



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 10:30 PM EDT

PDB ID : 4KSF / pdb_00004ksf
Title : Crystal Structure of Malonyl-CoA decarboxylase from Agrobacterium vitis,
Northeast Structural Genomics Consortium Target RiR35
Authors : Forouhar, F.; Neely, H.; Seetharaman, J.; Sahdev, S.; Xiao, R.; Ciccocanti, C.;
Lee, D.; Everett, J.K.; Acton, T.B.; Montelione, G.T.; Hunt, J.F.; Tong, L.;
Northeast Structural Genomics Consortium (NESG)
Deposited on : 2013-05-17
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
Mogul	:	2022.3.0, CSD as543be (2022)
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

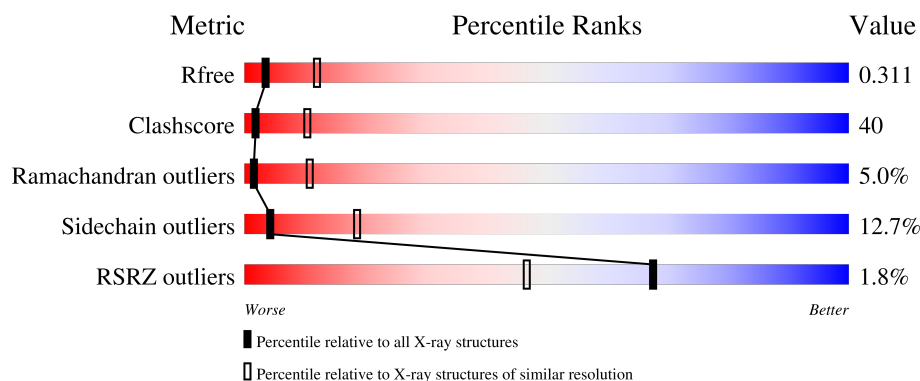
1 Overall quality at a glance

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	456	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3257 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 Malonyl-CoA decarboxylase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	Se	0	0	0
			3231	2042	589	590	3	7			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	450	GLU	-	expression tag	UNP B9K0V9
A	451	HIS	-	expression tag	UNP B9K0V9
A	452	HIS	-	expression tag	UNP B9K0V9
A	453	HIS	-	expression tag	UNP B9K0V9
A	454	HIS	-	expression tag	UNP B9K0V9
A	455	HIS	-	expression tag	UNP B9K0V9
A	456	HIS	-	expression tag	UNP B9K0V9

- Molecule 2 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ni	0	0
			1	1		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Cl	0	0
			2	2		

