



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 17, 2023 – 05:03 AM EDT

PDB ID : 2EFU
Title : The crystal structure of D-amino acid amidase from *Ochrobactrum anthropi* SV3 complexed with L-phenylalanine
Authors : Okazaki, S.; Suzuki, A.; Mizushima, T.; Komeda, H.; Asano, Y.; Yamane, T.
Deposited on : 2007-02-26
Resolution : 2.30 Å (reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<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 : 1.8.5 (274361), 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

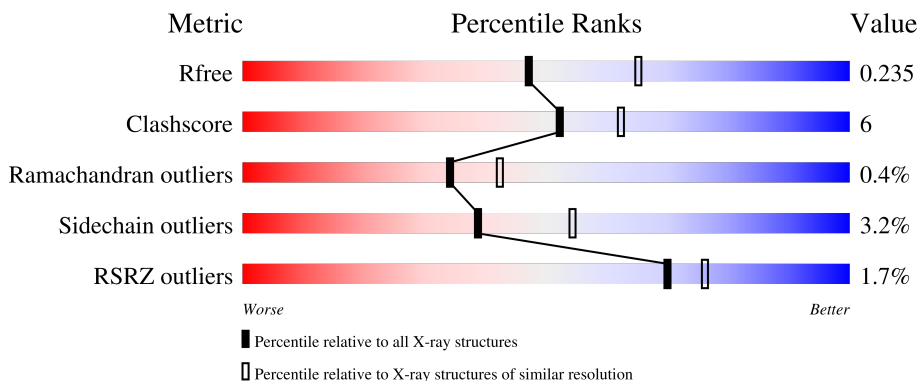
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


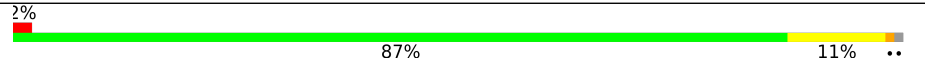
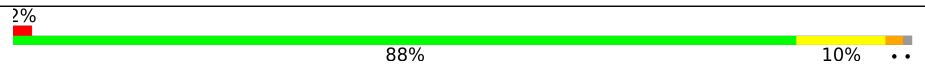

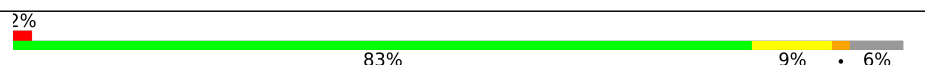
The reported resolution of this entry is 2.30 Å.

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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	363	 2% 87% 12%
1	B	363	 2% 87% 11%
1	C	363	 2% 88% 10%
1	D	363	 0% 85% 11% 3%
1	E	363	 2% 83% 9% 6%

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Mol	Chain	Length	Quality of chain
1	F	363	 A horizontal bar chart showing the quality of chain. The bar is divided into four segments: a small red segment at the beginning labeled '2%', a large green segment labeled '78%', a yellow segment labeled '12%', and a small grey segment at the end labeled '9%'.

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 17915 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.

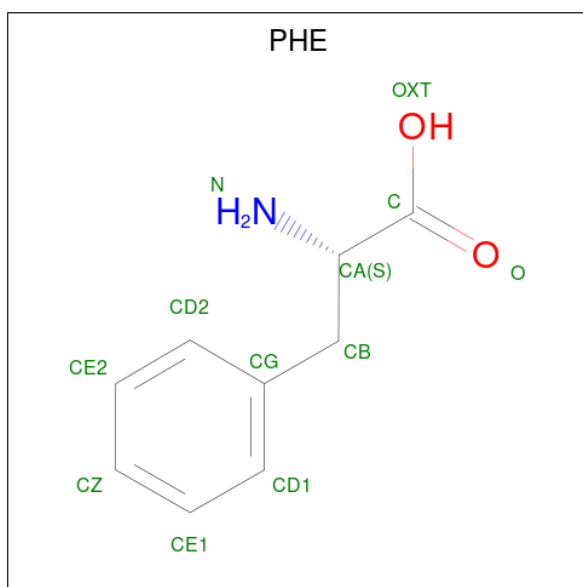
- Molecule 1 is a protein called D-Amino acid amidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	362	2819	1780	487	535	17	0	1	0
1	B	359	2806	1774	484	531	17	0	2	0
1	C	361	2805	1772	485	532	16	0	0	0
1	D	350	2726	1725	474	511	16	0	1	0
1	E	342	2665	1688	462	499	16	0	0	0
1	F	330	2589	1644	447	482	16	0	2	0

