



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:53 PM GMT

PDB ID : 1VL2
Title : Crystal structure of Argininosuccinate synthase (TM1780) from *Thermotoga maritima* at 1.65 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2004-07-08
Resolution : 1.65 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

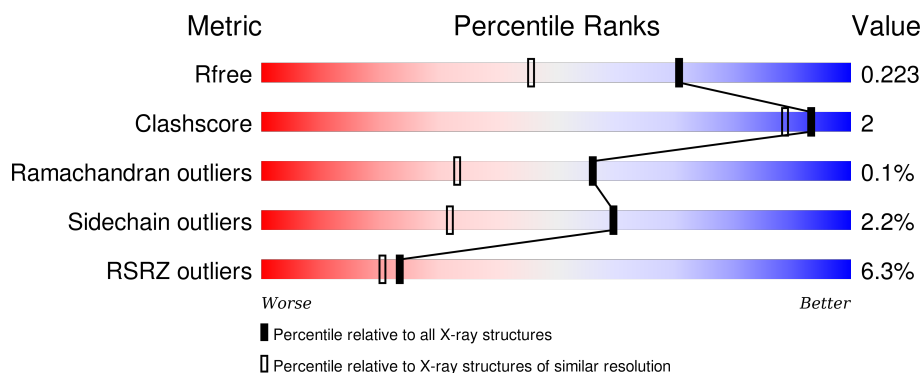
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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	1226 (1.66-1.66)
Clashscore	102246	1323 (1.66-1.66)
Ramachandran outliers	100387	1295 (1.66-1.66)
Sidechain outliers	100360	1295 (1.66-1.66)
RSRZ outliers	91569	1227 (1.66-1.66)

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	421	<div> <div>7%</div> <div> <div></div> <div>86%</div> <div>8%</div> <div>5%</div> </div> </div>
1	B	421	<div> <div>4%</div> <div> <div></div> <div>86%</div> <div>7%</div> <div>6%</div> </div> </div>
1	C	421	<div> <div>4%</div> <div> <div></div> <div>86%</div> <div>7%</div> <div>7%</div> </div> </div>
1	D	421	<div> <div>9%</div> <div> <div></div> <div>87%</div> <div>5%</div> <div>8%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13531 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 Argininosuccinate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	398	Total	C	N	O	S	0	2	0
			3117	2007	521	577	12			
1	B	394	Total	C	N	O	S	0	2	0
			3104	1997	516	579	12			
1	C	393	Total	C	N	O	S	0	2	0
			3089	1990	511	576	12			
1	D	389	Total	C	N	O	S	0	2	0
			3037	1961	501	563	12			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	LEADER SEQUENCE	UNP Q9X2A1
A	-10	GLY	-	LEADER SEQUENCE	UNP Q9X2A1
A	-9	SER	-	LEADER SEQUENCE	UNP Q9X2A1
A	-8	ASP	-	LEADER SEQUENCE	UNP Q9X2A1
A	-7	LYS	-	LEADER SEQUENCE	UNP Q9X2A1
A	-6	ILE	-	LEADER SEQUENCE	UNP Q9X2A1
A	-5	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
A	-4	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
A	-3	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
A	-2	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
A	-1	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
A	0	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
B	-11	MET	-	LEADER SEQUENCE	UNP Q9X2A1
B	-10	GLY	-	LEADER SEQUENCE	UNP Q9X2A1
B	-9	SER	-	LEADER SEQUENCE	UNP Q9X2A1
B	-8	ASP	-	LEADER SEQUENCE	UNP Q9X2A1
B	-7	LYS	-	LEADER SEQUENCE	UNP Q9X2A1
B	-6	ILE	-	LEADER SEQUENCE	UNP Q9X2A1
B	-5	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
B	-4	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
B	-3	HIS	-	LEADER SEQUENCE	UNP Q9X2A1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
B	-1	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
B	0	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
C	-11	MET	-	LEADER SEQUENCE	UNP Q9X2A1
C	-10	GLY	-	LEADER SEQUENCE	UNP Q9X2A1
C	-9	SER	-	LEADER SEQUENCE	UNP Q9X2A1
C	-8	ASP	-	LEADER SEQUENCE	UNP Q9X2A1
C	-7	LYS	-	LEADER SEQUENCE	UNP Q9X2A1
C	-6	ILE	-	LEADER SEQUENCE	UNP Q9X2A1
C	-5	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
C	-4	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
C	-3	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
C	-2	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
C	-1	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
C	0	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
D	-11	MET	-	LEADER SEQUENCE	UNP Q9X2A1
D	-10	GLY	-	LEADER SEQUENCE	UNP Q9X2A1
D	-9	SER	-	LEADER SEQUENCE	UNP Q9X2A1
D	-8	ASP	-	LEADER SEQUENCE	UNP Q9X2A1
D	-7	LYS	-	LEADER SEQUENCE	UNP Q9X2A1
D	-6	ILE	-	LEADER SEQUENCE	UNP Q9X2A1
D	-5	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
D	-4	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
D	-3	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
D	-2	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
D	-1	HIS	-	LEADER SEQUENCE	UNP Q9X2A1
D	0	HIS	-	LEADER SEQUENCE	UNP Q9X2A1

