



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:23 PM GMT

PDB ID : 3R74
Title : Crystal structure of 2-amino-2-desoxyisochorismate synthase (ADIC) synthase PhzE from Burkholderia lata 383
Authors : Li, Q.A.; Mavrodi, D.V.; Thomashow, L.S.; Roessle, M.; Blankenfeldt, W.
Deposited on : 2011-03-22
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

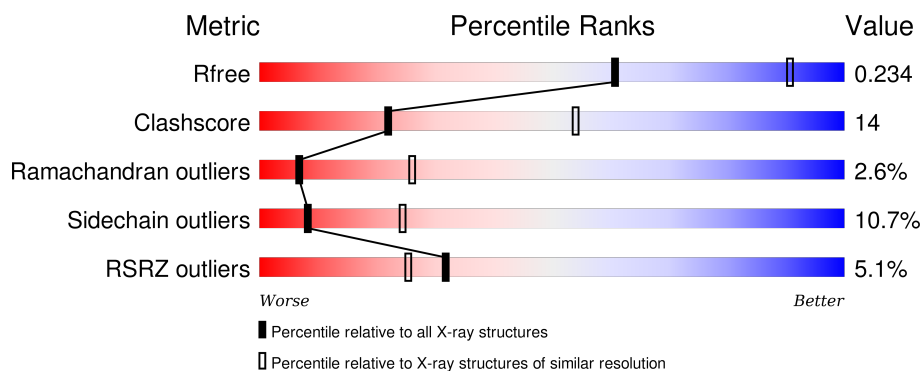
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

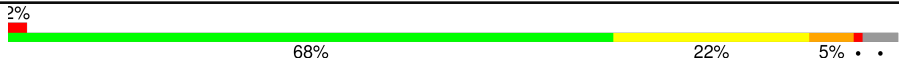

The reported resolution of this entry is 2.90 Å.

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	645	 2% 68% 22% 5% . .
1	B	645	 7% 69% 23% . .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9168 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 Anthranilate/para-aminobenzoate synthases component I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	617	Total	C	N	O	S	0	0	0
			4630	2901	831	876	22			
1	B	616	Total	C	N	O	S	0	0	0
			4458	2792	802	844	20			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP Q396C7
A	0	HIS	-	EXPRESSION TAG	UNP Q396C7
B	-1	GLY	-	EXPRESSION TAG	UNP Q396C7
B	0	HIS	-	EXPRESSION TAG	UNP Q396C7

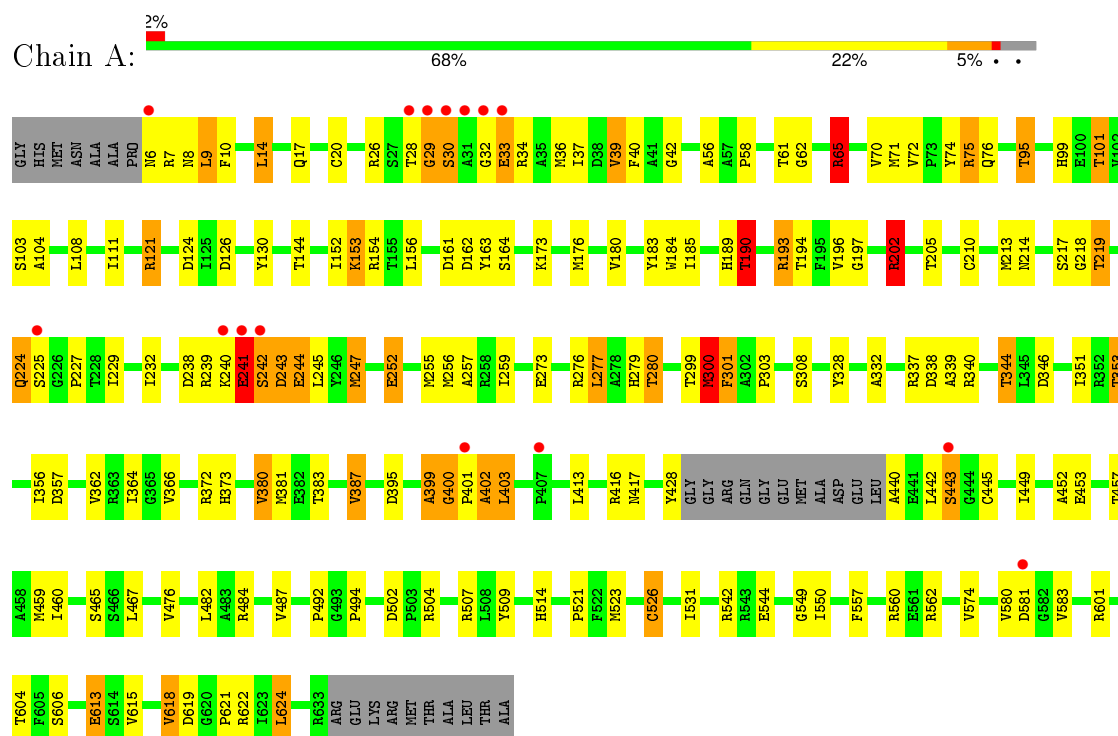
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	46	Total	O	0	0
			46	46		
2	B	34	Total	O	0	0
			34	34		

