1:C:441:GLN:HG2	2.17	0.45
1:D:182:LEU:HD21	1:D:234:SER:HB2	1.99	0.45
1:A:418:PRO:O	1:A:542:GLU:HG3	2.17	0.45
1:D:88:ALA:HB2	1:D:458:ASN:HB2	1.99	0.44
1:D:567:HIS:HA	1:D:574:THR:HG21	1.98	0.44
1:A:55:ALA:O	1:A:59:ARG:HB3	2.17	0.44
1:B:81:GLY:HA3	1:B:227:LEU:HD22	1.99	0.44
1:C:224:LYS:HE3	1:C:356:PRO:HD2	1.98	0.44
1:A:512:SER:HB2	1:A:529:LEU:HD21	1.99	0.44
1:A:263:GLU:OE2	1:A:299:SER:OG	2.28	0.44
1:B:560:PHE:HB2	1:C:560:PHE:HB2	1.99	0.44
1:A:51:VAL:HG21	1:A:159:LEU:HD13	1.99	0.44
1:A:175:MDO:HB1	1:B:322:TYR:HE2	1.83	0.44
1:C:123:GLU:HG3	1:C:198:ARG:HH22	1.83	0.43
1:D:43:LEU:HD22	1:D:134:LEU:HD22	2.00	0.43
1:D:537:VAL:HA	1:D:540:TYR:CE2	2.53	0.43
1:C:348:GLU:OE1	1:D:280:LYS:HE3	2.18	0.43
1:A:27:ILE:CD1	1:A:43:LEU:HB2	2.49	0.42
1:C:531:VAL:O	1:C:535:VAL:HG22	2.19	0.42
1:D:82:VAL:HG23	1:D:83:THR:OG1	2.18	0.42
1:C:322:TYR:CZ	1:D:459:GLN:HG2	2.54	0.42
1:A:437:SER:O	1:A:441:GLN:HG2	2.20	0.42
1:C:165:PRO:HA	1:C:197:ALA:HA	2.01	0.42
1:B:199:ILE:HB	1:B:203:VAL:HG22	2.01	0.42
1:D:180:ILE:HB	1:D:181:PRO:HD3	2.02	0.41
1:C:43:LEU:HD11	1:C:51:VAL:HG22	2.02	0.41
1:B:545:CYS:SG	1:B:589:SER:HA	2.61	0.41
1:D:83:THR:HG22	1:D:83:THR:O	2.20	0.41
1:C:102:GLU:HG3	1:C:221:LEU:HD12	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:379:TYR:O	1:C:383:VAL:HG23	2.20	0.41
1:D:79:ILE:O	1:D:84:THR:HG23	2.20	0.41
1:D:84:THR:HA	1:D:92:SER:O	2.21	0.41
1:B:163:VAL:HG22	1:B:199:ILE:HG12	2.03	0.41
1:D:524:THR:HG23	1:D:562:THR:HG21	2.01	0.41
1:C:295:LEU:HA	1:C:624:LYS:HD2	2.02	0.41
1:A:501:GLU:OE2	1:A:619:ARG:NH1	2.51	0.41
1:C:262:CYS:HB2	1:C:324:LEU:HD11	2.03	0.41
1:C:299:SER:HA	1:C:300:PRO:HD3	1.91	0.41
1:B:262:CYS:HB2	1:B:324:LEU:HD11	2.03	0.41
1:C:136:ARG:HH22	1:C:354:ASP:HB3	1.86	0.40
1:C:37:VAL:HG13	1:C:346:GLU:HG3	2.02	0.40
1:A:163:VAL:HA	1:A:198:ARG:O	2.22	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	625/705 (89%)	609 (97%)	16 (3%)	0	100	100
1	B	635/705 (90%)	620 (98%)	14 (2%)	1 (0%)	52	75
1	C	605/705 (86%)	595 (98%)	10 (2%)	0	100	100
1	D	633/705 (90%)	617 (98%)	15 (2%)	1 (0%)	52	75
All	All	2498/2820 (89%)	2441 (98%)	55 (2%)	2 (0%)	56	78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	178	ASP
1	B	90	SER