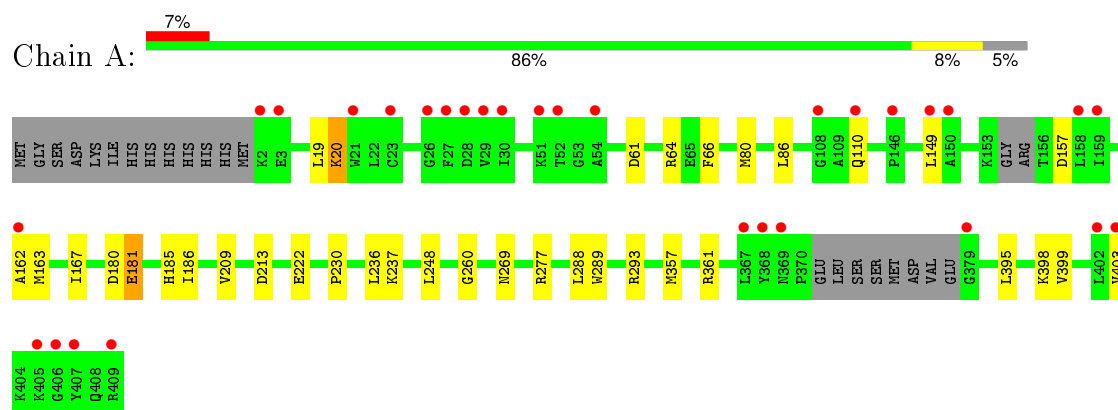
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	315	Total O 315 315	0	0
2	B	298	Total O 298 298	0	0
2	C	312	Total O 312 312	0	0
2	D	259	Total O 259 259	0	0

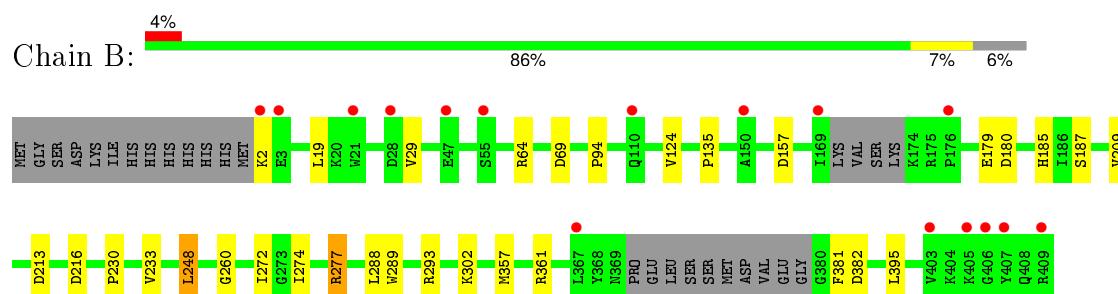
3 Residue-property plots [i](#)

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.