- Molecule 2 is BARIUM ION (three-letter code: BA) (formula: Ba).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total 4	Ba 4	0	0
2	B	2	Total 2	Ba 2	0	0
2	C	4	Total 4	Ba 4	0	0
2	D	5	Total 6	Ba 6	0	1
2	E	4	Total 4	Ba 4	0	0
2	F	6	Total 6	Ba 6	0	0

- Molecule 3 is PHENYLALANINE (three-letter code: PHE) (formula: C₉H₁₁NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	12	9	1	2	0	0
3	B	1	12	9	1	2	0	0
3	C	1	12	9	1	2	0	0
3	D	1	12	9	1	2	0	0
3	E	1	12	9	1	2	0	0
3	F	1	12	9	1	2	0	0

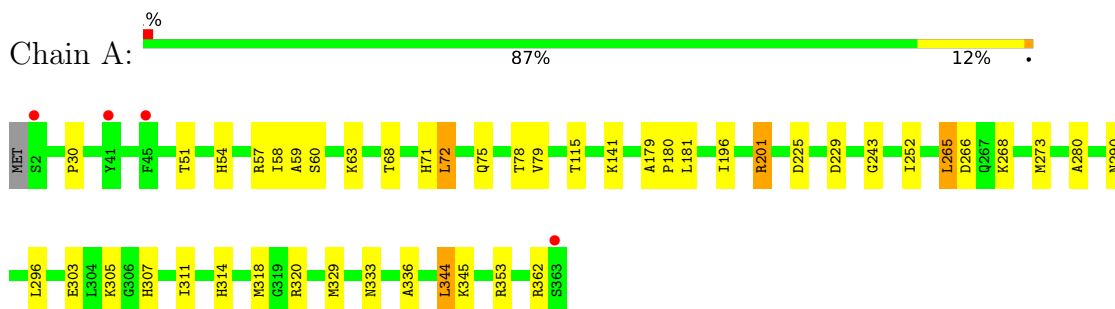
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	223	223	223	0	0
4	B	304	304	304	0	0
4	C	248	248	248	0	0
4	D	255	255	255	0	0
4	E	198	198	198	0	0
4	F	179	179	179	0	0

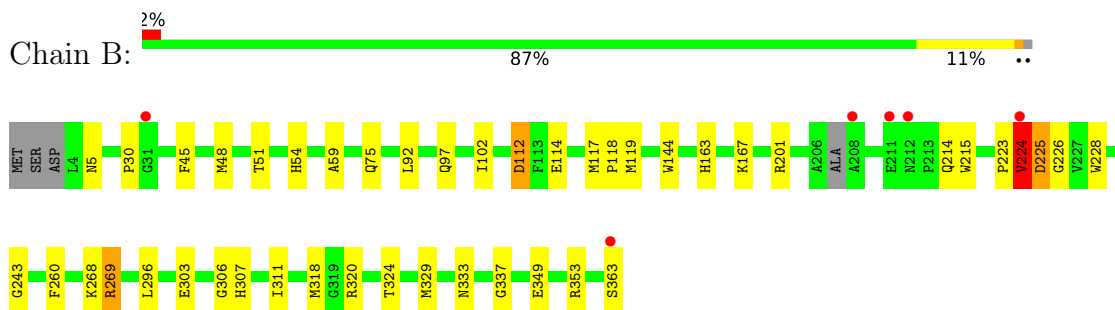
3 Residue-property plots [i](#)

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.