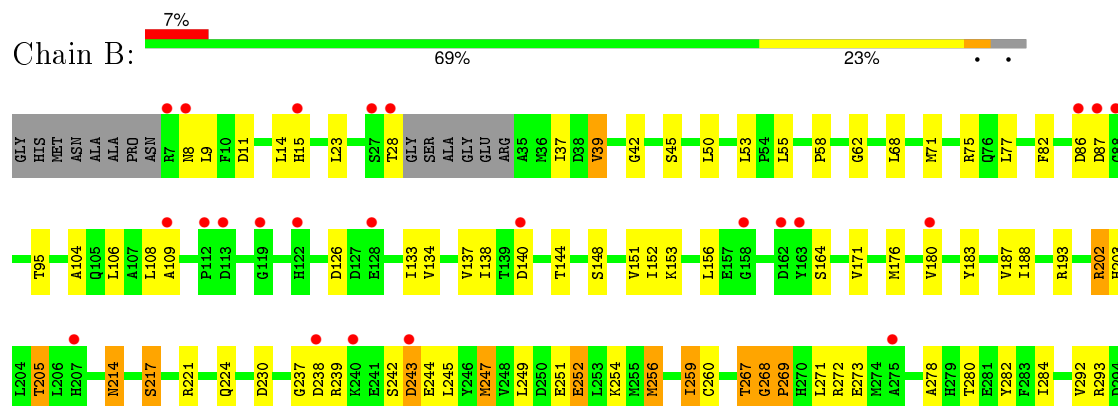
3 Residue-property plots

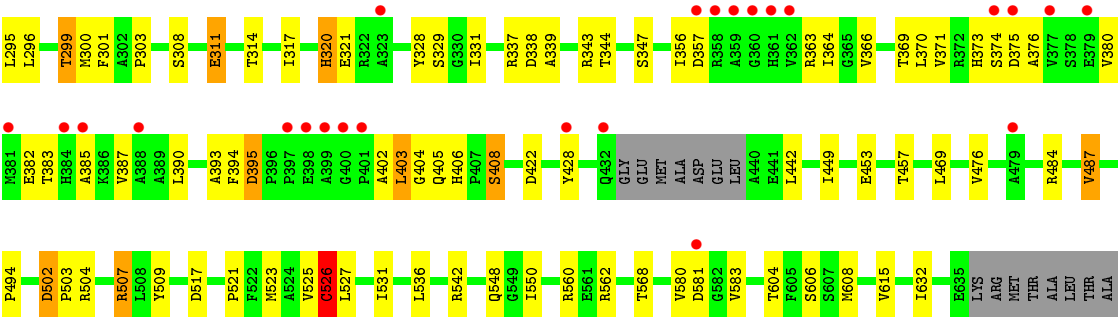
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Anthranilate/para-aminobenzoate synthases component I



• Molecule 1: Anthranilate/para-aminobenzoate synthases component I





4 Data and refinement statistics

Property	Value	Source
Space group	P 62 2 2	Depositor
Cell constants a, b, c, α , β , γ	172.36 Å 172.36 Å 216.44 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.92 – 2.90 19.93 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.92-2.90) 99.8 (19.93-2.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.38 (at 2.88 Å)	Xtriage
Refinement program	REFMAC 5.6.0077	Depositor
R, R_{free}	0.187 , 0.231 0.185 , 0.234	Depositor DCC
R_{free} test set	2120 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	63.9	Xtriage
Anisotropy	0.322	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 50.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 42360 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9168	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.57% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.92	5/4724 (0.1%)	0.95	13/6428 (0.2%)
1	B	0.73	1/4545 (0.0%)	0.85	6/6201 (0.1%)
All	All	0.83	6/9269 (0.1%)	0.90	19/12629 (0.2%)

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	2
1	B	0	4
All	All	0	6

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	526	CYS	CB-SG	10.83	2.00	1.82
1	B	526	CYS	CB-SG	7.47	1.95	1.82
1	A	20	CYS	CB-SG	-7.29	1.69	1.82
1	A	257	ALA	CA-CB	-5.30	1.41	1.52
1	A	210	CYS	CB-SG	-5.26	1.73	1.81
1	A	75	ARG	CB-CG	-5.20	1.38	1.52

