



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:14 PM UTC

PDB ID : 2YHO / pdb_00002yho
Title : The IDOL-UBE2D complex mediates sterol-dependent degradation of the LDL receptor
Authors : Fairall, L.; Goult, B.T.; Millard, C.J.; Tontono, P.; Schwabe, J.W.R.
Deposited on : 2011-05-04
Resolution : 2.10 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

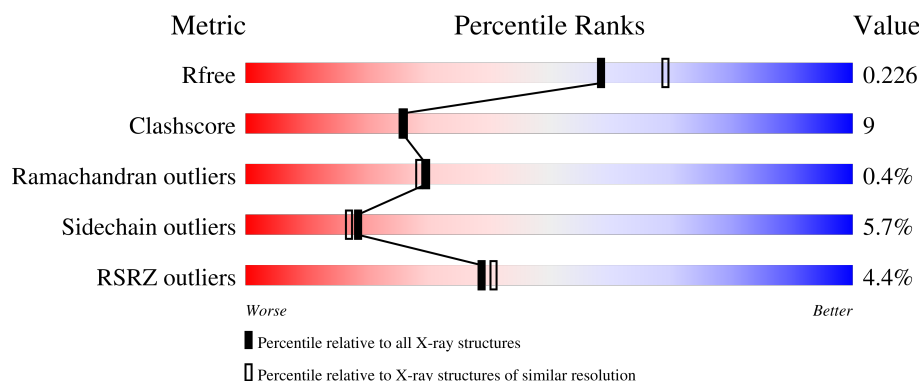
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	79	
1	C	79	
1	E	79	
1	G	79	
2	B	149	

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Mol	Chain	Length	Quality of chain
2	D	149	 81% 17% •
2	F	149	 81% 17% •
2	H	149	 % 80% 18% ••

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ACT	F	1148	-	-	X	-
4	ACT	G	1442	-	-	X	-
4	ACT	H	1148	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7208 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 E3 UBIQUITIN-PROTEIN LIGASE MYLIP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	67	Total	C	N	O	S	0	0	0
			512	312	94	94	12			
1	C	67	Total	C	N	O	S	0	0	0
			506	310	92	92	12			
1	E	70	Total	C	N	O	S	0	0	0
			522	317	95	98	12			
1	G	70	Total	C	N	O	S	0	0	0
			534	328	98	96	12			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	367	GLY	-	expression tag	UNP Q8WY64
A	368	ALA	-	expression tag	UNP Q8WY64
C	367	GLY	-	expression tag	UNP Q8WY64
C	368	ALA	-	expression tag	UNP Q8WY64
E	367	GLY	-	expression tag	UNP Q8WY64
E	368	ALA	-	expression tag	UNP Q8WY64
G	367	GLY	-	expression tag	UNP Q8WY64
G	368	ALA	-	expression tag	UNP Q8WY64

- Molecule 2 is a protein called UBIQUITIN-CONJUGATING ENZYME E2 D1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	149	Total	C	N	O	S	0	0	0
			1171	752	198	214	7			
2	D	149	Total	C	N	O	S	0	0	0
			1174	755	199	213	7			
2	F	149	Total	C	N	O	S	0	0	0
			1172	755	199	211	7			
2	H	147	Total	C	N	O	S	0	0	0
			1167	751	197	212	7			

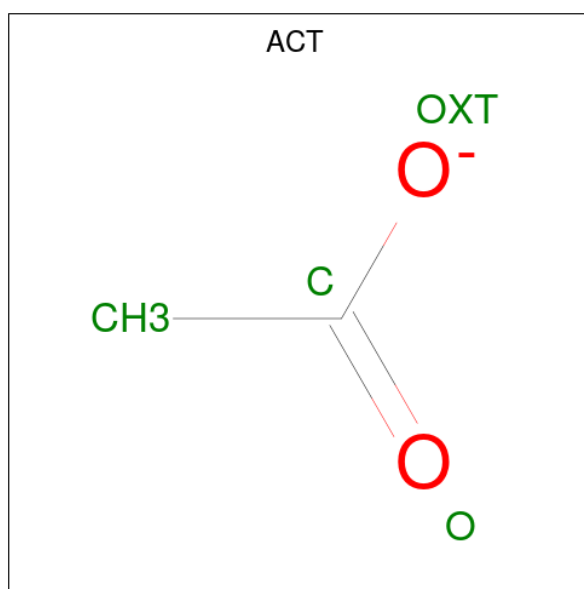
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP P51668
B	0	ALA	-	expression tag	UNP P51668
D	-1	GLY	-	expression tag	UNP P51668
D	0	ALA	-	expression tag	UNP P51668
F	-1	GLY	-	expression tag	UNP P51668
F	0	ALA	-	expression tag	UNP P51668
H	-1	GLY	-	expression tag	UNP P51668
H	0	ALA	-	expression tag	UNP P51668