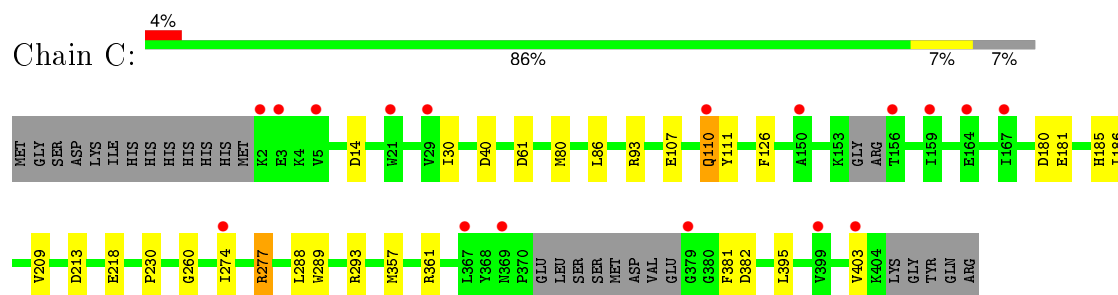
- Molecule 1: Argininosuccinate synthase



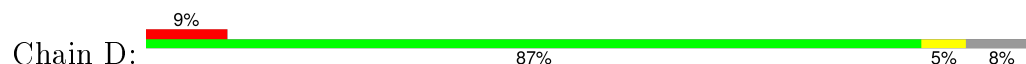
- Molecule 1: Argininosuccinate synthase

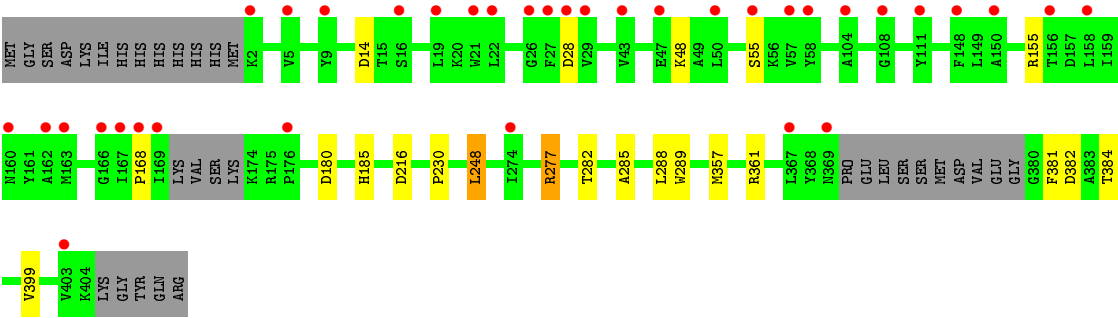


- Molecule 1: Argininosuccinate synthase



- Molecule 1: Argininosuccinate synthase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.32Å 114.91Å 149.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.21 – 1.65 49.21 – 1.65	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.21-1.65) 99.8 (49.21-1.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 1.65Å)	Xtriage
Refinement program	REFMAC 5.2.0001	Depositor
R, R_{free}	0.177 , 0.209 0.192 , 0.223	Depositor DCC
R_{free} test set	9757 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	15.3	Xtriage
Anisotropy	0.285	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	9 of 195745 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	13531	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 49.39 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 7.5130e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.84	1/3197 (0.0%)	0.91	6/4321 (0.1%)
1	B	0.81	0/3184	0.90	11/4308 (0.3%)
1	C	0.80	0/3168	0.89	9/4285 (0.2%)
1	D	0.81	0/3116	0.88	4/4225 (0.1%)
All	All	0.82	1/12665 (0.0%)	0.90	30/17139 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	66	PHE	CB-CG	5.60	1.60	1.51