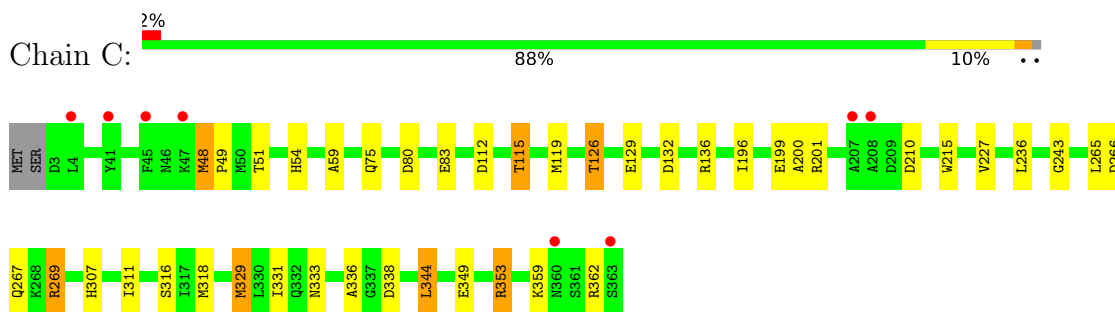
- Molecule 1: D-Amino acid amidase



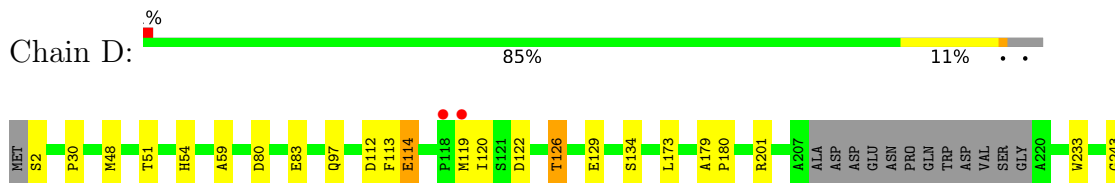
- Molecule 1: D-Amino acid amidase



- Molecule 1: D-Amino acid amidase

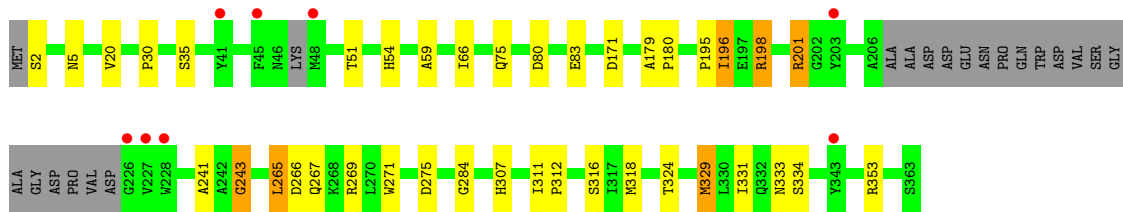
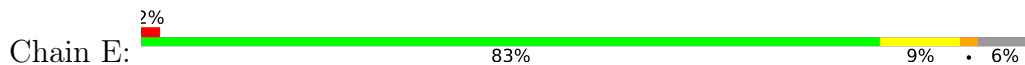


- Molecule 1: D-Amino acid amidase

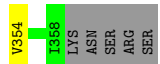
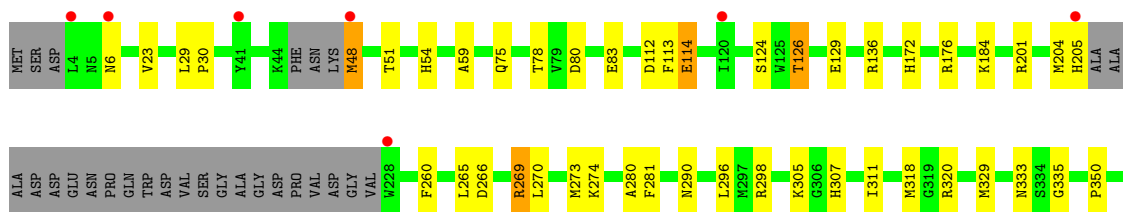
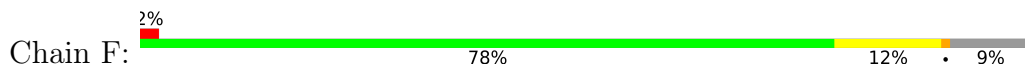




• Molecule 1: D-Amino acid amidase



• Molecule 1: D-Amino acid amidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	77.47Å 123.27Å 116.16Å 90.00° 104.05° 90.00°	Depositor
Resolution (Å)	47.67 – 2.30 47.66 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.67-2.30) 100.0 (47.66-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.86 (at 2.29Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.170 , 0.235 0.170 , 0.235	Depositor DCC
R_{free} test set	4735 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	23.1	Xtrriage
Anisotropy	0.075	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17915	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 2.67% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section:
BA

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	0.46	0/2891	0.59	0/3921
1	B	0.53	0/2880	0.65	1/3904 (0.0%)
1	C	0.49	0/2877	0.61	0/3902
1	D	0.50	0/2797	0.60	0/3788
1	E	0.46	0/2731	0.56	0/3697
1	F	0.49	0/2660	0.61	1/3602 (0.0%)
All	All	0.49	0/16836	0.61	2/22814 (0.0%)