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Zn 2 2	0	0
3	C	2	Total Zn 2 2	0	0
3	E	2	Total Zn 2 2	0	0
3	G	2	Total Zn 2 2	0	0

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	F	1	Total C O 4 2 2	0	0
4	G	1	Total C O 4 2 2	0	0
4	H	1	Total C O 4 2 2	0	0
4	H	1	Total C O 4 2 2	0	0
4	H	1	Total C O 4 2 2	0	0

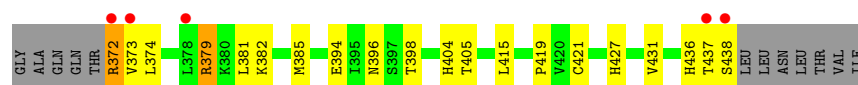
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	46	Total O 46 46	0	0
5	B	71	Total O 71 71	0	0
5	C	28	Total O 28 28	0	0
5	D	78	Total O 78 78	0	0
5	E	32	Total O 32 32	0	0
5	F	56	Total O 56 56	0	0
5	G	24	Total O 24 24	0	0
5	H	71	Total O 71 71	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: E3 UBIQUITIN-PROTEIN LIGASE MYLIP



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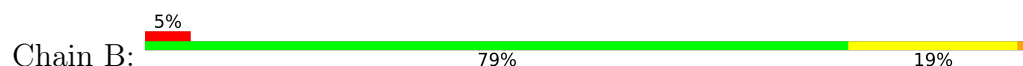
- Molecule 1: E3 UBIQUITIN-PROTEIN LIGASE MYLIP



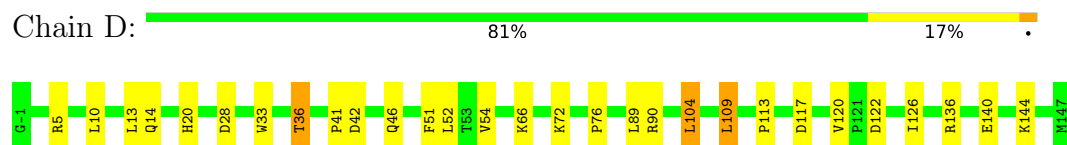
- Molecule 1: E3 UBIQUITIN-PROTEIN LIGASE MYLIP



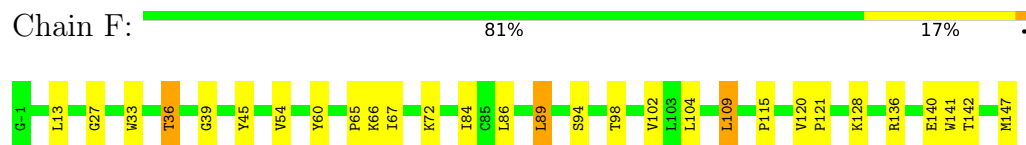
- Molecule 2: UBIQUITIN-CONJUGATING ENZYME E2 D1



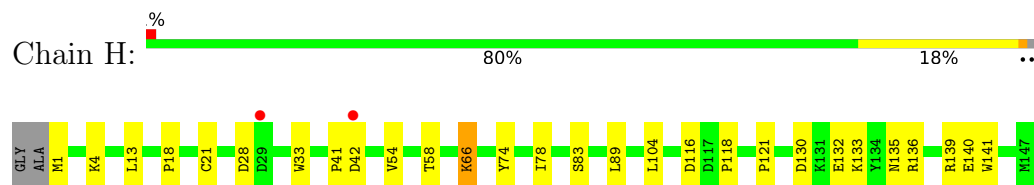
- Molecule 2: UBIQUITIN-CONJUGATING ENZYME E2 D1



- Molecule 2: UBIQUITIN-CONJUGATING ENZYME E2 D1



- Molecule 2: UBIQUITIN-CONJUGATING ENZYME E2 D1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.69Å 137.87Å 63.75Å 90.00° 106.39° 90.00°	Depositor
Resolution (Å)	55.91 – 2.10 55.91 – 2.10	Depositor EDS
% Data completeness (in resolution range)	95.5 (55.91-2.10) 99.6 (55.91-2.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.92 (at 2.10Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.186 , 0.233 0.185 , 0.226	Depositor DCC
R_{free} test set	2812 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	25.8	Xtriage
Anisotropy	0.739	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 42.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7208	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.40% 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: ZN, ACT