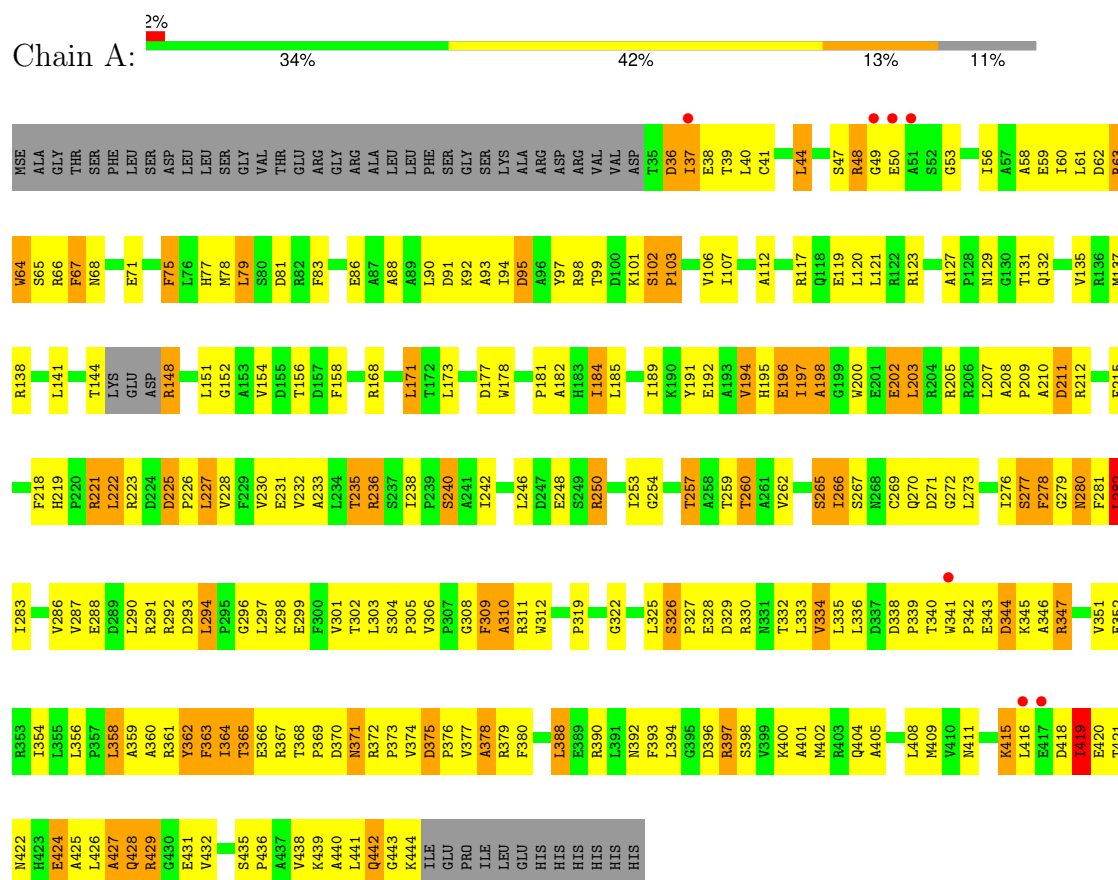
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	23	Total	O	0	0
			23	23		

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: Malonyl-CoA decarboxylase



4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	100.41 Å 100.41 Å 242.74 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.14 – 3.10 28.14 – 3.10	Depositor EDS
% Data completeness (in resolution range)	88.6 (28.14-3.10) 94.1 (28.14-3.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.61 (at 3.11 Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.220 , 0.291 0.233 , 0.311	Depositor DCC
R_{free} test set	2015 reflections (9.45%)	wwPDB-VP
Wilson B-factor (Å ²)	62.4	Xtriage
Anisotropy	0.122	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 68.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3257	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.78% 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: NI, CL

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	0.51	0/3292	1.08	27/4450 (0.6%)

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	211	ASP	N-CA-C	-8.25	101.54	111.69
1	A	39	THR	N-CA-C	-8.16	102.56	114.39
1	A	210	ALA	N-CA-C	-7.71	103.77	113.02
1	A	309	PHE	N-CA-C	-7.06	104.29	113.12
1	A	322	GLY	N-CA-C	-6.95	104.38	115.08
1	A	235	THR	N-CA-C	6.92	117.17	108.45
1	A	63	ARG	N-CA-C	-6.60	105.09	113.01
1	A	334	VAL	N-CA-C	-6.50	104.86	112.98
1	A	36	ASP	N-CA-C	-6.42	104.37	111.82
1	A	246	LEU	N-CA-C	6.41	121.36	112.45
1	A	310	ALA	N-CA-C	-6.18	104.62	111.36
1	A	277	SER	N-CA-C	6.11	119.08	110.23
1	A	200	TRP	N-CA-C	6.02	118.63	111.71
1	A	279	GLY	N-CA-C	-5.87	105.55	113.24
1	A	182	ALA	N-CA-C	5.74	117.61	111.36
1	A	374	VAL	N-CA-C	5.65	117.06	110.62
1	A	102	SER	CA-C-N	5.51	126.72	119.84
1	A	102	SER	C-N-CA	5.51	126.72	119.84
1	A	364	ILE	N-CA-C	5.49	118.74	111.17
1	A	79	LEU	N-CA-C	-5.40	104.94	112.45
1	A	378	ALA	N-CA-C	-5.26	104.98	111.40
1	A	75	PHE	N-CA-C	-5.21	106.61	113.12
1	A	262	VAL	N-CA-C	5.16	115.48	107.28
1	A	240	SER	N-CA-C	-5.12	106.98	113.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	293	ASP	N-CA-C	5.12	117.52	111.33
1	A	375	ASP	CA-C-N	5.04	124.35	118.85
1	A	375	ASP	C-N-CA	5.04	124.35	118.85

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	3231	0	3229	258	0
2	A	1	0	0	0	0
3	A	2	0	0	1	0
4	A	23	0	0	1	0
All	All	3257	0	3229	258	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 40.