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	300	MET	CG-SD-CE	-9.54	84.93	100.20
1	A	75	ARG	CB-CA-C	-7.76	94.87	110.40
1	B	268	GLY	C-N-CD	-7.03	105.14	120.60
1	B	469	LEU	CA-CB-CG	6.24	129.65	115.30
1	A	340	ARG	NE-CZ-NH1	5.91	123.25	120.30
1	B	272	ARG	NE-CZ-NH1	5.84	123.22	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	65	ARG	NE-CZ-NH1	5.78	123.19	120.30
1	A	121	ARG	NE-CZ-NH1	5.76	123.18	120.30
1	A	124	ASP	CB-CG-OD1	5.73	123.45	118.30
1	A	75	ARG	CB-CG-CD	-5.71	96.76	111.60
1	B	363	ARG	NE-CZ-NH1	5.60	123.10	120.30
1	B	502	ASP	CB-CG-OD2	5.48	123.23	118.30
1	A	507	ARG	NE-CZ-NH1	5.41	123.01	120.30
1	A	75	ARG	CA-CB-CG	5.26	124.98	113.40
1	A	624	LEU	CB-CG-CD1	-5.22	102.13	111.00
1	A	202	ARG	CB-CG-CD	-5.14	98.23	111.60
1	B	502	ASP	CB-CG-OD1	-5.12	113.69	118.30
1	A	300	MET	CA-C-N	-5.12	105.95	117.20
1	A	190	THR	N-CA-C	-5.07	97.30	111.00

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	300	MET	Peptide
1	A	6	ASN	Peptide
1	B	267	THR	Peptide
1	B	268	GLY	Peptide
1	B	300	MET	Peptide
1	B	428	TYR	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	4630	0	4479	140	0
1	B	4458	0	4197	123	0
2	A	46	0	0	1	0
2	B	34	0	0	1	0
All	All	9168	0	8676	246	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 14.