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	0.52	0/520	0.77	1/702 (0.1%)
1	C	0.49	0/513	0.81	0/693
1	E	0.45	0/530	0.77	0/718
1	G	0.52	0/542	0.80	1/732 (0.1%)
2	B	0.47	0/1208	0.87	5/1648 (0.3%)
2	D	0.50	0/1211	0.81	2/1652 (0.1%)
2	F	0.47	0/1209	0.83	2/1649 (0.1%)
2	H	0.46	0/1204	0.83	1/1641 (0.1%)
All	All	0.48	0/6937	0.82	12/9435 (0.1%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	40	PRO	CA-C-N	8.12	128.06	119.05
2	B	40	PRO	C-N-CA	8.12	128.06	119.05
2	D	120	VAL	CA-C-N	6.76	126.27	119.24
2	D	120	VAL	C-N-CA	6.76	126.27	119.24
2	B	119	LEU	N-CA-C	-6.75	105.18	113.41
2	H	28	ASP	N-CA-C	-6.00	104.67	112.23
2	B	120	VAL	CA-C-N	5.45	126.65	119.84
2	B	120	VAL	C-N-CA	5.45	126.65	119.84
1	G	407	CYS	N-CA-C	5.26	117.81	109.50
2	F	120	VAL	CA-C-N	5.06	124.67	119.05
2	F	120	VAL	C-N-CA	5.06	124.67	119.05
1	A	374	LEU	N-CA-C	-5.01	105.95	111.71

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	512	0	491	20	0
1	C	506	0	491	10	0
1	E	522	0	486	10	0
1	G	534	0	519	15	0
2	B	1171	0	1146	21	0
2	D	1174	0	1157	21	0
2	F	1172	0	1157	18	0
2	H	1167	0	1151	18	0
3	A	2	0	0	0	0
3	C	2	0	0	0	0
3	E	2	0	0	0	0
3	G	2	0	0	0	0
4	A	8	0	6	0	0
4	B	8	0	6	1	0
4	F	4	0	3	3	0
4	G	4	0	3	2	0
4	H	12	0	9	3	0
5	A	46	0	0	0	0
5	B	71	0	0	1	0
5	C	28	0	0	0	0
5	D	78	0	0	8	0
5	E	32	0	0	0	0
5	F	56	0	0	3	0
5	G	24	0	0	0	0
5	H	71	0	0	2	0
All	All	7208	0	6625	127	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 9.