All (258) 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:336:LEU:HA	1:A:341:TRP:HH2	1.16	1.04
1:A:197:ILE:CD1	1:A:202:GLU:HB3	1.89	1.03
1:A:230:VAL:HG12	1:A:266:ILE:HG13	1.51	0.93
1:A:222:LEU:H	1:A:222:LEU:HD22	1.32	0.91
1:A:197:ILE:HD11	1:A:202:GLU:HB3	1.53	0.90
1:A:336:LEU:HA	1:A:341:TRP:CH2	2.06	0.90
1:A:86:GLU:OE2	1:A:88:ALA:HB3	1.71	0.88
1:A:236:ARG:HH21	1:A:236:ARG:HB3	1.38	0.87
1:A:236:ARG:HA	1:A:259:THR:HG22	1.56	0.84
1:A:341:TRP:H	1:A:342:PRO:HD2	1.42	0.84
1:A:37:ILE:HD12	1:A:63:ARG:HG3	1.59	0.84
1:A:373:PRO:HG2	1:A:379:ARG:HG2	1.59	0.82
1:A:306:VAL:O	1:A:306:VAL:HG12	1.80	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:308:GLY:HA2	1:A:311:ARG:HG3	1.63	0.80
1:A:361:ARG:HE	1:A:365:THR:HG21	1.45	0.79
1:A:341:TRP:N	1:A:342:PRO:HD2	1.96	0.79
1:A:370:ASP:HB3	1:A:372:ARG:HH11	1.46	0.78
1:A:205:ARG:HD3	1:A:248:GLU:HB3	1.66	0.77
1:A:173:LEU:HD11	1:A:215:PHE:HB3	1.67	0.75
1:A:260:THR:HB	1:A:299:GLU:HB2	1.69	0.75
1:A:222:LEU:HD22	1:A:222:LEU:N	2.02	0.74
1:A:131:THR:O	1:A:135:VAL:HG23	1.89	0.73
1:A:236:ARG:HD3	1:A:257:THR:O	1.88	0.72
1:A:222:LEU:H	1:A:222:LEU:CD2	2.02	0.72
1:A:312:TRP:CZ2	1:A:366:GLU:HG3	2.26	0.71
1:A:442:GLN:HG3	1:A:443:GLY:H	1.55	0.71
1:A:59:GLU:O	1:A:63:ARG:HG2	1.91	0.70
1:A:221:ARG:NH2	3:A:503:CL:CL	2.61	0.70
1:A:342:PRO:HD3	1:A:397:ARG:HH21	1.58	0.69
1:A:306:VAL:HG21	1:A:363:PHE:HZ	1.57	0.69
1:A:364:ILE:HG13	1:A:365:THR:HG22	1.75	0.69
1:A:364:ILE:HA	1:A:432:VAL:HG11	1.74	0.69
1:A:368:THR:HB	1:A:369:PRO:HD2	1.74	0.68
1:A:277:SER:HB3	1:A:280:ASN:HD21	1.59	0.68
1:A:47:SER:HA	1:A:50:GLU:OE1	1.94	0.67
1:A:197:ILE:HD12	1:A:202:GLU:HB3	1.77	0.67
1:A:370:ASP:HB3	1:A:372:ARG:NH1	2.10	0.67
1:A:117:ARG:O	1:A:121:LEU:HG	1.94	0.67
1:A:250:ARG:HB2	1:A:250:ARG:HH21	1.58	0.67
1:A:360:ALA:O	1:A:364:ILE:HG12	1.94	0.66
1:A:336:LEU:HD23	1:A:341:TRP:CZ2	2.31	0.66
1:A:397:ARG:HG3	1:A:397:ARG:HH11	1.61	0.66
1:A:428:GLN:O	1:A:429:ARG:HG3	1.96	0.65
1:A:79:LEU:O	1:A:83:PHE:HB2	1.96	0.65
1:A:230:VAL:CG1	1:A:266:ILE:HG13	2.26	0.65
1:A:168:ARG:HA	1:A:171:LEU:HD22	1.79	0.65
1:A:343:GLU:HB2	1:A:347:ARG:HH11	1.62	0.64
1:A:168:ARG:O	1:A:168:ARG:HD3	1.98	0.64
1:A:342:PRO:HD3	1:A:397:ARG:NH2	2.12	0.64
1:A:336:LEU:HD23	1:A:341:TRP:HZ2	1.63	0.63