All (246) 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:380:VAL:O	1:B:383:THR:HG22	1.46	1.13
1:A:459:MET:CE	1:B:254:LYS:HG3	1.82	1.08
1:B:151:VAL:HG22	1:B:369:THR:HG22	1.31	1.07
1:A:213:MET:HG3	1:A:256:MET:HE3	1.37	1.05
1:A:459:MET:HE2	1:B:254:LYS:HG3	1.43	1.01
1:B:366:VAL:HG11	1:B:387:VAL:HG22	1.46	0.96
1:B:366:VAL:HG11	1:B:387:VAL:CG2	1.99	0.92
1:A:176:MET:CE	1:A:185:ILE:HD12	1.99	0.92
1:A:366:VAL:HG11	1:A:387:VAL:HG13	1.59	0.83
1:A:176:MET:HE2	1:A:185:ILE:HD12	1.59	0.82
1:A:176:MET:HE1	1:A:185:ILE:HB	1.63	0.78
1:B:203:HIS:NE2	1:B:299:THR:HG23	1.99	0.78
1:B:137:VAL:HG21	1:B:152:ILE:HD11	1.67	0.76
1:A:229:ILE:HD13	1:B:406:HIS:CD2	2.22	0.74
1:B:82:PHE:HB3	1:B:314:THR:HG21	1.69	0.74
1:A:219:THR:CG2	1:A:279:HIS:CE1	2.71	0.74
1:B:104:ALA:O	1:B:108:LEU:HD12	1.88	0.73
1:A:460:ILE:HG12	1:A:613:GLU:HG2	1.71	0.73
1:B:403:LEU:HD12	1:B:404:GLY:N	2.03	0.73
1:A:351:ILE:O	1:A:353:THR:HG22	1.89	0.72
1:B:476:VAL:HG13	1:B:507:ARG:HG3	1.72	0.70
1:B:383:THR:O	1:B:387:VAL:HG23	1.91	0.70
1:B:137:VAL:HG21	1:B:152:ILE:CD1	2.22	0.69
1:B:366:VAL:CG1	1:B:387:VAL:HG22	2.22	0.69
1:B:317:ILE:HG23	1:B:321:GLU:OE1	1.92	0.69
1:B:403:LEU:C	1:B:403:LEU:HD12	2.13	0.69
1:A:219:THR:CG2	1:A:279:HIS:ND1	2.57	0.67
1:B:271:LEU:HD22	1:B:273:GLU:HG2	1.75	0.67
1:B:82:PHE:CZ	1:B:311:GLU:HG2	2.29	0.67
1:A:373:HIS:HB3	2:A:674:HOH:O	1.94	0.67
1:A:442:LEU:O	1:A:443:SER:O	2.12	0.67
1:A:277:LEU:C	1:A:277:LEU:HD23	2.14	0.67
1:A:460:ILE:CG1	1:A:613:GLU:HG2	2.25	0.66
1:B:376:ALA:O	1:B:380:VAL:HG23	1.96	0.66
1:A:401:PRO:O	1:A:402:ALA:HB2	1.96	0.65
1:A:255:MET:HE2	1:A:299:THR:HB	1.78	0.65
1:A:255:MET:CE	1:A:299:THR:HA	2.27	0.65
1:A:277:LEU:HD13	1:B:224:GLN:HG2	1.80	0.64
1:B:364:ILE:HD13	1:B:390:LEU:HD13	1.81	0.63
1:B:71:MET:CE	1:B:188:ILE:HD13	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:241:GLU:C	1:A:243:ASP:H	2.02	0.63
1:A:366:VAL:CG1	1:A:387:VAL:HG13	2.29	0.63
1:A:217:SER:OG	1:A:280:THR:CG2	2.47	0.62
1:A:273:GLU:OE1	1:B:402:ALA:HB1	1.98	0.62
1:B:259:ILE:HG22	1:B:260:CYS:SG	2.40	0.62
1:A:176:MET:HE3	1:A:185:ILE:HG21	1.82	0.62
1:A:255:MET:HE2	1:A:299:THR:CB	2.29	0.61
1:A:255:MET:CE	1:A:299:THR:CA	2.78	0.61
1:A:217:SER:HB2	1:A:245:LEU:HD13	1.81	0.61
1:A:276:ARG:HB2	1:B:224:GLN:HA	1.81	0.61
1:A:202:ARG:HD3	1:A:214:ASN:CB	2.31	0.61
1:A:219:THR:HG22	1:A:279:HIS:CE1	2.36	0.61
1:A:217:SER:OG	1:A:218:GLY:N	2.32	0.61
1:A:255:MET:HE3	1:A:299:THR:CA	2.32	0.60
1:A:618:VAL:HG12	1:A:619:ASP:N	2.16	0.60
1:B:295:LEU:O	1:B:299:THR:HB	2.01	0.60
1:B:62:GLY:O	1:B:339:ALA:HB1	2.01	0.60
1:A:255:MET:HE3	1:A:299:THR:C	2.22	0.60
1:A:190:THR:HG22	1:A:193:ARG:H	1.66	0.60
1:B:259:ILE:HG22	1:B:260:CYS:N	2.17	0.59
1:B:133:ILE:HD12	1:B:320:HIS:O	2.02	0.59