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	B	0	2
1	F	0	1
All	All	0	3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	114	GLU	N-CA-C	-7.49	90.78	111.00
1	B	226	GLY	N-CA-C	-5.01	100.56	113.10

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	224	VAL	Peptide
1	B	225	ASP	Peptide
1	F	113	PHE	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	2819	0	2719	32	0
1	B	2806	0	2711	26	0
1	C	2805	0	2706	26	0
1	D	2726	0	2651	31	0
1	E	2665	0	2587	31	0
1	F	2589	0	2522	39	0
2	A	4	0	0	0	0
2	B	2	0	0	0	0
2	C	4	0	0	1	0
2	D	6	0	0	0	0
2	E	4	0	0	0	0
2	F	6	0	0	0	0
3	A	12	0	8	0	0
3	B	12	0	8	0	0
3	C	12	0	8	0	0
3	D	12	0	8	0	0
3	E	12	0	8	0	0
3	F	12	0	8	0	0
4	A	223	0	0	4	0
4	B	304	0	0	7	0
4	C	248	0	0	4	0
4	D	255	0	0	2	0
4	E	198	0	0	1	0
4	F	179	0	0	4	0
All	All	17915	0	15944	177	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 6.

The worst 5 of 177 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)
2:C:3001:BA:BA	4:C:3068:HOH:O	1.25	1.27
1:A:353:ARG:NH1	4:A:3239:HOH:O	1.92	1.02
1:F:265:LEU:CD1	1:F:273:MET:CE	2.38	1.02
1:F:265:LEU:HD12	1:F:273:MET:CE	1.92	0.99
1:A:51:THR:H	1:A:54:HIS:HD2	1.05	0.97

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	361/363 (99%)	353 (98%)	7 (2%)	1 (0%)	41	50
1	B	357/363 (98%)	342 (96%)	12 (3%)	3 (1%)	19	23
1	C	359/363 (99%)	348 (97%)	10 (3%)	1 (0%)	41	50
1	D	347/363 (96%)	332 (96%)	14 (4%)	1 (0%)	41	50
1	E	336/363 (93%)	326 (97%)	8 (2%)	2 (1%)	25	31
1	F	326/363 (90%)	314 (96%)	12 (4%)	0	100	100
All	All	2086/2178 (96%)	2015 (97%)	63 (3%)	8 (0%)	34	42

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	224	VAL
1	C	243	GLY
1	A	243	GLY
1	B	225	ASP
1	B	243	GLY

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	301/301 (100%)	292 (97%)	9 (3%)	41	57
1	B	300/301 (100%)	293 (98%)	7 (2%)	50	67
1	C	299/301 (99%)	288 (96%)	11 (4%)	34	48
1	D	291/301 (97%)	282 (97%)	9 (3%)	40	55
1	E	285/301 (95%)	277 (97%)	8 (3%)	43	60
1	F	277/301 (92%)	265 (96%)	12 (4%)	29	40
All	All	1753/1806 (97%)	1697 (97%)	56 (3%)	39	54

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	114	GLU
1	F	307	HIS
1	D	329	MET
1	F	269	ARG
1	F	114	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	267	GLN
1	F	205	HIS
1	D	54	HIS
1	E	205	HIS
1	D	6	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 32 ligands modelled in this entry, 26 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PHE	A	2001	-	11,12,12	0.82	0	14,15,15	1.01	2 (14%)
3	PHE	B	2002	-	11,12,12	0.76	0	14,15,15	0.95	2 (14%)
3	PHE	E	2005	-	11,12,12	0.77	0	14,15,15	0.95	2 (14%)
3	PHE	C	2003	-	11,12,12	0.79	0	14,15,15	0.82	1 (7%)
3	PHE	F	2006	2	11,12,12	0.78	0	14,15,15	1.20	2 (14%)
3	PHE	D	2004	2	11,12,12	0.74	0	14,15,15	0.98	2 (14%)

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	PHE	A	2001	-	-	0/8/8/8	0/1/1/1
3	PHE	B	2002	-	-	1/8/8/8	0/1/1/1
3	PHE	E	2005	-	-	0/8/8/8	0/1/1/1
3	PHE	C	2003	-	-	0/8/8/8	0/1/1/1
3	PHE	F	2006	2	-	4/8/8/8	0/1/1/1
3	PHE	D	2004	2	-	0/8/8/8	0/1/1/1

