



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:37 PM UTC

PDB ID : 3TSY / pdb_00003tsy
Title : 4-Coumaroyl-CoA Ligase::Stilbene Synthase fusion protein
Authors : Yi, H.; Jez, J.M.
Deposited on : 2011-09-13
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

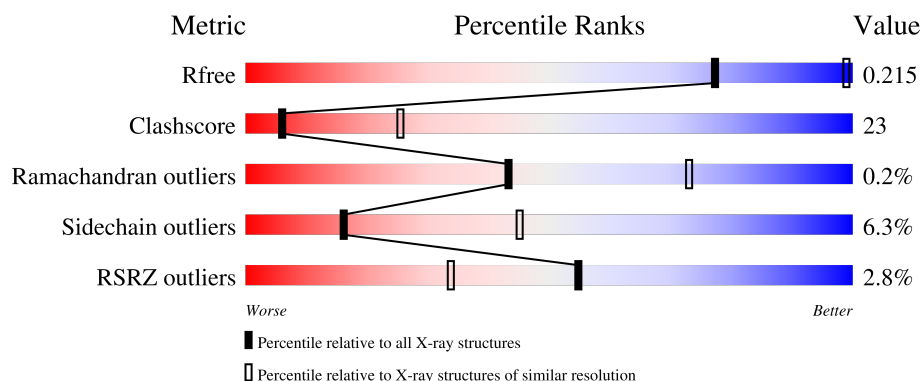
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	979	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6323 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 Fusion Protein 4-coumarate–CoA ligase 1, Resveratrol synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	828	6323	4030	1060	1198	35	0	0	0

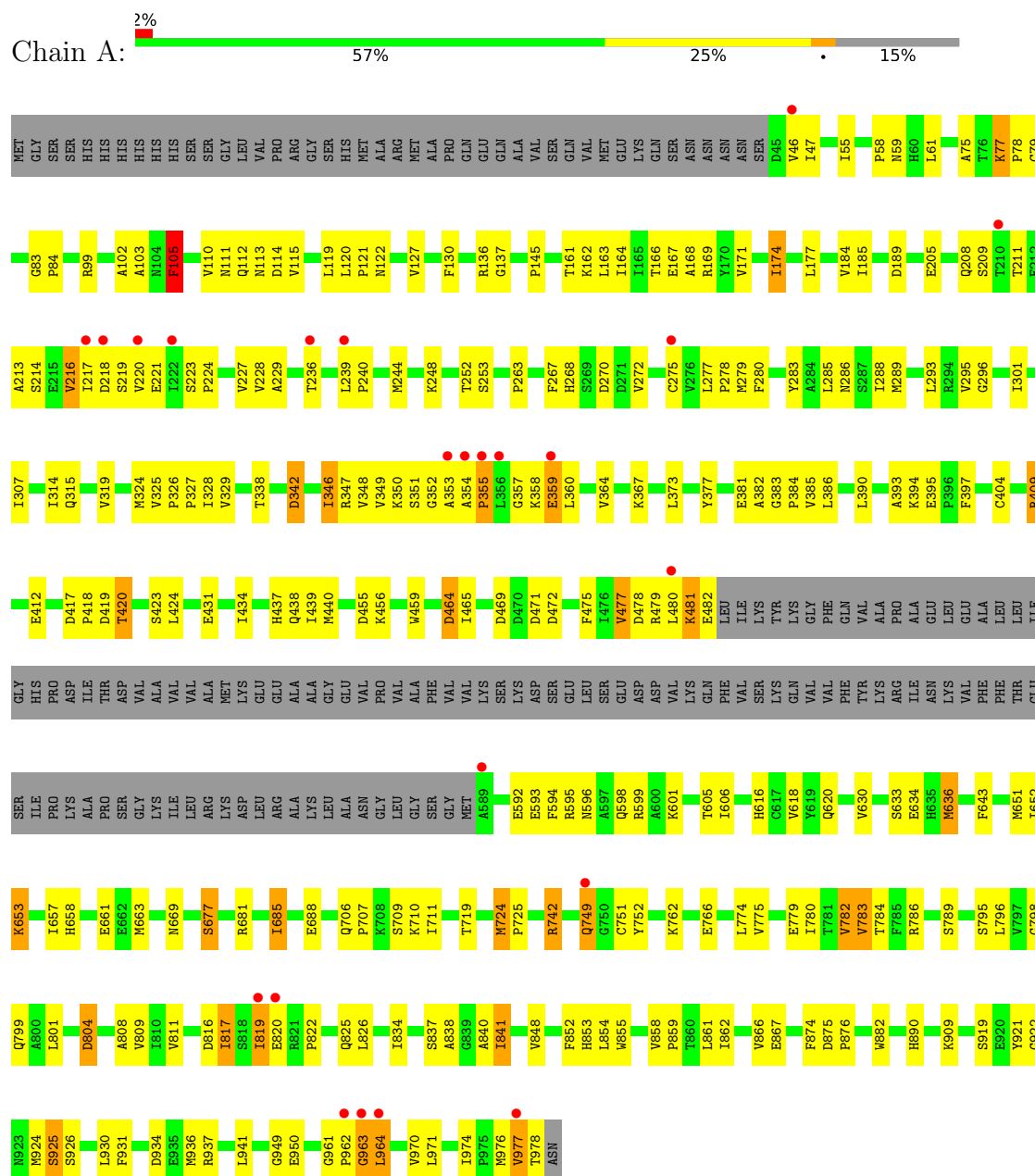
There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP Q42524
A	2	GLY	-	expression tag	UNP Q42524
A	3	SER	-	expression tag	UNP Q42524
A	4	SER	-	expression tag	UNP Q42524
A	5	HIS	-	expression tag	UNP Q42524
A	6	HIS	-	expression tag	UNP Q42524
A	7	HIS	-	expression tag	UNP Q42524
A	8	HIS	-	expression tag	UNP Q42524
A	9	HIS	-	expression tag	UNP Q42524
A	10	HIS	-	expression tag	UNP Q42524
A	11	SER	-	expression tag	UNP Q42524
A	12	SER	-	expression tag	UNP Q42524
A	13	GLY	-	expression tag	UNP Q42524
A	14	LEU	-	expression tag	UNP Q42524
A	15	VAL	-	expression tag	UNP Q42524
A	16	PRO	-	expression tag	UNP Q42524
A	17	ARG	-	expression tag	UNP Q42524
A	18	GLY	-	expression tag	UNP Q42524
A	19	SER	-	expression tag	UNP Q42524
A	20	HIS	-	expression tag	UNP Q42524
A	21	MET	-	expression tag	UNP Q42524
A	22	ALA	-	expression tag	UNP Q42524
A	23	ARG	-	expression tag	UNP Q42524
A	585	GLY	-	linker	UNP Q42524
A	586	SER	-	linker	UNP Q42524
A	587	GLY	-	linker	UNP Q42524

3 Residue-property plots