1:A:219:THR:HG23	1:A:279:HIS:ND1	2.17	0.59
1:B:171:VAL:HG13	1:B:393:ALA:HB1	1.82	0.59
1:A:183:TYR:CE2	1:A:202:ARG:HB2	2.38	0.58
1:B:71:MET:HE1	1:B:188:ILE:HD13	1.85	0.58
1:A:72:VAL:HG11	1:A:300:MET:HE3	1.85	0.58
1:A:255:MET:HE3	1:A:299:THR:HA	1.85	0.58
1:A:29:GLY:O	1:A:30:SER:CB	2.52	0.57
1:A:217:SER:HB3	1:A:280:THR:HG22	1.85	0.57
1:B:387:VAL:O	1:B:387:VAL:HG12	2.03	0.57
1:A:219:THR:HG22	1:A:279:HIS:ND1	2.21	0.56
1:B:509:TYR:CE1	1:B:531:ILE:HG23	2.39	0.56
1:A:176:MET:CE	1:A:185:ILE:HB	2.35	0.56
1:B:137:VAL:HG11	1:B:152:ILE:HD11	1.86	0.56
1:A:467:LEU:HD23	1:A:467:LEU:N	2.19	0.56
1:A:244:GLU:HA	1:A:247:MET:HE1	1.88	0.56
1:B:144:THR:O	1:B:144:THR:CG2	2.54	0.56
1:A:217:SER:CB	1:A:280:THR:HG22	2.36	0.55
1:A:417:ASN:HD21	1:B:269:PRO:HD2	1.71	0.55
1:A:189:HIS:HD2	1:A:194:THR:OG1	1.88	0.55
1:A:440:ALA:O	1:A:443:SER:HB2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:372:ARG:NH1	1:B:548:GLN:HE21	2.05	0.55
1:B:151:VAL:HG22	1:B:369:THR:CG2	2.21	0.55
1:B:183:TYR:CE2	1:B:202:ARG:HB2	2.42	0.54
1:A:76:GLN:HB3	1:A:300:MET:CE	2.37	0.54
1:B:580:VAL:HG12	1:B:583:VAL:HG23	1.90	0.53
1:A:241:GLU:O	1:A:243:ASP:N	2.38	0.53
1:A:76:GLN:HB3	1:A:300:MET:HE3	1.90	0.53
1:A:10:PHE:CE2	1:A:14:LEU:HD12	2.43	0.53
1:A:460:ILE:HG12	1:A:613:GLU:CG	2.38	0.53
1:B:50:LEU:HD23	1:B:53:LEU:HD11	1.91	0.53
1:B:138:ILE:HD13	1:B:374:SER:O	2.09	0.53
1:A:36:MET:HE2	1:A:103:SER:HA	1.89	0.53
1:A:176:MET:CE	1:A:185:ILE:CD1	2.81	0.52
1:B:406:HIS:CD2	1:B:408:SER:OG	2.63	0.52
1:B:449:ILE:HG21	1:B:457:THR:HG23	1.91	0.52
1:A:205:THR:HG22	1:A:346:ASP:HA	1.92	0.52
1:B:205:THR:HG22	1:B:205:THR:O	2.09	0.52
1:A:401:PRO:O	1:A:402:ALA:CB	2.58	0.52
1:B:55:LEU:CD2	1:B:68:LEU:HD21	2.40	0.51
1:B:23:LEU:HD23	1:B:39:VAL:HB	1.93	0.51
1:B:507:ARG:NH1	2:B:670:HOH:O	2.44	0.51
1:A:202:ARG:HD3	1:A:214:ASN:HB3	1.92	0.51
1:A:36:MET:CE	1:A:103:SER:HA	2.41	0.51
1:B:403:LEU:CD1	1:B:403:LEU:C	2.78	0.51
1:B:108:LEU:HD21	1:B:176:MET:HB3	1.92	0.51
1:B:217:SER:HB3	1:B:280:THR:HG22	1.92	0.51
1:A:399:ALA:O	1:A:400:GLY:C	2.48	0.51
1:A:238:ASP:O	1:A:240:LYS:N	2.44	0.50
1:A:9:LEU:HD13	1:A:39:VAL:CG2	2.41	0.50
1:A:255:MET:CE	1:A:299:THR:HB	2.42	0.50
1:B:82:PHE:CE2	1:B:311:GLU:HG2	2.46	0.50
1:A:255:MET:HE2	1:A:299:THR:HA	1.93	0.50
1:A:95:THR:O	1:A:95:THR:HG22	2.11	0.50
1:A:255:MET:HE2	1:A:299:THR:CA	2.42	0.50
1:A:452:ALA:HB3	1:A:492:PRO:O	2.12	0.50
1:A:40:PHE:CE2	1:A:99:HIS:CD2	3.00	0.50
1:B:251:GLU:HA	1:B:254:LYS:HD3	1.92	0.50
1:A:459:MET:HE3	1:B:254:LYS:HG3	1.82	0.49
1:A:383:THR:O	1:A:387:VAL:HG22	2.11	0.49
1:B:509:TYR:CZ	1:B:531:ILE:HG23	2.47	0.49
1:A:26:ARG:HG2	1:A:184:TRP:CD1	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:557:PHE:CE1	1:A:601:ARG:HD3	2.48	0.49
1:A:449:ILE:HG21	1:A:457:THR:HG23	1.93	0.49