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	538/592 (91%)	527 (98%)	11 (2%)	63 86
1	B	546/592 (92%)	529 (97%)	17 (3%)	47 75
1	C	526/592 (89%)	521 (99%)	5 (1%)	82 95
1	D	544/592 (92%)	530 (97%)	14 (3%)	54 81
All	All	2154/2368 (91%)	2107 (98%)	47 (2%)	60 84

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	82	VAL
1	A	94	THR
1	A	231	ASN
1	A	268	ARG
1	A	278	LYS
1	A	279	VAL
1	A	334	LEU
1	A	353	ASN
1	A	392	LYS
1	A	481	LEU
1	A	602	LEU
1	B	59	ARG
1	B	82	VAL
1	B	102	GLU
1	B	107	CYS
1	B	201	ASP
1	B	203	VAL
1	B	231	ASN
1	B	268	ARG
1	B	334	LEU
1	B	455	GLU
1	B	481	LEU
1	B	552	LEU
1	B	553	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	555	LEU
1	B	574	THR
1	B	618	VAL
1	B	640	VAL
1	C	231	ASN
1	C	268	ARG
1	C	279	VAL
1	C	555	LEU
1	C	575	ASP
1	D	82	VAL
1	D	84	THR
1	D	96	ARG
1	D	224	LYS
1	D	231	ASN
1	D	268	ARG
1	D	279	VAL
1	D	324	LEU
1	D	325	ARG
1	D	353	ASN
1	D	481	LEU
1	D	555	LEU
1	D	576	THR
1	D	602	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	231	ASN
1	A	350	ASN
1	A	413	ASN
1	A	459	GLN
1	A	671	HIS
1	B	162	ASN
1	B	231	ASN
1	C	231	ASN
1	C	621	GLN
1	D	231	ASN

5.3.3 RNA

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	A	175	1	11,13,14	2.76	5 (45%)	13,18,20	3.35	3 (23%)
1	MDO	B	175	1	11,13,14	2.75	5 (45%)	13,18,20	3.18	3 (23%)
1	MDO	C	175	1	11,13,14	2.83	5 (45%)	13,18,20	3.02	3 (23%)
1	MDO	D	175	1	11,13,14	2.78	5 (45%)	13,18,20	3.07	3 (23%)

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
1	MDO	A	175	1	-	0/4/23/24	0/1/1/1
1	MDO	B	175	1	-	0/4/23/24	0/1/1/1
1	MDO	C	175	1	-	0/4/23/24	0/1/1/1
1	MDO	D	175	1	-	0/4/23/24	0/1/1/1

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	175	MDO	C2-N3	-3.30	1.32	1.39
1	B	175	MDO	C2-N3	-3.21	1.32	1.39
1	A	175	MDO	C2-N3	-3.18	1.33	1.39
1	D	175	MDO	C2-N3	-3.14	1.33	1.39
1	D	175	MDO	CA2-N2	-2.37	1.33	1.39
1	B	175	MDO	CA2-N2	-2.37	1.33	1.39
1	A	175	MDO	CA2-N2	-2.36	1.33	1.39
1	C	175	MDO	CA2-N2	-2.34	1.33	1.39
1	A	175	MDO	CA-C1	2.97	1.55	1.51
1	D	175	MDO	CA-C1	2.98	1.55	1.51
1	B	175	MDO	CA-C1	3.08	1.55	1.51

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	175	MDO	CA-C1	3.30	1.55	1.51
1	B	175	MDO	O-C	3.66	1.43	1.19
1	A	175	MDO	O-C	3.68	1.43	1.19
1	C	175	MDO	O-C	3.71	1.43	1.19
1	D	175	MDO	O-C	3.73	1.44	1.19
1	B	175	MDO	O2-C2	6.18	1.36	1.23
1	A	175	MDO	O2-C2	6.25	1.36	1.23
1	D	175	MDO	O2-C2	6.33	1.36	1.23
1	C	175	MDO	O2-C2	6.33	1.36	1.23