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: Fusion Protein 4-coumarate–CoA ligase 1, Resveratrol synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	117.55Å 117.55Å 243.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.10 – 3.10 49.10 – 3.10	Depositor EDS
% Data completeness (in resolution range)	93.8 (49.10-3.10) 93.8 (49.10-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.66 (at 3.12Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, R_{free}	0.177 , 0.208 0.188 , 0.215	Depositor DCC
R_{free} test set	1495 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	73.4	Xtriage
Anisotropy	0.326	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 58.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6323	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.81% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.55	0/6452	0.99	21/8767 (0.2%)

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	359	GLU	N-CA-C	-11.03	99.33	113.12
1	A	749	GLN	N-CA-C	8.36	120.17	111.14
1	A	963	GLY	N-CA-C	-7.89	104.86	115.36
1	A	477	VAL	N-CA-C	7.74	118.62	112.12
1	A	383	GLY	N-CA-C	6.72	126.05	112.34
1	A	801	LEU	N-CA-C	6.51	119.70	111.69
1	A	601	LYS	N-CA-C	6.47	118.13	111.14
1	A	477	VAL	CB-CA-C	-6.17	104.86	110.91
1	A	921	TYR	N-CA-C	6.12	121.68	113.72
1	A	841	ILE	N-CA-C	-5.97	99.04	107.75
1	A	105	PHE	N-CA-C	-5.96	104.78	111.28
1	A	137	GLY	N-CA-C	-5.71	107.44	115.32
1	A	220	VAL	N-CA-C	-5.68	105.61	113.00
1	A	925	SER	CB-CA-C	-5.66	110.06	116.63
1	A	439	ILE	CB-CA-C	-5.64	105.13	111.45
1	A	385	VAL	N-CA-C	5.50	116.50	108.58
1	A	383	GLY	CA-C-N	5.40	139.96	127.00
1	A	383	GLY	C-N-CA	5.40	139.96	127.00
1	A	115	VAL	N-CA-C	5.35	117.00	108.87
1	A	75	ALA	N-CA-C	5.32	117.77	111.33
1	A	420	THR	N-CA-C	-5.17	101.22	109.23

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	6323	0	6379	288	0
All	All	6323	0	6379	288	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 23.