1:B:55:LEU:HD21	1:B:68:LEU:HD21	1.95	0.49
1:A:9:LEU:HD13	1:A:39:VAL:HG22	1.94	0.49
1:B:252:GLU:OE1	1:B:303:PRO:HG2	2.13	0.49
1:A:242:SER:O	1:A:243:ASP:O	2.30	0.49
1:A:523:MET:HA	1:A:606:SER:O	2.13	0.48
1:B:523:MET:HA	1:B:606:SER:O	2.13	0.48
1:B:521:PRO:HA	1:B:604:THR:O	2.12	0.48
1:B:148:SER:HB2	1:B:247:MET:CE	2.43	0.48
1:A:58:PRO:HB3	1:A:337:ARG:NH2	2.29	0.48
1:A:509:TYR:CZ	1:A:531:ILE:HG23	2.49	0.48
1:B:476:VAL:HG13	1:B:507:ARG:CG	2.43	0.48
1:A:72:VAL:CG1	1:A:300:MET:HE3	2.44	0.47
1:A:101:THR:O	1:A:101:THR:HG22	2.13	0.47
1:B:525:VAL:HG22	1:B:608:MET:HE2	1.95	0.47
1:B:256:MET:CE	1:B:259:ILE:HG21	2.44	0.47
1:A:252:GLU:OE1	1:A:303:PRO:HG2	2.13	0.47
1:A:217:SER:OG	1:A:280:THR:HG22	2.14	0.47
1:A:521:PRO:HA	1:A:604:THR:O	2.15	0.47
1:A:549:GLY:O	1:A:550:ILE:HD13	2.15	0.47
1:B:371:VAL:HG23	1:B:373:HIS:H	1.80	0.47
1:A:71:MET:HE2	1:A:332:ALA:HA	1.97	0.47
1:A:413:LEU:HD22	1:B:269:PRO:HB2	1.96	0.47
1:B:58:PRO:HB3	1:B:337:ARG:NH2	2.30	0.46
1:A:130:TYR:HD2	1:A:380:VAL:HG22	1.80	0.46
1:B:144:THR:O	1:B:144:THR:HG22	2.14	0.46
1:B:252:GLU:HG2	1:B:284:ILE:HD12	1.97	0.46
1:A:161:ASP:O	1:A:162:ASP:C	2.54	0.46
1:B:271:LEU:HD21	1:B:278:ALA:HB1	1.98	0.46
1:A:14:LEU:HD21	1:A:111:ILE:HA	1.97	0.46
1:B:106:LEU:O	1:B:109:ALA:HB3	2.14	0.46
1:A:243:ASP:OD1	1:A:244:GLU:N	2.48	0.46
1:B:371:VAL:HG23	1:B:373:HIS:N	2.31	0.46
1:B:296:LEU:O	1:B:299:THR:HG22	2.15	0.45
1:A:403:LEU:CB	1:B:273:GLU:OE1	2.64	0.45
1:A:62:GLY:O	1:A:339:ALA:HB1	2.16	0.45
1:A:229:ILE:CD1	1:B:406:HIS:CD2	2.98	0.45
1:A:604:THR:HG22	1:A:604:THR:O	2.17	0.45
1:B:394:PHE:O	1:B:395:ASP:CB	2.63	0.45
1:A:244:GLU:HA	1:A:247:MET:CE	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:SER:OG	1:A:280:THR:HG21	2.15	0.45
1:B:271:LEU:CD2	1:B:273:GLU:HG2	2.44	0.45
1:B:356:ILE:HG22	1:B:357:ASP:N	2.31	0.45
1:B:140:ASP:O	1:B:144:THR:HB	2.16	0.45
1:A:37:ILE:HD13	1:A:37:ILE:HG21	1.72	0.45
1:B:380:VAL:O	1:B:383:THR:CG2	2.40	0.44
1:B:237:GLY:O	1:B:239:ARG:N	2.51	0.44
1:A:241:GLU:C	1:A:243:ASP:N	2.70	0.44
1:A:416:ARG:HH12	1:B:280:THR:HG21	1.81	0.44
1:A:357:ASP:OD1	1:A:357:ASP:C	2.56	0.44
1:B:494:PRO:O	1:B:504:ARG:NH2	2.42	0.44
1:A:42:GLY:HA3	1:A:95:THR:O	2.17	0.44
1:B:214:ASN:HD22	1:B:214:ASN:C	2.22	0.44
1:B:387:VAL:O	1:B:387:VAL:CG1	2.66	0.43
1:A:10:PHE:CE2	1:A:14:LEU:CD1	3.01	0.43
1:B:11:ASP:O	1:B:15:HIS:CD2	2.70	0.43
1:B:269:PRO:HD3	1:B:282:TYR:CE2	2.54	0.43
1:B:269:PRO:HD3	1:B:282:TYR:CZ	2.53	0.43
1:A:449:ILE:HG21	1:A:457:THR:CG2	2.48	0.43
1:B:328:TYR:O	1:B:329:SER:OG	2.29	0.43
1:A:108:LEU:O	1:A:173:LYS:HE3	2.19	0.43
1:A:351:ILE:C	1:A:353:THR:HG22	2.39	0.43
1:A:74:TYR:HA	1:A:301:PHE:CE1	2.54	0.43
1:A:300:MET:CE	1:A:301:PHE:CZ	3.02	0.43
1:B:183:TYR:CZ	1:B:202:ARG:HB2	2.53	0.43