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	180	ASP	CB-CG-OD2	7.64	125.18	118.30
1	A	293	ARG	NE-CZ-NH2	-7.11	116.75	120.30
1	C	293	ARG	NE-CZ-NH1	7.06	123.83	120.30
1	D	180	ASP	CB-CG-OD2	6.61	124.25	118.30
1	D	277	ARG	NE-CZ-NH2	-6.46	117.07	120.30
1	C	293	ARG	NE-CZ-NH2	-6.38	117.11	120.30
1	B	180	ASP	CB-CG-OD2	6.38	124.04	118.30
1	B	64	ARG	NE-CZ-NH1	-6.20	117.20	120.30
1	C	180	ASP	CB-CG-OD2	6.03	123.72	118.30
1	B	157	ASP	CB-CG-OD2	5.80	123.52	118.30
1	A	157	ASP	CB-CG-OD2	5.72	123.45	118.30
1	B	293	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	B	277	ARG	NE-CZ-NH1	5.55	123.08	120.30
1	A	213	ASP	CB-CG-OD2	5.54	123.29	118.30
1	B	69	ASP	CB-CG-OD2	5.53	123.28	118.30
1	C	213	ASP	CB-CG-OD2	5.43	123.19	118.30
1	D	14	ASP	CB-CG-OD2	5.41	123.17	118.30
1	C	382	ASP	CB-CG-OD2	5.38	123.14	118.30
1	B	248	LEU	CA-CB-CG	5.34	127.58	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	293	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	D	248	LEU	CA-CB-CG	5.31	127.52	115.30
1	C	40	ASP	CB-CG-OD2	5.27	123.04	118.30
1	C	14	ASP	CB-CG-OD2	5.26	123.03	118.30
1	C	61	ASP	CB-CG-OD2	5.26	123.03	118.30
1	B	382	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	66	PHE	CB-CG-CD1	5.17	124.42	120.80
1	B	216	ASP	CB-CG-OD2	5.08	122.87	118.30
1	B	213	ASP	CB-CG-OD2	5.06	122.85	118.30
1	C	277	ARG	NE-CZ-NH2	-5.05	117.78	120.30
1	A	61	ASP	CB-CG-OD2	5.02	122.82	118.30

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	3117	0	3063	15	0
1	B	3104	0	3043	17	0
1	C	3089	0	3035	11	0
1	D	3037	0	2962	12	0
2	A	315	0	0	6	0
2	B	298	0	0	2	0
2	C	312	0	0	2	0
2	D	259	0	0	3	0
All	All	13531	0	12103	47	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 2.