All (288) 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:A:816:ASP:O	1:A:817:ILE:CG2	1.84	1.26
1:A:218:ASP:CB	1:A:219:SER:HA	1.74	1.17
1:A:326:PRO:CG	1:A:327:PRO:HD3	1.74	1.16
1:A:326:PRO:HD3	1:A:354:ALA:CB	1.76	1.14
1:A:326:PRO:HD3	1:A:354:ALA:HB2	1.30	1.09
1:A:382:ALA:HB1	1:A:386:LEU:HD21	1.23	1.09
1:A:816:ASP:O	1:A:817:ILE:HG22	0.94	1.09
1:A:841:ILE:HB	1:A:962:PRO:CA	1.82	1.08
1:A:218:ASP:HB3	1:A:219:SER:CA	1.84	1.08
1:A:677:SER:HB2	1:A:681:ARG:HE	1.21	1.04
1:A:706:GLN:OE1	1:A:819:ILE:HG13	1.59	1.01
1:A:120:LEU:HD21	1:A:166:THR:HA	1.42	1.01
1:A:841:ILE:HB	1:A:962:PRO:HA	1.00	0.98
1:A:841:ILE:CB	1:A:962:PRO:HA	1.94	0.97
1:A:326:PRO:HG2	1:A:327:PRO:CD	1.94	0.97
1:A:99:ARG:HH22	1:A:217:ILE:HG22	1.24	0.97
1:A:119:LEU:O	1:A:120:LEU:HD23	1.65	0.96
1:A:326:PRO:HG2	1:A:327:PRO:HD3	0.98	0.96
1:A:817:ILE:H	1:A:820:GLU:HG3	1.31	0.94
1:A:819:ILE:H	1:A:819:ILE:HD13	1.29	0.94
1:A:382:ALA:HB1	1:A:386:LEU:CD2	1.99	0.93
1:A:120:LEU:HD21	1:A:166:THR:CA	1.98	0.92
1:A:841:ILE:HG22	1:A:962:PRO:HB3	1.50	0.91
1:A:163:LEU:HD12	1:A:164:ILE:H	1.37	0.90
1:A:120:LEU:CD2	1:A:166:THR:HA	2.01	0.89
1:A:382:ALA:CB	1:A:386:LEU:HD21	2.02	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:742:ARG:HG3	1:A:742:ARG:HH11	1.39	0.87
1:A:816:ASP:C	1:A:817:ILE:HG22	1.97	0.87
1:A:817:ILE:H	1:A:820:GLU:CG	1.89	0.85
1:A:218:ASP:HB3	1:A:219:SER:HA	0.89	0.85
1:A:325:VAL:HB	1:A:326:PRO:HD2	1.60	0.84
1:A:386:LEU:HD22	1:A:434:ILE:HG21	1.60	0.83
1:A:605:THR:HG22	1:A:825:GLN:HG2	1.60	0.81
1:A:820:GLU:OE2	1:A:822:PRO:HD3	1.80	0.80
1:A:798:GLY:HA3	1:A:852:PHE:CZ	2.16	0.80
1:A:326:PRO:CG	1:A:327:PRO:CD	2.58	0.79
1:A:677:SER:HB2	1:A:681:ARG:NE	1.98	0.79
1:A:817:ILE:HA	1:A:820:GLU:OE1	1.83	0.79
1:A:268:HIS:HD2	1:A:270:ASP:H	1.29	0.78
1:A:119:LEU:O	1:A:120:LEU:CD2	2.33	0.77
1:A:798:GLY:HA3	1:A:852:PHE:HZ	1.48	0.77
1:A:924:MET:HE1	1:A:931:PHE:CG	2.19	0.77
1:A:862:ILE:HD13	1:A:964:LEU:HD11	1.67	0.76
1:A:819:ILE:HD13	1:A:819:ILE:N	2.00	0.76
1:A:214:SER:O	1:A:217:ILE:HG23	1.86	0.75
1:A:59:ASN:HB2	1:A:248:LYS:HG3	1.68	0.75
1:A:99:ARG:NH2	1:A:217:ILE:HG22	2.01	0.74
1:A:120:LEU:HD21	1:A:166:THR:C	2.11	0.74
1:A:820:GLU:OE2	1:A:820:GLU:C	2.30	0.74
1:A:841:ILE:O	1:A:962:PRO:CB	2.36	0.74
1:A:780:ILE:HG22	1:A:782:VAL:HG13	1.67	0.73
1:A:822:PRO:HB2	1:A:974:ILE:HD13	1.69	0.73
1:A:817:ILE:CA	1:A:820:GLU:OE1	2.36	0.73
1:A:205:GLU:O	1:A:208:GLN:HG2	1.87	0.73