1:A:277:LEU:CD2	1:A:277:LEU:C	2.86	0.43
1:B:296:LEU:HA	1:B:299:THR:HG22	2.01	0.43
1:A:402:ALA:O	1:A:403:LEU:CB	2.67	0.43
1:A:70:VAL:O	1:A:71:MET:HE2	2.18	0.43
1:B:338:ASP:OD2	1:B:338:ASP:C	2.56	0.43
1:B:383:THR:O	1:B:387:VAL:CG2	2.65	0.43
1:A:232:ILE:CD1	1:B:403:LEU:HD11	2.49	0.43
1:A:476:VAL:HG21	1:A:504:ARG:HG3	2.01	0.42
1:B:299:THR:O	1:B:299:THR:HG23	2.19	0.42
1:B:148:SER:HB2	1:B:247:MET:HE3	2.01	0.42
1:B:75:ARG:O	1:B:77:LEU:N	2.52	0.42
1:B:108:LEU:HD21	1:B:176:MET:CB	2.48	0.42
1:A:416:ARG:NH1	1:B:280:THR:HG21	2.34	0.42
1:B:245:LEU:O	1:B:249:LEU:HD13	2.19	0.42
1:B:134:VAL:HG13	1:B:370:LEU:CD1	2.50	0.42
1:A:190:THR:HG22	1:A:193:ARG:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:ILE:HG12	1:A:362:VAL:HG22	2.00	0.42
1:A:467:LEU:HD11	1:A:621:PRO:O	2.20	0.42
1:A:197:GLY:HA3	1:A:353:THR:HB	2.01	0.42
1:A:300:MET:HE1	1:A:301:PHE:CZ	2.54	0.42
1:A:372:ARG:HH11	1:B:548:GLN:HE21	1.66	0.42
1:A:153:LYS:HG2	1:A:154:ARG:N	2.27	0.42
1:B:632:ILE:CG2	1:B:632:ILE:O	2.67	0.42
1:A:328:TYR:CE1	1:A:351:ILE:HG22	2.55	0.42
1:A:413:LEU:CD2	1:B:269:PRO:HB2	2.50	0.42
1:A:126:ASP:C	1:A:126:ASP:OD1	2.59	0.41
1:A:224:GLN:HA	1:A:225:SER:HA	1.89	0.41
1:A:163:TYR:CG	1:A:164:SER:N	2.87	0.41
1:A:618:VAL:CG1	1:A:619:ASP:N	2.83	0.41
1:B:356:ILE:CG2	1:B:357:ASP:N	2.83	0.41
1:A:104:ALA:O	1:A:108:LEU:HG	2.20	0.41
1:A:176:MET:CE	1:A:185:ILE:CB	2.97	0.41
1:B:292:VAL:HG11	1:B:343:ARG:HD2	2.03	0.41
1:B:8:ASN:OD1	1:B:9:LEU:N	2.53	0.41
1:B:55:LEU:HD12	1:B:293:ARG:HH11	1.84	0.41
1:A:344:THR:O	1:A:344:THR:HG22	2.21	0.41
1:A:61:THR:HG23	1:A:65:ARG:NH1	2.36	0.41
1:B:245:LEU:HD11	1:B:282:TYR:CE1	2.56	0.41
1:A:256:MET:HE1	1:A:259:ILE:HD11	2.02	0.41
1:B:134:VAL:HG13	1:B:370:LEU:HD13	2.03	0.41
1:A:156:LEU:HD23	1:A:364:ILE:HD12	2.03	0.41
1:A:380:VAL:HG12	1:A:381:MET:N	2.36	0.41
1:B:356:ILE:HG22	1:B:357:ASP:O	2.21	0.41
1:A:338:ASP:OD1	1:A:338:ASP:C	2.59	0.41
1:B:242:SER:O	1:B:243:ASP:O	2.39	0.41
1:B:331:ILE:HG23	1:B:347:SER:OG	2.21	0.41
1:B:382:GLU:HA	1:B:385:ALA:HB3	2.03	0.41
1:B:259:ILE:CG2	1:B:260:CYS:SG	3.09	0.41
1:B:502:ASP:HA	1:B:503:PRO:HD3	1.98	0.41
1:A:494:PRO:O	1:A:504:ARG:NH2	2.47	0.40
1:A:32:GLY:O	1:A:33:GLU:CB	2.68	0.40
1:B:526:CYS:O	1:B:527:LEU:C	2.59	0.40
1:B:217:SER:HB2	1:B:245:LEU:HD13	2.03	0.40
1:B:487:VAL:HG22	1:B:632:ILE:HD11	2.04	0.40
1:B:317:ILE:CG2	1:B:321:GLU:OE1	2.67	0.40
1:B:23:LEU:HD12	1:B:187:VAL:CG1	2.51	0.40
1:A:502:ASP:OD1	1:A:504:ARG:HB3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:42:GLY:HA3	1:B:95:THR:O	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	613/645 (95%)	567 (92%)	24 (4%)	22 (4%)	4	18
1	B	610/645 (95%)	559 (92%)	41 (7%)	10 (2%)	12	40
All	All	1223/1290 (95%)	1126 (92%)	65 (5%)	32 (3%)	7	26