All (127) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:58:THR:H	4:H:1150:ACT:H1	1.36	0.87
1:G:372:ARG:HG2	1:G:373:VAL:H	1.40	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:84:ILE:H	4:F:1148:ACT:H1	1.38	0.86
1:A:398:THR:HG21	1:C:431:VAL:HG12	1.60	0.83
2:D:42:ASP:H	2:D:46:GLN:HE21	1.29	0.81
1:E:394:GLU:HB2	1:E:436:HIS:HE1	1.48	0.79
1:G:372:ARG:HG2	1:G:373:VAL:N	1.99	0.77
1:E:416:GLN:H	1:E:416:GLN:NE2	1.84	0.75
1:A:379:ARG:HH22	2:B:15:ARG:CZ	2.01	0.74
1:G:419:PRO:HA	1:G:422:ARG:HH21	1.52	0.74
2:D:42:ASP:H	2:D:46:GLN:NE2	1.86	0.73
1:G:383:GLU:O	4:G:1442:ACT:H1	1.94	0.68
1:A:379:ARG:NH2	2:B:15:ARG:CZ	2.58	0.67
1:A:372:ARG:HG3	1:A:373:VAL:H	1.60	0.66
2:B:1:MET:HG3	2:B:3:LEU:HB3	1.77	0.66
2:F:84:ILE:H	4:F:1148:ACT:CH3	2.09	0.66
2:D:122:ASP:O	2:D:126:ILE:HG12	1.96	0.65
2:D:41:PRO:O	5:D:2031:HOH:O	2.15	0.64
1:E:394:GLU:HB2	1:E:436:HIS:CE1	2.30	0.64
1:A:398:THR:OG1	1:A:431:VAL:HG11	1.99	0.63
2:D:20:HIS:HD2	5:D:2019:HOH:O	1.81	0.63
1:G:386:LEU:O	4:G:1442:ACT:H2	1.99	0.62
1:A:379:ARG:HH22	2:B:15:ARG:NH2	1.96	0.62
2:D:20:HIS:CD2	5:D:2019:HOH:O	2.53	0.62
2:B:122:ASP:O	2:B:126:ILE:HG12	1.99	0.61
2:H:136:ARG:O	2:H:140:GLU:HG3	2.00	0.60
2:H:66:LYS:HE2	5:H:2033:HOH:O	2.02	0.60
1:E:416:GLN:H	1:E:416:GLN:CD	2.09	0.59
2:F:115:PRO:HB2	2:F:128:LYS:HE2	1.84	0.59
1:G:372:ARG:C	1:G:374:LEU:H	2.09	0.59
1:C:376:GLU:O	1:C:380:LYS:HG2	2.03	0.59
1:A:372:ARG:CG	1:A:373:VAL:H	2.15	0.58
1:A:437:THR:HG22	1:A:438:SER:N	2.18	0.58
1:C:372:ARG:C	1:C:374:LEU:H	2.12	0.58
5:D:2024:HOH:O	1:E:441:ASN:HA	2.04	0.58
1:A:415:LEU:HD13	1:A:419:PRO:HG3	1.86	0.57
1:C:372:ARG:O	1:C:373:VAL:HG12	2.05	0.57
2:B:120:VAL:HG11	2:B:123:ILE:HD12	1.85	0.57
2:F:13:LEU:C	2:F:13:LEU:HD23	2.29	0.57
1:A:437:THR:O	1:A:438:SER:C	2.47	0.57
2:B:30:LEU:HD22	5:B:2068:HOH:O	2.05	0.56
2:B:13:LEU:C	2:B:13:LEU:HD23	2.30	0.56
1:G:424:ARG:NH1	1:G:426:GLU:HG2	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:385:MET:HE2	1:E:435:THR:HB	1.86	0.56
2:F:36:THR:HG21	5:F:2020:HOH:O	2.04	0.56
2:B:67:ILE:O	4:B:1148:ACT:H2	2.06	0.56
1:E:395:ILE:HD13	1:E:406:VAL:HA	1.88	0.56
2:D:136:ARG:O	2:D:140:GLU:HG3	2.06	0.55
1:G:379:ARG:HG2	1:G:383:GLU:OE1	2.05	0.55
2:D:41:PRO:O	2:D:42:ASP:HB2	2.06	0.55
4:H:1148:ACT:H1	5:H:2034:HOH:O	2.06	0.54
1:G:424:ARG:HH12	1:G:426:GLU:HG2	1.72	0.54
2:H:18:PRO:HG2	2:H:21:CYS:HB2	1.90	0.54
1:E:394:GLU:OE1	1:E:437:THR:HG22	2.07	0.54
1:C:398:THR:HG23	1:C:405:THR:HG22	1.90	0.53
2:D:10:LEU:O	2:D:14:GLN:HG3	2.09	0.53
2:H:13:LEU:C	2:H:13:LEU:HD23	2.33	0.52
1:E:394:GLU:CB	1:E:436:HIS:CE1	2.92	0.52
1:C:438:SER:CB	2:F:27:GLY:HA3	2.41	0.52
2:F:86:LEU:HD13	2:F:109:LEU:HD22	1.92	0.51
2:F:60:TYR:HE1	2:F:65:PRO:HD3	1.76	0.50
1:E:378:LEU:HD22	1:E:382:LYS:HE3	1.93	0.50
2:D:33:TRP:HB2	2:D:54:VAL:HB	1.93	0.50
2:F:36:THR:HG22	5:F:2019:HOH:O	2.12	0.50
2:D:13:LEU:C	2:D:13:LEU:HD23	2.37	0.50