All (47) 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:C:230:PRO:HG3	1:C:288:LEU:HD11	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:233:VAL:HG23	1:B:248:LEU:HG	1.69	0.74
1:C:357[B]:MET:SD	2:D:532:HOH:O	2.50	0.68
1:D:230:PRO:HG3	1:D:288:LEU:HD11	1.74	0.67
1:A:230:PRO:HG3	1:A:288:LEU:HD11	1.76	0.67
2:A:571:HOH:O	1:B:357[B]:MET:SD	2.52	0.67
1:A:357[B]:MET:SD	2:B:547:HOH:O	2.52	0.66
2:C:628:HOH:O	1:D:357[B]:MET:HG2	1.95	0.66
2:A:650:HOH:O	1:B:357[B]:MET:HG2	1.97	0.65
1:A:80:MET:HG2	1:A:86:LEU:HD23	1.79	0.65
1:D:357[B]:MET:SD	2:D:441:HOH:O	2.55	0.63
1:B:274:ILE:HD13	1:D:399:VAL:HG21	1.81	0.63
1:B:230:PRO:HG3	1:B:288:LEU:HD11	1.83	0.61
1:A:237:LYS:HB2	2:A:634:HOH:O	2.03	0.58
1:B:19:LEU:HD13	1:B:29:VAL:HG11	1.86	0.58
1:B:381:PHE:CD1	1:C:395:LEU:HD11	2.39	0.56
1:C:110:GLN:HG2	1:C:111:TYR:CD2	2.42	0.55
1:C:181:GLU:HG3	1:C:186:ILE:HG12	1.91	0.53
1:A:162:ALA:HA	1:A:167:ILE:HD12	1.92	0.51
1:A:395:LEU:HD11	1:D:381:PHE:CD1	2.46	0.51
2:C:628:HOH:O	1:D:357[B]:MET:CG	2.58	0.50
1:B:2:LYS:N	2:B:646:HOH:O	2.45	0.50
1:B:233:VAL:CG2	1:B:248:LEU:HG	2.40	0.49
2:A:434:HOH:O	1:B:357[B]:MET:SD	2.60	0.49
1:C:93:ARG:HD2	1:C:126:PHE:CE2	2.48	0.49
1:A:222:GLU:HG3	1:A:236:LEU:HD21	1.96	0.48
1:A:64:ARG:HD3	2:A:544:HOH:O	2.14	0.48
1:D:382:ASP:OD1	1:D:384:THR:HB	2.15	0.47
1:C:30:ILE:HD13	1:C:107:GLU:HG3	1.98	0.46
1:B:124:VAL:CG2	1:B:272:ILE:HD12	2.46	0.46
1:B:395:LEU:HD11	1:C:381:PHE:CD1	2.50	0.46
1:A:209:VAL:O	1:A:260:GLY:HA2	2.16	0.46
1:A:20:LYS:HG3	1:A:167:ILE:HD11	1.98	0.45
1:D:216:ASP:CB	2:D:483:HOH:O	2.63	0.45
1:C:80:MET:HG2	1:C:86:LEU:HD23	1.99	0.45
1:A:398:LYS:HG2	1:B:135:PRO:HB3	2.00	0.44
1:A:237:LYS:CB	2:A:634:HOH:O	2.64	0.44
1:A:181:GLU:HB2	1:A:186:ILE:HG12	2.00	0.43
1:C:209:VAL:O	1:C:260:GLY:HA2	2.17	0.43
1:B:274:ILE:HD13	1:D:399:VAL:CG2	2.46	0.43
1:D:48:LYS:HE3	1:D:168:PRO:O	2.19	0.42
1:A:399:VAL:HG21	1:C:274:ILE:HD13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:179:GLU:HA	1:B:187:SER:O	2.20	0.41
1:D:282:THR:HG22	1:D:285:ALA:HB3	2.02	0.41
1:B:209:VAL:O	1:B:260:GLY:HA2	2.20	0.41
1:D:28:ASP:OD1	1:D:55:SER:HB3	2.21	0.41
1:A:269:ASN:HB3	1:B:302:LYS:HD3	2.03	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	394/421 (94%)	380 (96%)	13 (3%)	1 (0%)	46	24
1	B	390/421 (93%)	376 (96%)	14 (4%)	0	100	100
1	C	389/421 (92%)	373 (96%)	15 (4%)	1 (0%)	46	24
1	D	385/421 (91%)	373 (97%)	12 (3%)	0	100	100
All	All	1558/1684 (92%)	1502 (96%)	54 (4%)	2 (0%)	56	33

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	403	VAL
1	C	403	VAL

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	321/356 (90%)	310 (97%)	11 (3%)	44	14
1	B	321/356 (90%)	316 (98%)	5 (2%)	70	48
1	C	320/356 (90%)	314 (98%)	6 (2%)	65	40
1	D	310/356 (87%)	304 (98%)	6 (2%)	65	40
All	All	1272/1424 (89%)	1244 (98%)	28 (2%)	60	32

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	LEU
1	A	20	LYS
1	A	110	GLN
1	A	149	LEU
1	A	163	MET
1	A	181	GLU
1	A	185	HIS
1	A	248	LEU
1	A	277	ARG
1	A	289	TRP
1	A	361	ARG
1	B	94	PRO
1	B	185	HIS
1	B	277	ARG
1	B	289	TRP
1	B	361	ARG
1	C	110	GLN
1	C	185	HIS
1	C	218	GLU
1	C	277	ARG
1	C	289	TRP
1	C	361	ARG
1	D	155	ARG
1	D	185	HIS
1	D	248	LEU
1	D	277	ARG
1	D	289	TRP
1	D	361	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	110	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	398/421 (94%)	0.31	30 (7%) 17 15	8, 16, 38, 49	0
1	B	394/421 (93%)	0.21	16 (4%) 41 40	8, 16, 33, 57	0
1	C	393/421 (93%)	0.21	17 (4%) 39 38	8, 16, 35, 61	0
1	D	389/421 (92%)	0.46	36 (9%) 11 9	8, 17, 35, 57	0
All	All	1574/1684 (93%)	0.30	99 (6%) 23 20	8, 16, 36, 61	0