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	30	SER
1	A	242	SER
1	A	243	ASP
1	A	301	PHE
1	A	402	ALA
1	A	403	LEU
1	A	443	SER
1	B	238	ASP
1	B	243	ASP
1	B	269	PRO
1	B	301	PHE
1	B	395	ASP
1	A	8	ASN
1	A	28	THR
1	A	33	GLU
1	A	34	ARG
1	A	399	ALA

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Mol	Chain	Res	Type
1	A	400	GLY
1	B	320	HIS
1	A	239	ARG
1	A	526	CYS
1	A	618	VAL
1	B	453	GLU
1	B	526	CYS
1	B	581	ASP
1	A	453	GLU
1	B	164	SER
1	A	56	ALA
1	A	241	GLU
1	A	445	CYS
1	A	227	PRO
1	A	29	GLY

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	465/507 (92%)	415 (89%)	50 (11%)	8	24
1	B	423/507 (83%)	378 (89%)	45 (11%)	8	25
All	All	888/1014 (88%)	793 (89%)	95 (11%)	8	24

All (95) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ARG
1	A	9	LEU
1	A	14	LEU
1	A	17	GLN
1	A	39	VAL
1	A	65	ARG
1	A	75	ARG
1	A	95	THR

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Mol	Chain	Res	Type
1	A	101	THR
1	A	121	ARG
1	A	144	THR
1	A	152	ILE
1	A	153	LYS
1	A	180	VAL
1	A	190	THR
1	A	193	ARG
1	A	196	VAL
1	A	202	ARG
1	A	219	THR
1	A	224	GLN
1	A	241	GLU
1	A	244	GLU
1	A	247	MET
1	A	252	GLU
1	A	277	LEU
1	A	280	THR
1	A	308	SER
1	A	344	THR
1	A	353	THR
1	A	380	VAL
1	A	387	VAL
1	A	395	ASP
1	A	428	TYR
1	A	465	SER
1	A	482	LEU
1	A	484	ARG
1	A	487	VAL
1	A	514	HIS
1	A	542	ARG
1	A	544	GLU
1	A	560	ARG
1	A	562	ARG
1	A	574	VAL
1	A	580	VAL
1	A	581	ASP
1	A	583	VAL
1	A	613	GLU
1	A	615	VAL
1	A	622	ARG
1	A	624	LEU

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Mol	Chain	Res	Type
1	B	14	LEU
1	B	28	THR
1	B	37	ILE
1	B	39	VAL
1	B	45	SER
1	B	86	ASP
1	B	87	ASP
1	B	126	ASP
1	B	153	LYS
1	B	156	LEU
1	B	180	VAL
1	B	193	ARG
1	B	202	ARG
1	B	205	THR
1	B	214	ASN
1	B	217	SER
1	B	221	ARG
1	B	230	ASP
1	B	244	GLU
1	B	247	MET
1	B	252	GLU
1	B	256	MET
1	B	259	ILE
1	B	267	THR
1	B	299	THR
1	B	308	SER
1	B	311	GLU
1	B	344	THR
1	B	375	ASP
1	B	403	LEU
1	B	405	GLN
1	B	408	SER
1	B	422	ASP
1	B	442	LEU
1	B	484	ARG
1	B	487	VAL
1	B	507	ARG
1	B	517	ASP
1	B	536	LEU
1	B	542	ARG
1	B	550	ILE
1	B	560	ARG

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Mol	Chain	Res	Type
1	B	562	ARG
1	B	568	THR
1	B	615	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	105	GLN
1	A	189	HIS
1	A	224	GLN
1	A	361	HIS
1	A	417	ASN
1	A	477	HIS
1	A	547	ASN
1	B	15	HIS
1	B	207	HIS
1	B	214	ASN
1	B	265	GLN
1	B	361	HIS
1	B	406	HIS
1	B	477	HIS
1	B	547	ASN
1	B	548	GLN

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 ⓘ

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, 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	617/645 (95%)	-0.38	15 (2%) 62 57	26, 56, 119, 187	1 (0%)
1	B	616/645 (95%)	0.03	48 (7%) 16 10	33, 91, 154, 195	0
All	All	1233/1290 (95%)	-0.18	63 (5%) 32 25	26, 70, 147, 195	1 (0%)

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	30	SER	6.4
1	A	29	GLY	5.5
1	B	359	ALA	5.4
1	A	401	PRO	5.3
1	B	28	THR	5.2
1	A	28	THR	5.2
1	B	397	PRO	5.1
1	B	400	GLY	5.0
1	B	112	PRO	4.6
1	A	32	GLY	4.4
1	B	358	ARG	4.2
1	B	399	ALA	4.1
1	A	31	ALA	4.0
1	B	360	GLY	3.9
1	B	275	ALA	3.8
1	A	242	SER	3.7
1	B	379	GLU	3.6
1	B	401	PRO	3.5
1	A	443	SER	3.5
1	B	388	ALA	3.3
1	B	362	VAL	3.3
1	A	240	LYS	3.3
1	B	162	ASP	3.2
1	B	243	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	119	GLY	3.2
1	B	158	GLY	3.2
1	A	241	GLU	3.2
1	A	33	GLU	3.1
1	B	398	GLU	3.1
1	B	180	VAL	3.1
1	B	109	ALA	2.9
1	B	240	LYS	2.7
1	B	8	ASN	2.7
1	B	384	HIS	2.7
1	B	140	ASP	2.6
1	B	88	GLY	2.6
1	B	113	ASP	2.6
1	B	7	ARG	2.6
1	B	374	SER	2.6
1	A	6	ASN	2.5
1	B	238	ASP	2.5
1	B	581	ASP	2.4
1	B	357	ASP	2.4
1	B	15	HIS	2.4
1	A	407	PRO	2.3
1	B	86	ASP	2.3
1	B	323	ALA	2.3
1	B	385	ALA	2.3
1	B	27	SER	2.3
1	B	128	GLU	2.2
1	B	381	MET	2.2
1	A	225	SER	2.2
1	B	428	TYR	2.2
1	B	163	TYR	2.2
1	B	207	HIS	2.2
1	B	432	GLN	2.2
1	A	581	ASP	2.1
1	B	377	VAL	2.1
1	B	361	HIS	2.1
1	B	375	ASP	2.1
1	B	479	ALA	2.0
1	B	87	ASP	2.0
1	B	122	HIS	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](#)

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.