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	175	MDO	O2-C2-CA2	-8.47	126.38	130.95
1	B	175	MDO	O2-C2-CA2	-7.95	126.66	130.95
1	C	175	MDO	O2-C2-CA2	-7.59	126.85	130.95
1	D	175	MDO	O2-C2-CA2	-7.43	126.93	130.95
1	B	175	MDO	N3-C1-N2	-2.66	109.50	111.56
1	D	175	MDO	N3-C1-N2	-2.59	109.56	111.56
1	A	175	MDO	N3-C1-N2	-2.58	109.56	111.56
1	C	175	MDO	N3-C1-N2	-2.52	109.61	111.56
1	C	175	MDO	CA2-C2-N3	7.15	107.13	103.39
1	D	175	MDO	CA2-C2-N3	7.42	107.26	103.39
1	B	175	MDO	CA2-C2-N3	7.47	107.29	103.39
1	A	175	MDO	CA2-C2-N3	7.79	107.46	103.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	175	MDO	1	0
1	D	175	MDO	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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, 95^{th} 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	635/705 (90%)	0.05	14 (2%)	65	69	21, 38, 60, 72	0
1	B	643/705 (91%)	0.09	15 (2%)	64	67	21, 37, 63, 84	0
1	C	617/705 (87%)	0.01	9 (1%)	76	79	20, 36, 54, 76	0
1	D	641/705 (90%)	0.10	21 (3%)	50	55	21, 37, 63, 77	0
All	All	2536/2820 (89%)	0.06	59 (2%)	64	67	20, 37, 61, 84	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	314	LEU	5.1
1	C	314	LEU	3.7
1	B	572	ILE	3.5
1	C	581	LEU	3.4
1	A	577	LEU	3.3
1	D	77	ALA	3.3
1	D	577	LEU	3.2
1	D	94	THR	3.2
1	C	576	THR	3.2
1	B	56	GLU	3.1
1	B	314	LEU	3.0
1	D	92	SER	2.9
1	D	602	LEU	2.9
1	B	94	THR	2.8
1	A	581	LEU	2.7
1	C	586	LYS	2.7
1	A	515	ALA	2.6
1	A	202	ASP	2.6
1	D	563	ILE	2.6
1	D	576	THR	2.6
1	D	586	LYS	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	591	ARG	2.5
1	D	71	ARG	2.5
1	D	95	ASN	2.5
1	A	586	LYS	2.5
1	D	57	GLN	2.5
1	B	677	LEU	2.4
1	B	57	GLN	2.4
1	D	56	GLU	2.4
1	B	95	ASN	2.4
1	D	202	ASP	2.4
1	D	574	THR	2.4
1	B	55	ALA	2.4
1	C	217	ARG	2.4
1	B	573	GLU	2.4
1	D	449	THR	2.3
1	A	576	THR	2.3
1	A	588	LEU	2.2
1	B	217	ARG	2.2
1	A	517	GLU	2.2
1	B	99	GLU	2.2
1	A	565	ALA	2.2
1	A	518	CYS	2.2
1	B	545	CYS	2.2
1	D	75	ASP	2.2
1	C	671	HIS	2.2
1	A	311	ILE	2.1
1	C	73	ALA	2.1
1	C	522	ASN	2.1
1	A	47	HIS	2.1
1	D	599	VAL	2.1
1	A	505	LYS	2.1
1	B	92	SER	2.1
1	D	217	ARG	2.1
1	A	566	LEU	2.1
1	B	75	ASP	2.1
1	C	573	GLU	2.0
1	B	621	GLN	2.0
1	D	96	ARG	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} 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
1	MDO	C	175	13/14	0.95	0.13	-	30,32,32,32	0
1	MDO	A	175	13/14	0.95	0.14	-	28,29,29,30	0
1	MDO	D	175	13/14	0.90	0.19	-	31,32,33,33	0
1	MDO	B	175	13/14	0.93	0.16	-	31,32,33,33	0

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.