1:A:685:ILE:HG21	1:A:783:VAL:HG12	1.70	0.72
1:A:817:ILE:O	1:A:817:ILE:HG13	1.88	0.72
1:A:268:HIS:CD2	1:A:270:ASP:H	2.06	0.72
1:A:837:SER:HB2	1:A:964:LEU:HD23	1.73	0.71
1:A:651:MET:HA	1:A:651:MET:HE2	1.73	0.70
1:A:419:ASP:OD1	1:A:420:THR:HG23	1.93	0.69
1:A:742:ARG:HG3	1:A:742:ARG:NH1	2.04	0.69
1:A:482:GLU:O	1:A:482:GLU:HG2	1.92	0.69
1:A:163:LEU:HD12	1:A:164:ILE:N	2.07	0.69
1:A:724:MET:HA	1:A:725:PRO:C	2.18	0.68
1:A:130:PHE:CE1	1:A:285:LEU:HD21	2.29	0.68
1:A:780:ILE:CG2	1:A:782:VAL:HG13	2.23	0.68
1:A:358:LYS:O	1:A:358:LYS:HG3	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:465:ILE:CD1	1:A:477:VAL:CG2	2.73	0.67
1:A:326:PRO:CD	1:A:327:PRO:CD	2.74	0.66
1:A:122:ASN:HD21	1:A:279:MET:H	1.42	0.66
1:A:326:PRO:HD3	1:A:354:ALA:HB1	1.77	0.65
1:A:685:ILE:HG23	1:A:782:VAL:HG22	1.78	0.65
1:A:822:PRO:HB2	1:A:974:ILE:CD1	2.25	0.65
1:A:357:GLY:O	1:A:358:LYS:HB3	1.94	0.65
1:A:742:ARG:HH11	1:A:742:ARG:CG	2.10	0.65
1:A:465:ILE:CD1	1:A:477:VAL:HG23	2.27	0.65
1:A:817:ILE:N	1:A:820:GLU:OE1	2.30	0.64
1:A:862:ILE:O	1:A:866:VAL:HG23	1.98	0.64
1:A:167:GLU:CD	1:A:169:ARG:HH12	2.05	0.64
1:A:386:LEU:CD2	1:A:434:ILE:HG21	2.27	0.64
1:A:481:LYS:HG2	1:A:482:GLU:OE1	1.98	0.63
1:A:858:VAL:O	1:A:862:ILE:HG12	1.99	0.62
1:A:751:CYS:HB3	1:A:890:HIS:NE2	2.15	0.61
1:A:326:PRO:CD	1:A:327:PRO:HD3	2.30	0.61
1:A:465:ILE:HG13	1:A:477:VAL:HG23	1.82	0.61
1:A:217:ILE:HG13	1:A:218:ASP:OD2	2.01	0.61
1:A:77:LYS:HE2	1:A:296:GLY:O	2.01	0.60
1:A:248:LYS:HZ3	1:A:437:HIS:HB3	1.67	0.60
1:A:469:ASP:OD2	1:A:475:PHE:HE2	1.84	0.60
1:A:326:PRO:CD	1:A:354:ALA:CB	2.68	0.60
1:A:417:ASP:HB3	1:A:420:THR:OG1	2.02	0.60
1:A:283:TYR:OH	1:A:350:LYS:HE3	2.02	0.60
1:A:465:ILE:HG13	1:A:477:VAL:CG2	2.32	0.60
1:A:112:GLN:H	1:A:136:ARG:HH21	1.49	0.59
1:A:239:LEU:HG	1:A:240:PRO:HD2	1.85	0.59
1:A:219:SER:OG	1:A:221:GLU:N	2.32	0.59
1:A:342:ASP:OD1	1:A:342:ASP:C	2.46	0.58
1:A:841:ILE:HG22	1:A:962:PRO:CB	2.30	0.58
1:A:357:GLY:H	1:A:360:LEU:HD12	1.68	0.58
1:A:227:VAL:HG21	1:A:244:MET:HE2	1.86	0.58
1:A:114:ASP:HB2	1:A:162:LYS:HD3	1.85	0.58
1:A:119:LEU:HD22	1:A:145:PRO:HA	1.86	0.58
1:A:277:LEU:CD2	1:A:325:VAL:HG13	2.34	0.57
1:A:465:ILE:HD11	1:A:477:VAL:HG23	1.85	0.57
1:A:841:ILE:O	1:A:962:PRO:HB2	2.03	0.57
1:A:278:PRO:HB3	1:A:280:PHE:CZ	2.39	0.57
1:A:795:SER:O	1:A:799:GLN:HG2	2.05	0.57
1:A:167:GLU:CD	1:A:169:ARG:NH1	2.63	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:386:LEU:HD22	1:A:434:ILE:HD13	1.87	0.57