1:A:97:TYR:CZ	1:A:101:LYS:HG3	2.34	0.63
1:A:259:THR:HG23	1:A:260:THR:HG22	1.79	0.63
1:A:266:ILE:N	1:A:266:ILE:HD12	2.14	0.63
1:A:197:ILE:HD11	1:A:203:LEU:N	2.15	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:LEU:HD11	1:A:393:PHE:HB2	1.82	0.62
1:A:396:ASP:O	1:A:397:ARG:HB2	1.99	0.61
1:A:419:ILE:C	1:A:419:ILE:HD13	2.25	0.61
1:A:77:HIS:C	1:A:79:LEU:H	2.08	0.61
1:A:119:GLU:HA	1:A:119:GLU:OE2	2.01	0.60
1:A:359:ALA:O	1:A:362:TYR:HB3	2.00	0.60
1:A:117:ARG:HD2	1:A:154:VAL:HG23	1.83	0.60
1:A:306:VAL:O	1:A:306:VAL:CG1	2.49	0.60
1:A:278:PHE:HA	1:A:280:ASN:OD1	2.03	0.59
1:A:415:LYS:HD2	1:A:416:LEU:H	1.66	0.59
1:A:209:PRO:HB2	1:A:211:ASP:HB3	1.84	0.59
1:A:419:ILE:HG23	1:A:420:GLU:OE2	2.02	0.59
1:A:219:HIS:HB3	1:A:222:LEU:HD23	1.85	0.58
1:A:47:SER:HA	1:A:50:GLU:CD	2.28	0.58
1:A:326:SER:HB3	1:A:329:ASP:OD2	2.03	0.58
1:A:141:LEU:HD11	1:A:154:VAL:HG13	1.84	0.58
1:A:129:ASN:ND2	1:A:132:GLN:HB3	2.19	0.57
1:A:44:LEU:HD22	1:A:123:ARG:HB3	1.85	0.57
1:A:98:ARG:HG3	1:A:99:THR:HG23	1.85	0.57
1:A:370:ASP:OD2	1:A:372:ARG:HD2	2.04	0.57
1:A:361:ARG:NE	1:A:365:THR:HG21	2.17	0.57
1:A:388:LEU:HD13	1:A:438:VAL:HG11	1.87	0.57
1:A:310:ALA:HB2	1:A:405:ALA:HA	1.86	0.57
1:A:61:LEU:HD12	1:A:127:ALA:CB	2.35	0.56
1:A:306:VAL:HG21	1:A:363:PHE:CZ	2.40	0.56
1:A:341:TRP:N	1:A:342:PRO:CD	2.69	0.56
1:A:68:ASN:HB3	1:A:71:GLU:HG3	1.88	0.56
1:A:77:HIS:HE1	1:A:148:ARG:HH21	1.51	0.56
1:A:48:ARG:HG2	1:A:49:GLY:N	2.21	0.56
1:A:205:ARG:HG3	1:A:205:ARG:HH11	1.71	0.56
1:A:225:ASP:N	1:A:225:ASP:OD2	2.39	0.55
1:A:375:ASP:OD1	1:A:377:VAL:HG22	2.06	0.55
1:A:400:LYS:O	1:A:404:GLN:HG2	2.06	0.55
1:A:138:ARG:HB2	1:A:158:PHE:CD1	2.41	0.55
1:A:309:PHE:HB3	1:A:405:ALA:CB	2.36	0.55
1:A:92:LYS:O	1:A:95:ASP:HB3	2.06	0.55
1:A:441:LEU:O	1:A:442:GLN:C	2.50	0.55
1:A:341:TRP:CD1	1:A:394:LEU:HD11	2.42	0.55
1:A:37:ILE:HD12	1:A:63:ARG:CG	2.34	0.55
1:A:152:GLY:O	1:A:156:THR:HG23	2.08	0.54
1:A:302:THR:O	1:A:411:ASN:HA	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:439:LYS:O	1:A:442:GLN:N	2.34	0.54
1:A:75:PHE:O	1:A:79:LEU:HB2	2.08	0.54
1:A:209:PRO:C	1:A:211:ASP:H	2.16	0.54
1:A:192:GLU:HB3	1:A:197:ILE:HG22	1.90	0.54
1:A:287:VAL:O	1:A:291:ARG:HG2	2.08	0.53
1:A:342:PRO:HG2	1:A:343:GLU:H	1.73	0.53