All (99) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	367	LEU	8.2
1	D	167	ILE	6.4
1	D	367	LEU	6.2
1	A	405	LYS	6.0
1	B	169	ILE	5.6
1	A	406	GLY	5.5
1	C	403	VAL	5.1
1	C	274	ILE	5.1
1	D	21	TRP	4.9
1	A	150	ALA	4.7
1	D	2	LYS	4.5
1	C	21	TRP	4.5
1	A	3	GLU	4.3
1	B	406	GLY	4.2
1	A	407	TYR	4.0
1	A	403	VAL	3.9
1	A	28	ASP	3.9
1	D	162	ALA	3.9
1	D	403	VAL	3.8
1	C	379	GLY	3.8
1	A	379	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	5	VAL	3.6
1	A	21	TRP	3.6
1	D	108	GLY	3.6
1	B	407	TYR	3.6
1	D	9	TYR	3.6
1	D	168	PRO	3.5
1	D	27	PHE	3.4
1	D	169	ILE	3.3
1	B	367	LEU	3.3
1	C	2	LYS	3.1
1	B	176	PRO	3.1
1	D	369	ASN	3.1
1	B	2	LYS	3.1
1	D	111	TYR	3.0
1	A	27	PHE	3.0
1	B	405	LYS	3.0
1	D	47	GLU	3.0
1	D	50	LEU	3.0
1	B	150	ALA	2.9
1	A	23	CYS	2.9
1	A	29	VAL	2.9
1	A	52	THR	2.9
1	D	19	LEU	2.8
1	D	148	PHE	2.8
1	D	29	VAL	2.8
1	A	149	LEU	2.8
1	A	369	ASN	2.8
1	D	163	MET	2.8
1	B	403	VAL	2.8
1	D	57	VAL	2.7
1	C	159	ILE	2.7
1	D	16	SER	2.7
1	C	156	THR	2.7
1	B	21	TRP	2.7
1	A	367	LEU	2.7
1	B	3	GLU	2.7
1	A	146	PRO	2.7
1	D	28	ASP	2.7
1	C	3	GLU	2.6
1	C	29	VAL	2.6
1	D	55	SER	2.6
1	A	402	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	22	LEU	2.6
1	D	26	GLY	2.5
1	B	55	SER	2.5
1	D	166	GLY	2.4
1	D	158	LEU	2.4
1	A	108	GLY	2.4
1	D	43	VAL	2.4
1	A	162	ALA	2.3
1	A	110	GLN	2.3
1	C	5	VAL	2.3
1	D	176	PRO	2.3
1	A	158	LEU	2.3
1	A	26	GLY	2.3
1	A	2	LYS	2.2
1	D	58	TYR	2.2
1	B	28	ASP	2.2
1	C	110	GLN	2.2
1	A	30	ILE	2.2
1	C	369	ASN	2.2
1	A	51	LYS	2.2
1	C	399	VAL	2.2
1	C	167	ILE	2.2
1	D	274	ILE	2.2
1	D	150	ALA	2.2
1	A	159	ILE	2.2
1	D	160	ASN	2.2
1	B	409	ARG	2.1
1	A	54	ALA	2.1
1	C	150	ALA	2.1
1	D	104	ALA	2.1
1	B	47	GLU	2.1
1	C	164	GLU	2.1
1	D	156	THR	2.0
1	A	409	ARG	2.0
1	A	368	TYR	2.0
1	B	110	GLN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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.