1:A:841:ILE:CB	1:A:962:PRO:CA	2.68	0.56
1:A:862:ILE:CD1	1:A:964:LEU:HD11	2.35	0.56
1:A:840:ALA:HB2	1:A:855:TRP:CE3	2.40	0.56
1:A:819:ILE:N	1:A:819:ILE:CD1	2.66	0.56
1:A:228:VAL:HG13	1:A:229:ALA:N	2.20	0.56
1:A:419:ASP:OD1	1:A:419:ASP:C	2.48	0.56
1:A:112:GLN:HG2	1:A:113:ASN:ND2	2.21	0.55
1:A:752:TYR:HD2	1:A:961:GLY:HA3	1.71	0.55
1:A:685:ILE:CG2	1:A:782:VAL:HG22	2.35	0.55
1:A:325:VAL:CG2	1:A:328:ILE:HG13	2.37	0.55
1:A:465:ILE:CG1	1:A:477:VAL:HG23	2.37	0.55
1:A:275:CYS:O	1:A:275:CYS:SG	2.64	0.55
1:A:677:SER:CB	1:A:681:ARG:HE	2.09	0.54
1:A:841:ILE:C	1:A:962:PRO:HB3	2.31	0.54
1:A:841:ILE:CG2	1:A:962:PRO:HB3	2.31	0.54
1:A:924:MET:HE1	1:A:931:PHE:CD1	2.42	0.54
1:A:834:ILE:HD12	1:A:964:LEU:HG	1.90	0.54
1:A:936:MET:HE2	1:A:950:GLU:OE2	2.08	0.54
1:A:219:SER:HB3	1:A:221:GLU:O	2.08	0.53
1:A:364:VAL:HG11	1:A:373:LEU:HD21	1.90	0.53
1:A:809:VAL:HG12	1:A:811:VAL:HG23	1.90	0.53
1:A:418:PRO:O	1:A:419:ASP:CG	2.52	0.53
1:A:112:GLN:O	1:A:113:ASN:HB2	2.08	0.53
1:A:268:HIS:HD2	1:A:270:ASP:N	2.03	0.53
1:A:479:ARG:HG3	1:A:480:LEU:H	1.74	0.53
1:A:924:MET:HE1	1:A:931:PHE:CD2	2.44	0.53
1:A:326:PRO:CD	1:A:327:PRO:HD2	2.39	0.52
1:A:606:ILE:HG23	1:A:809:VAL:HG13	1.92	0.52
1:A:685:ILE:HD12	1:A:783:VAL:HG12	1.91	0.52
1:A:592:GLU:OE1	1:A:592:GLU:N	2.30	0.52
1:A:477:VAL:HG23	1:A:478:ASP:N	2.25	0.52
1:A:592:GLU:H	1:A:592:GLU:CD	2.14	0.52
1:A:651:MET:HE2	1:A:651:MET:CA	2.38	0.52
1:A:786:ARG:NH2	1:A:848:VAL:O	2.43	0.52
1:A:219:SER:OG	1:A:221:GLU:HB3	2.10	0.51
1:A:417:ASP:O	1:A:420:THR:O	2.27	0.51
1:A:103:ALA:HB1	1:A:213:ALA:HB3	1.92	0.51
1:A:338:THR:HG21	1:A:367:LYS:HD2	1.91	0.51
1:A:286:ASN:ND2	1:A:384:PRO:HD2	2.25	0.51
1:A:643:PHE:CD1	1:A:796:LEU:HG	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:LEU:HB3	1:A:121:PRO:HD2	1.92	0.51
1:A:867:GLU:HG3	1:A:882:TRP:CH2	2.45	0.51
1:A:890:HIS:CE1	1:A:925:SER:O	2.64	0.50
1:A:278:PRO:HB3	1:A:280:PHE:CE2	2.46	0.50
1:A:228:VAL:CG1	1:A:229:ALA:N	2.75	0.50
1:A:263:PRO:O	1:A:393:ALA:HA	2.12	0.50
1:A:112:GLN:N	1:A:136:ARG:HH21	2.10	0.50
1:A:616:HIS:HB3	1:A:657:ILE:O	2.12	0.49
1:A:479:ARG:HG3	1:A:480:LEU:N	2.26	0.49
1:A:706:GLN:HB3	1:A:707:PRO:CD	2.42	0.49
1:A:820:GLU:C	1:A:820:GLU:CD	2.81	0.49
1:A:275:CYS:HB3	1:A:288:ILE:HG21	1.94	0.49
1:A:949:GLY:O	1:A:950:GLU:HB2	2.12	0.49
1:A:174:ILE:HD13	1:A:185:ILE:HD12	1.94	0.49