1:A:397:ARG:HH11	1:A:397:ARG:CG	2.21	0.53
1:A:61:LEU:HD12	1:A:127:ALA:HB3	1.89	0.53
1:A:141:LEU:C	1:A:141:LEU:HD23	2.33	0.53
1:A:192:GLU:OE1	1:A:231:GLU:OE2	2.26	0.53
1:A:36:ASP:C	1:A:38:GLU:H	2.16	0.53
1:A:185:LEU:HD11	1:A:207:LEU:HD21	1.91	0.53
1:A:290:LEU:HB3	1:A:297:LEU:CD1	2.38	0.53
1:A:250:ARG:HB2	1:A:250:ARG:NH2	2.23	0.53
1:A:371:ASN:C	1:A:371:ASN:HD22	2.17	0.53
1:A:398:SER:O	1:A:402:MSE:HG2	2.09	0.52
1:A:332:THR:HB	1:A:354:ILE:CD1	2.39	0.52
1:A:90:LEU:O	1:A:94:ILE:HG13	2.09	0.52
1:A:296:GLY:O	1:A:298:LYS:HE3	2.09	0.52
1:A:396:ASP:O	1:A:397:ARG:CB	2.56	0.52
1:A:56:ILE:O	1:A:60:ILE:HG13	2.09	0.52
1:A:361:ARG:O	1:A:362:TYR:C	2.53	0.52
1:A:265:SER:C	1:A:266:ILE:HD12	2.35	0.51
1:A:62:ASP:O	1:A:65:SER:HB2	2.10	0.51
1:A:117:ARG:CD	1:A:154:VAL:HG23	2.39	0.51
1:A:287:VAL:HG23	1:A:288:GLU:N	2.26	0.51
1:A:189:ILE:HA	1:A:197:ILE:HG21	1.93	0.51
1:A:192:GLU:CB	1:A:197:ILE:HG22	2.41	0.51
1:A:325:LEU:HD22	1:A:329:ASP:HB2	1.93	0.51
1:A:197:ILE:HD12	1:A:198:ALA:N	2.26	0.50
1:A:238:ILE:HD12	1:A:301:VAL:HG21	1.93	0.50
1:A:347:ARG:O	1:A:351:VAL:HG23	2.11	0.50
1:A:191:TYR:CD2	1:A:269:CYS:HB3	2.46	0.50
1:A:266:ILE:N	1:A:266:ILE:CD1	2.74	0.50
1:A:195:HIS:O	1:A:196:GLU:C	2.54	0.50
1:A:97:TYR:HE2	1:A:106:VAL:HG22	1.77	0.50
1:A:325:LEU:HD22	1:A:329:ASP:CB	2.42	0.49
1:A:77:HIS:CE1	1:A:148:ARG:HH21	2.31	0.49
1:A:393:PHE:CE2	1:A:394:LEU:HD22	2.47	0.49
1:A:64:TRP:O	1:A:65:SER:C	2.56	0.49
1:A:103:PRO:O	1:A:107:ILE:HG12	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:HIS:C	1:A:79:LEU:N	2.67	0.48
1:A:212:ARG:HH12	1:A:250:ARG:CZ	2.26	0.48
1:A:341:TRP:H	1:A:342:PRO:CD	2.21	0.48
1:A:191:TYR:CE2	1:A:269:CYS:HB3	2.48	0.48
1:A:197:ILE:HD12	1:A:197:ILE:C	2.39	0.48
1:A:441:LEU:HD23	1:A:444:LYS:HD3	1.95	0.48
1:A:304:SER:O	1:A:409:MSE:HE2	2.14	0.48
1:A:340:THR:C	1:A:341:TRP:HE3	2.21	0.48
1:A:326:SER:HB3	1:A:329:ASP:CG	2.39	0.48
1:A:365:THR:O	1:A:366:GLU:C	2.55	0.48
1:A:181:PRO:O	1:A:184:ILE:HG23	2.13	0.48
1:A:435:SER:HB2	1:A:436:PRO:HD2	1.96	0.48
1:A:283:ILE:O	1:A:287:VAL:HG13	2.13	0.47
1:A:358:LEU:O	1:A:361:ARG:HB3	2.13	0.47
1:A:294:LEU:HD12	1:A:294:LEU:N	2.30	0.47
1:A:419:ILE:HD13	1:A:419:ILE:O	2.14	0.47
1:A:47:SER:O	1:A:48:ARG:O	2.32	0.47
1:A:86:GLU:CD	1:A:88:ALA:HB3	2.40	0.47