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	2006	PHE	OXT-C-O	-3.44	116.28	124.09
3	A	2001	PHE	OXT-C-O	-2.89	117.53	124.09
3	F	2006	PHE	OXT-C-CA	2.80	122.92	113.38
3	D	2004	PHE	OXT-C-O	-2.65	118.08	124.09
3	E	2005	PHE	OXT-C-CA	2.45	121.72	113.38

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	F	2006	PHE	C-CA-CB-CG
3	F	2006	PHE	OXT-C-CA-N
3	F	2006	PHE	N-CA-CB-CG
3	F	2006	PHE	O-C-CA-N
3	B	2002	PHE	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	362/363 (99%)	-0.25	4 (1%) 80 85	12, 27, 39, 54	0
1	B	359/363 (98%)	-0.36	6 (1%) 70 76	9, 17, 44, 55	0
1	C	361/363 (99%)	-0.27	8 (2%) 62 69	10, 22, 40, 46	0
1	D	350/363 (96%)	-0.32	3 (0%) 84 88	9, 19, 37, 52	0
1	E	342/363 (94%)	-0.08	8 (2%) 60 67	12, 28, 49, 59	0
1	F	330/363 (90%)	-0.05	7 (2%) 63 70	16, 30, 43, 54	0
All	All	2104/2178 (96%)	-0.23	36 (1%) 70 76	9, 24, 44, 59	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	363	SER	5.4
1	E	45	PHE	4.5
1	E	48	MET	4.1
1	F	4	LEU	4.0
1	F	228	TRP	3.7

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](#)

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(Å ²)	Q<0.9
2	BA	A	3020	1/1	0.79	0.12	46,46,46,46	1
3	PHE	E	2005	12/12	0.82	0.24	33,38,40,40	0
3	PHE	F	2006	12/12	0.82	0.23	40,42,42,42	0
2	BA	E	3018	1/1	0.83	0.16	50,50,50,50	1
2	BA	F	3021	1/1	0.85	0.17	42,42,42,42	1
3	PHE	D	2004	12/12	0.86	0.22	37,40,43,43	0
2	BA	B	3010	1/1	0.87	0.43	49,49,49,49	1
2	BA	D	3014	1/1	0.89	0.56	45,45,45,45	1
3	PHE	C	2003	12/12	0.90	0.17	36,38,39,39	0
2	BA	A	3004	1/1	0.92	0.08	62,62,62,62	1
3	PHE	B	2002	12/12	0.92	0.15	33,34,35,35	0
2	BA	D	3022	1/1	0.92	0.11	53,53,53,53	1
2	BA	E	3012	1/1	0.92	0.15	44,44,44,44	1
2	BA	C	3013	1/1	0.92	0.24	46,46,46,46	1
2	BA	E	3019	1/1	0.92	0.14	48,48,48,48	1
2	BA	F	3016	1/1	0.93	0.06	48,48,48,48	1
2	BA	A	3009	1/1	0.93	0.34	48,48,48,48	1
3	PHE	A	2001	12/12	0.93	0.15	31,33,33,33	0
2	BA	D	3017	1/1	0.93	0.09	57,57,57,57	1
2	BA	C	3011	1/1	0.96	0.07	47,47,47,47	1
2	BA	E	3024	1/1	0.97	0.07	44,44,44,44	1
2	BA	F	3008	1/1	0.97	0.20	24,24,24,24	1
2	BA	F	3007	1/1	0.98	0.18	67,67,67,67	1
2	BA	D	3015	1/1	0.98	0.03	52,52,52,52	1
2	BA	B	3002	1/1	0.99	0.09	32,32,32,32	1
2	BA	F	3025	1/1	0.99	0.07	36,36,36,36	1
2	BA	C	3005	1/1	0.99	0.09	22,22,22,22	1
2	BA	F	3006	1/1	0.99	0.06	30,30,30,30	1
2	BA	C	3001	1/1	1.00	0.08	27,27,27,27	1
2	BA	A	3003	1/1	1.00	0.12	21,21,21,21	1
2	BA	D	3023[A]	1/1	1.00	0.07	33,33,33,33	1
2	BA	D	3023[B]	1/1	1.00	0.07	39,39,39,39	1

6.5 Other polymers [i](#)

There are no such residues in this entry.