1:A:358:LYS:O	1:A:358:LYS:CG	2.60	0.49
1:A:119:LEU:O	1:A:166:THR:HA	2.13	0.49
1:A:217:ILE:HG13	1:A:218:ASP:N	2.27	0.49
1:A:816:ASP:N	1:A:820:GLU:HG2	2.28	0.49
1:A:119:LEU:O	1:A:120:LEU:CG	2.61	0.49
1:A:122:ASN:ND2	1:A:279:MET:H	2.09	0.49
1:A:595:ARG:NH1	1:A:598:GLN:OE1	2.46	0.49
1:A:630:VAL:HG12	1:A:661:GLU:HG3	1.95	0.49
1:A:326:PRO:HD2	1:A:327:PRO:HD2	1.95	0.49
1:A:762:LYS:O	1:A:766:GLU:HG3	2.12	0.49
1:A:83:GLY:N	1:A:84:PRO:HD2	2.27	0.49
1:A:779:GLU:HG3	1:A:924:MET:O	2.12	0.49
1:A:841:ILE:C	1:A:962:PRO:CB	2.86	0.48
1:A:465:ILE:HD12	1:A:477:VAL:HG21	1.96	0.48
1:A:820:GLU:OE2	1:A:820:GLU:O	2.31	0.48
1:A:352:GLY:O	1:A:353:ALA:HB3	2.12	0.48
1:A:834:ILE:HD12	1:A:964:LEU:HD12	1.95	0.48
1:A:46:VAL:HG13	1:A:423:SER:CB	2.44	0.48
1:A:347:ARG:HG3	1:A:348:VAL:HG23	1.96	0.48
1:A:267:PHE:HB3	1:A:295:VAL:HG21	1.96	0.47
1:A:326:PRO:N	1:A:327:PRO:CD	2.77	0.47
1:A:277:LEU:HD21	1:A:325:VAL:HG13	1.96	0.47
1:A:354:ALA:HA	1:A:355:PRO:HD3	1.61	0.47
1:A:620:GLN:HG3	1:A:652:ILE:O	2.15	0.47
1:A:272:VAL:HB	1:A:319:VAL:HA	1.97	0.47
1:A:706:GLN:OE1	1:A:819:ILE:CG1	2.48	0.47
1:A:816:ASP:C	1:A:817:ILE:CG2	2.69	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:780:ILE:O	1:A:783:VAL:HG13	2.15	0.47
1:A:99:ARG:HH22	1:A:217:ILE:CG2	2.12	0.47
1:A:252:THR:HG22	1:A:438:GLN:HB3	1.97	0.47
1:A:275:CYS:SG	1:A:301:ILE:HA	2.55	0.47
1:A:465:ILE:CD1	1:A:477:VAL:HG21	2.45	0.47
1:A:934:ASP:O	1:A:937:ARG:HG3	2.14	0.47
1:A:685:ILE:CD1	1:A:783:VAL:HG12	2.45	0.47
1:A:707:PRO:HD2	1:A:710:LYS:HD3	1.97	0.46
1:A:653:LYS:HG3	1:A:919:SER:OG	2.15	0.46
1:A:377:TYR:CE2	1:A:386:LEU:HD12	2.50	0.46
1:A:633:SER:HB3	1:A:636:MET:HE3	1.97	0.46
1:A:455:ASP:OD2	1:A:459:TRP:HB2	2.16	0.46
1:A:465:ILE:CG1	1:A:477:VAL:CG2	2.94	0.46
1:A:593:GLU:O	1:A:594:PHE:C	2.57	0.46
1:A:817:ILE:N	1:A:820:GLU:HG3	2.15	0.46
1:A:820:GLU:CD	1:A:820:GLU:O	2.58	0.46
1:A:834:ILE:HD12	1:A:964:LEU:CD1	2.45	0.46
1:A:875:ASP:N	1:A:876:PRO:CD	2.79	0.46
1:A:633:SER:O	1:A:636:MET:HG3	2.17	0.45
1:A:263:PRO:HD2	1:A:394:LYS:HB2	1.98	0.45
1:A:890:HIS:HE1	1:A:925:SER:O	1.98	0.45
1:A:216:VAL:C	1:A:218:ASP:N	2.73	0.45
1:A:841:ILE:O	1:A:962:PRO:CA	2.64	0.45
1:A:465:ILE:HD11	1:A:477:VAL:CG2	2.45	0.45
1:A:465:ILE:O	1:A:477:VAL:HG22	2.17	0.45
1:A:595:ARG:HH12	1:A:598:GLN:HG2	1.82	0.45
1:A:826:LEU:HD23	1:A:971:LEU:CD2	2.47	0.45
1:A:658:HIS:CE1	1:A:688:GLU:HG3	2.51	0.45
1:A:481:LYS:HE2	1:A:481:LYS:HB3	1.54	0.45