1:A:236:ARG:HH21	1:A:236:ARG:CB	2.18	0.47
1:A:308:GLY:HA2	1:A:311:ARG:CG	2.37	0.47
1:A:338:ASP:O	1:A:341:TRP:HZ3	1.98	0.47
1:A:309:PHE:HB3	1:A:405:ALA:HB1	1.95	0.47
1:A:218:PHE:CZ	1:A:226:PRO:HB3	2.49	0.47
1:A:397:ARG:CG	1:A:397:ARG:NH1	2.77	0.47
1:A:426:LEU:O	1:A:427:ALA:C	2.58	0.47
1:A:212:ARG:NH1	1:A:250:ARG:CZ	2.78	0.46
1:A:421:THR:OG1	1:A:422:ASN:N	2.48	0.46
1:A:64:TRP:CH2	1:A:137:MSE:HG3	2.50	0.46
1:A:36:ASP:O	1:A:40:LEU:HD23	2.16	0.46
1:A:439:LYS:O	1:A:442:GLN:HB3	2.16	0.46
1:A:290:LEU:HB3	1:A:297:LEU:HD12	1.98	0.46
1:A:230:VAL:HG13	1:A:282:LEU:HD13	1.97	0.46
1:A:248:GLU:C	1:A:250:ARG:H	2.24	0.46
1:A:326:SER:C	1:A:328:GLU:N	2.73	0.46
1:A:326:SER:OG	1:A:328:GLU:HB3	2.15	0.46
1:A:97:TYR:CE1	1:A:101:LYS:HG3	2.51	0.45
1:A:151:LEU:O	1:A:154:VAL:HG12	2.16	0.45
1:A:408:LEU:HG	1:A:409:MSE:N	2.30	0.45
1:A:117:ARG:HE	1:A:154:VAL:HA	1.81	0.45
1:A:178:TRP:HA	1:A:178:TRP:CE3	2.52	0.45
1:A:281:PHE:O	1:A:282:LEU:C	2.58	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:419:ILE:HG23	1:A:420:GLU:N	2.32	0.45
1:A:330:ARG:O	1:A:334:VAL:HG23	2.16	0.45
1:A:64:TRP:HA	1:A:67:PHE:CE1	2.51	0.45
1:A:312:TRP:CZ3	1:A:358:LEU:HD12	2.52	0.45
1:A:333:LEU:C	1:A:335:LEU:H	2.25	0.45
1:A:343:GLU:CB	1:A:347:ARG:HH11	2.29	0.44
1:A:441:LEU:HD23	1:A:444:LYS:CD	2.48	0.44
1:A:44:LEU:CD2	1:A:123:ARG:HB3	2.45	0.44
1:A:129:ASN:HD21	1:A:132:GLN:HB3	1.83	0.44
1:A:287:VAL:CG2	1:A:288:GLU:N	2.80	0.44
1:A:208:ALA:N	1:A:209:PRO:HD2	2.33	0.44
1:A:401:ALA:HA	1:A:404:GLN:HB2	1.99	0.44
1:A:83:PHE:O	1:A:117:ARG:HB3	2.18	0.44
1:A:205:ARG:HG3	1:A:205:ARG:NH1	2.32	0.44
1:A:47:SER:HB2	1:A:50:GLU:OE2	2.18	0.44
1:A:48:ARG:HG2	1:A:49:GLY:H	1.83	0.44
1:A:227:LEU:HD12	1:A:270:GLN:HG3	1.98	0.44
1:A:235:THR:HA	1:A:253:ILE:HD11	2.00	0.43
1:A:440:ALA:C	1:A:442:GLN:H	2.26	0.43
1:A:240:SER:HA	1:A:392:ASN:OD1	2.18	0.43
1:A:344:ASP:O	1:A:345:LYS:C	2.61	0.43
1:A:378:ALA:C	1:A:380:PHE:N	2.74	0.43
1:A:340:THR:HG21	1:A:343:GLU:HG3	1.99	0.43
1:A:440:ALA:O	1:A:442:GLN:HG2	2.19	0.43
1:A:189:ILE:HG23	1:A:197:ILE:HG13	2.01	0.43
1:A:168:ARG:HD3	1:A:168:ARG:C	2.43	0.43
1:A:332:THR:HB	1:A:354:ILE:HD13	2.01	0.43
1:A:278:PHE:CD1	1:A:278:PHE:N	2.87	0.43
1:A:286:VAL:O	1:A:290:LEU:HG	2.18	0.43
1:A:309:PHE:HB3	1:A:405:ALA:HB2	2.00	0.43