1:A:834:ILE:HD12	1:A:964:LEU:CG	2.46	0.44
1:A:592:GLU:N	1:A:592:GLU:CD	2.75	0.44
1:A:122:ASN:HD21	1:A:279:MET:N	2.11	0.44
1:A:219:SER:C	1:A:221:GLU:N	2.73	0.44
1:A:706:GLN:CD	1:A:819:ILE:HG13	2.37	0.44
1:A:838:ALA:HA	1:A:963:GLY:HA2	2.00	0.44
1:A:79:CYS:SG	1:A:293:LEU:CD2	3.05	0.44
1:A:381:GLU:HB3	1:A:440:MET:HE2	2.00	0.44
1:A:168:ALA:HB2	1:A:189:ASP:OD2	2.17	0.44
1:A:325:VAL:HG22	1:A:328:ILE:HG13	2.00	0.44
1:A:55:ILE:HG12	1:A:409:ARG:HD2	2.00	0.43
1:A:593:GLU:O	1:A:596:ASN:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:268:HIS:CD2	1:A:270:ASP:HB2	2.53	0.43
1:A:58:PRO:HB2	1:A:61:LEU:HD12	2.01	0.43
1:A:120:LEU:HD23	1:A:166:THR:HA	1.96	0.43
1:A:267:PHE:CB	1:A:295:VAL:HG21	2.49	0.43
1:A:277:LEU:HD22	1:A:325:VAL:HG13	2.00	0.43
1:A:219:SER:OG	1:A:221:GLU:CB	2.66	0.43
1:A:224:PRO:HB3	1:A:248:LYS:HB2	2.01	0.43
1:A:711:ILE:HD12	1:A:774:LEU:HB2	1.99	0.43
1:A:325:VAL:O	1:A:329:VAL:HG23	2.18	0.43
1:A:127:VAL:HG22	1:A:289:MET:SD	2.59	0.43
1:A:168:ALA:O	1:A:171:VAL:HG23	2.19	0.43
1:A:102:ALA:O	1:A:105:PHE:HB2	2.18	0.42
1:A:796:LEU:HA	1:A:796:LEU:HD12	1.81	0.42
1:A:853:HIS:O	1:A:854:LEU:HD12	2.19	0.42
1:A:268:HIS:HD2	1:A:270:ASP:HB2	1.85	0.42
1:A:326:PRO:CD	1:A:354:ALA:HB2	2.23	0.42
1:A:749:GLN:HA	1:A:749:GLN:NE2	2.35	0.42
1:A:77:LYS:HE3	1:A:78:PRO:O	2.19	0.42
1:A:357:GLY:C	1:A:359:GLU:H	2.27	0.42
1:A:837:SER:HB3	1:A:861:LEU:HD13	2.01	0.42
1:A:119:LEU:C	1:A:120:LEU:HG	2.45	0.42
1:A:816:ASP:O	1:A:817:ILE:CB	2.63	0.42
1:A:964:LEU:HD13	1:A:964:LEU:HA	1.81	0.42
1:A:977:VAL:O	1:A:978:THR:C	2.62	0.42
1:A:314:ILE:CG2	1:A:346:ILE:HD11	2.50	0.42
1:A:373:LEU:N	1:A:373:LEU:HD12	2.35	0.42
1:A:941:LEU:HD13	1:A:976:MET:SD	2.60	0.42
1:A:795:SER:HA	1:A:852:PHE:CE2	2.55	0.42
1:A:804:ASP:N	1:A:804:ASP:OD1	2.52	0.42
1:A:822:PRO:CB	1:A:974:ILE:CD1	2.97	0.42
1:A:858:VAL:HB	1:A:859:PRO:HD3	2.01	0.42
1:A:223:SER:HA	1:A:224:PRO:HD3	1.98	0.41
1:A:817:ILE:H	1:A:820:GLU:CD	2.28	0.41
1:A:924:MET:O	1:A:925:SER:HB3	2.19	0.41
1:A:111:ASN:O	1:A:112:GLN:C	2.64	0.41
1:A:471:ASP:O	1:A:472:ASP:HB2	2.20	0.41
1:A:324:MET:CE	1:A:349:VAL:HG13	2.50	0.41
1:A:105:PHE:O	1:A:110:VAL:HB	2.20	0.41
1:A:351:SER:OG	1:A:354:ALA:O	2.22	0.41
1:A:817:ILE:O	1:A:817:ILE:CG1	2.59	0.41
1:A:862:ILE:HD13	1:A:964:LEU:CD1	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:685:ILE:HG23	1:A:782:VAL:CG2	2.48	0.41
1:A:874:PHE:CZ	1:A:970:VAL:HG22	2.55	0.41
1:A:113:ASN:N	1:A:113:ASN:HD22	2.18	0.41
1:A:431:GLU:HA	1:A:464:ASP:O	2.20	0.41
1:A:706:GLN:HB3	1:A:707:PRO:HD2	2.02	0.41
1:A:775:VAL:O	1:A:808:ALA:HA	2.20	0.41
1:A:120:LEU:CD2	1:A:166:THR:C	2.88	0.41
1:A:658:HIS:NE2	1:A:663:MET:HE1	2.36	0.41
1:A:417:ASP:HB2	1:A:424:LEU:HD11	2.03	0.40
1:A:325:VAL:HG22	1:A:328:ILE:CD1	2.52	0.40
1:A:390:LEU:HB3	1:A:397:PHE:HB2	2.04	0.40
1:A:925:SER:OG	1:A:926:SER:N	2.53	0.40
1:A:652:ILE:HD13	1:A:922:GLY:HA2	2.03	0.40
1:A:326:PRO:CD	1:A:354:ALA:HB1	2.46	0.40
1:A:595:ARG:NH2	1:A:599:ARG:HB3	2.37	0.40
1:A:749:GLN:O	1:A:752:TYR:CE2	2.75	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	824/979 (84%)	794 (96%)	28 (3%)	2 (0%)	43 73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	817	ILE
1	A	355	PRO

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	694/821 (84%)	650 (94%)	44 (6%)	16	45

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	ILE
1	A	77	LYS
1	A	105	PHE
1	A	161	THR
1	A	174	ILE
1	A	177	LEU
1	A	184	VAL
1	A	209	SER
1	A	211	THR
1	A	216	VAL
1	A	236	THR
1	A	253	SER
1	A	307	ILE
1	A	315	GLN
1	A	342	ASP
1	A	346	ILE
1	A	395	GLU
1	A	404	CYS
1	A	409	ARG
1	A	412	GLU
1	A	456	LYS
1	A	464	ASP
1	A	481	LYS
1	A	618	VAL
1	A	634	GLU
1	A	636	MET
1	A	653	LYS
1	A	669	ASN
1	A	677	SER
1	A	685	ILE

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Mol	Chain	Res	Type
1	A	709	SER
1	A	719	THR
1	A	724	MET
1	A	742	ARG
1	A	782	VAL
1	A	783	VAL
1	A	784	THR
1	A	789	SER
1	A	804	ASP
1	A	819	ILE
1	A	909	LYS
1	A	930	LEU
1	A	964	LEU
1	A	977	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	GLN
1	A	113	ASN
1	A	122	ASN
1	A	268	HIS
1	A	635	HIS
1	A	749	GLN
1	A	890	HIS

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 oligosaccharides 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	828/979 (84%)	-0.24	23 (2%) 55 34	26, 80, 135, 198	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	355	PRO	6.1
1	A	354	ALA	5.1
1	A	820	GLU	5.0
1	A	353	ALA	4.7
1	A	962	PRO	4.6
1	A	275	CYS	4.6
1	A	480	LEU	4.2
1	A	963	GLY	4.2
1	A	236	THR	3.8
1	A	46	VAL	3.5
1	A	356	LEU	3.2
1	A	589	ALA	2.9
1	A	819	ILE	2.8
1	A	210	THR	2.5
1	A	977	VAL	2.5
1	A	239	LEU	2.4
1	A	749	GLN	2.4
1	A	222	ILE	2.3
1	A	964	LEU	2.3
1	A	218	ASP	2.3
1	A	359	GLU	2.1
1	A	217	ILE	2.1
1	A	220	VAL	2.1

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 oligosaccharides 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.