1:A:326:SER:O	1:A:327:PRO:C	2.62	0.43
1:A:260:THR:CB	1:A:299:GLU:HB2	2.45	0.43
1:A:92:LYS:HA	4:A:618:HOH:O	2.19	0.42
1:A:151:LEU:HA	1:A:154:VAL:HG12	2.01	0.42
1:A:375:ASP:CG	1:A:376:PRO:HD2	2.44	0.42
1:A:119:GLU:OE1	1:A:123:ARG:HD3	2.19	0.42
1:A:93:ALA:C	1:A:95:ASP:N	2.74	0.42
1:A:297:LEU:C	1:A:298:LYS:HD3	2.44	0.42
1:A:439:LYS:O	1:A:442:GLN:CB	2.68	0.42
1:A:392:ASN:O	1:A:408:LEU:HD12	2.19	0.42
1:A:77:HIS:CE1	1:A:148:ARG:HE	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:424:GLU:O	1:A:425:ALA:C	2.62	0.42
1:A:368:THR:HB	1:A:369:PRO:CD	2.47	0.42
1:A:90:LEU:HA	1:A:112:ALA:HB1	2.01	0.42
1:A:189:ILE:HG12	1:A:203:LEU:HG	2.00	0.42
1:A:344:ASP:C	1:A:346:ALA:N	2.75	0.42
1:A:354:ILE:O	1:A:358:LEU:HB2	2.20	0.42
1:A:428:GLN:HE21	1:A:428:GLN:HB2	1.55	0.41
1:A:278:PHE:C	1:A:280:ASN:N	2.73	0.41
1:A:119:GLU:O	1:A:120:LEU:C	2.64	0.41
1:A:254:GLY:HA3	1:A:257:THR:HG23	2.02	0.41
1:A:352:GLU:HA	1:A:393:PHE:CE1	2.55	0.41
1:A:95:ASP:O	1:A:98:ARG:HG2	2.20	0.41
1:A:198:ALA:HB3	1:A:202:GLU:HB2	2.03	0.41
1:A:271:ASP:C	1:A:273:LEU:H	2.28	0.41
1:A:344:ASP:O	1:A:347:ARG:N	2.46	0.41
1:A:319:PRO:HA	1:A:330:ARG:HH22	1.85	0.41
1:A:228:VAL:HG23	1:A:267:SER:O	2.21	0.41
1:A:47:SER:CA	1:A:50:GLU:CD	2.93	0.41
1:A:242:ILE:HA	1:A:303:LEU:HD21	2.03	0.41
1:A:250:ARG:HH21	1:A:250:ARG:CB	2.30	0.41
1:A:53:GLY:O	1:A:56:ILE:HB	2.20	0.41
1:A:92:LYS:C	1:A:95:ASP:HB3	2.46	0.41
1:A:345:LYS:HD3	1:A:345:LYS:N	2.36	0.41
1:A:415:LYS:HD2	1:A:416:LEU:N	2.34	0.41
1:A:91:ASP:C	1:A:93:ALA:N	2.77	0.41
1:A:177:ASP:HA	1:A:207:LEU:HG	2.03	0.41
1:A:367:ARG:HB3	1:A:371:ASN:HA	2.02	0.41
1:A:440:ALA:C	1:A:442:GLN:N	2.79	0.41
1:A:344:ASP:OD2	1:A:346:ALA:HB3	2.21	0.40
1:A:370:ASP:HB3	1:A:372:ARG:CD	2.51	0.40
1:A:189:ILE:HA	1:A:197:ILE:CG2	2.51	0.40
1:A:232:VAL:HG12	1:A:233:ALA:N	2.36	0.40
1:A:343:GLU:HB2	1:A:347:ARG:NH1	2.33	0.40
1:A:361:ARG:O	1:A:365:THR:HG23	2.21	0.40
1:A:78:MSE:HA	1:A:81:ASP:HB2	2.03	0.40
1:A:185:LEU:HD12	1:A:185:LEU:HA	1.85	0.40
1:A:288:GLU:HA	1:A:291:ARG:HG3	2.03	0.40
1:A:419:ILE:C	1:A:419:ILE:CD1	2.93	0.40
1:A:138:ARG:HD3	1:A:272:GLY:O	2.21	0.40
1:A:359:ALA:O	1:A:360:ALA:C	2.65	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	403/456 (88%)	335 (83%)	48 (12%)	20 (5%)	1	11

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	48	ARG
1	A	194	VAL
1	A	198	ALA
1	A	419	ILE
1	A	427	ALA
1	A	442	GLN
1	A	37	ILE
1	A	196	GLU
1	A	429	ARG
1	A	103	PRO
1	A	363	PHE
1	A	58	ALA
1	A	223	ARG
1	A	282	LEU
1	A	305	PRO
1	A	265	SER
1	A	292	ARG
1	A	339	PRO
1	A	362	TYR
1	A	276	ILE

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	338/372 (91%)	295 (87%)	43 (13%)	4 18

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	CYS
1	A	44	LEU
1	A	64	TRP
1	A	66	ARG
1	A	67	PHE
1	A	95	ASP
1	A	102	SER
1	A	144	THR
1	A	148	ARG
1	A	171	LEU
1	A	184	ILE
1	A	194	VAL
1	A	197	ILE
1	A	202	GLU
1	A	203	LEU
1	A	221	ARG
1	A	222	LEU
1	A	225	ASP
1	A	227	LEU
1	A	236	ARG
1	A	250	ARG
1	A	257	THR
1	A	260	THR
1	A	266	ILE
1	A	278	PHE
1	A	280	ASN
1	A	282	LEU
1	A	294	LEU
1	A	326	SER
1	A	344	ASP
1	A	347	ARG
1	A	358	LEU
1	A	365	THR
1	A	371	ASN
1	A	388	LEU
1	A	390	ARG

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Mol	Chain	Res	Type
1	A	397	ARG
1	A	415	LYS
1	A	418	ASP
1	A	419	ILE
1	A	424	GLU
1	A	428	GLN
1	A	431	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	77	HIS
1	A	125	ASN
1	A	132	GLN
1	A	195	HIS
1	A	280	ASN
1	A	371	ASN
1	A	404	GLN
1	A	406	HIS
1	A	428	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 [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	400/456 (87%)	0.14	7 (1%)	67 47	29, 56, 88, 112	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	51	ALA	4.1
1	A	37	ILE	3.4
1	A	50	GLU	2.7
1	A	49	GLY	2.5
1	A	417	GLU	2.4
1	A	416	LEU	2.3
1	A	341	TRP	2.2

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](#)

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	NI	A	501	1/1	0.92	0.06	37,37,37,37	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	CL	A	502	1/1	0.95	0.08	41,41,41,41	0
3	CL	A	503	1/1	0.96	0.09	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.