2:H:41:PRO:O	2:H:42:ASP:CB	2.59	0.49
1:A:394:GLU:OE1	1:A:436:HIS:HD2	1.96	0.48
2:H:18:PRO:HB3	2:H:104:LEU:HG	1.96	0.47
2:F:136:ARG:O	2:F:140:GLU:HG3	2.13	0.47
1:A:372:ARG:HD3	1:A:372:ARG:HA	1.58	0.47
2:H:104:LEU:HD23	2:H:104:LEU:HA	1.79	0.47
2:B:3:LEU:HD11	2:B:7:GLN:NE2	2.30	0.47
2:B:102:VAL:O	2:B:106:ILE:HG13	2.15	0.47
2:D:42:ASP:N	2:D:46:GLN:HE21	2.06	0.46
1:A:398:THR:HG23	1:A:405:THR:OG1	2.15	0.46
1:A:381:LEU:HG	1:A:385:MET:HE3	1.98	0.46
1:A:381:LEU:HD23	1:C:381:LEU:HD13	1.98	0.46
2:F:33:TRP:HB2	2:F:54:VAL:HB	1.98	0.46
2:H:116:ASP:C	2:H:118:PRO:HD3	2.41	0.46
2:H:4:LYS:HD2	2:H:4:LYS:N	2.29	0.45
2:B:3:LEU:HD11	2:B:7:GLN:HE21	1.81	0.45
2:D:36:THR:CG2	5:D:2020:HOH:O	2.64	0.45
2:H:118:PRO:HB2	2:H:121:PRO:HA	1.98	0.45
1:C:409:GLU:HG2	1:C:410:SER:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:36:THR:HG22	5:D:2020:HOH:O	2.17	0.45
2:F:98:THR:O	2:F:102:VAL:HG23	2.16	0.45
2:H:78:ILE:HA	2:H:83:SER:O	2.17	0.45
2:H:130:ASP:OD2	2:H:133:LYS:HB2	2.17	0.45
2:F:89:LEU:HD12	2:F:89:LEU:HA	1.75	0.45
2:F:142:THR:HG22	2:F:147:MET:HE3	1.99	0.45
1:C:374:LEU:HD12	1:C:374:LEU:HA	1.83	0.44
2:H:89:LEU:HD13	4:H:1148:ACT:H3	1.97	0.44
2:D:51:PHE:C	2:D:52:LEU:HD12	2.42	0.44
1:G:372:ARG:CG	1:G:373:VAL:N	2.77	0.44
1:A:381:LEU:CD2	1:C:381:LEU:HD13	2.48	0.44
2:B:104:LEU:HD23	2:B:104:LEU:HA	1.87	0.44
2:H:74:TYR:HB2	2:H:141:TRP:CE3	2.53	0.44
2:F:39:GLY:HA3	2:F:45:TYR:O	2.18	0.44
2:B:64:PRO:HB3	2:B:93:TRP:CG	2.54	0.43
1:G:430:HIS:HE1	1:G:432:TYR:CE1	2.36	0.43
2:F:67:ILE:O	4:F:1148:ACT:H2	2.18	0.43
2:D:104:LEU:HD22	5:D:2058:HOH:O	2.17	0.43
2:D:144:LYS:HB2	2:D:144:LYS:HE3	1.89	0.42
1:G:372:ARG:CG	1:G:373:VAL:H	2.23	0.42
1:A:396:ASN:C	1:A:431:VAL:HG22	2.44	0.42
2:F:121:PRO:HD2	5:F:2047:HOH:O	2.19	0.42
1:A:379:ARG:HA	1:A:382:LYS:HD3	2.01	0.42
2:B:126:ILE:N	2:B:126:ILE:HD13	2.34	0.42
2:B:18:PRO:HB3	2:B:104:LEU:HG	2.02	0.42
2:D:52:LEU:HD12	2:D:52:LEU:N	2.35	0.42
1:G:374:LEU:C	1:G:374:LEU:HD12	2.45	0.41
2:B:115:PRO:HG3	2:B:127:TYR:CE2	2.55	0.41
1:G:440:LEU:HD22	1:G:440:LEU:N	2.34	0.41
2:B:74:TYR:CZ	2:B:123:ILE:HG12	2.55	0.41
2:D:90:ARG:NE	5:D:2054:HOH:O	2.46	0.41
2:F:72:LYS:HE2	2:F:141:TRP:CZ3	2.56	0.41
2:B:29:ASP:OD1	2:B:31:PHE:HB2	2.20	0.41
1:A:372:ARG:CG	1:A:373:VAL:N	2.82	0.41
2:H:136:ARG:HG2	2:H:140:GLU:OE2	2.20	0.41
2:B:40:PRO:HA	2:B:41:PRO:HD3	1.77	0.40
1:G:439:LEU:O	1:G:439:LEU:HG	2.21	0.40
2:B:33:TRP:HB2	2:B:54:VAL:HB	2.03	0.40
2:D:109:LEU:HD12	2:D:109:LEU:HA	1.92	0.40
2:H:135:ASN:O	2:H:139:ARG:HG3	2.21	0.40
1:A:404:HIS:CE1	1:A:421:CYS:HB3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:76:PRO:HG2	2:D:113:PRO:HB3	2.04	0.40
2:H:33:TRP:HB2	2:H:54:VAL:HB	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	65/79 (82%)	59 (91%)	6 (9%)	0	100	100
1	C	65/79 (82%)	60 (92%)	4 (6%)	1 (2%)	8	4
1	E	68/79 (86%)	64 (94%)	3 (4%)	1 (2%)	8	4
1	G	68/79 (86%)	62 (91%)	5 (7%)	1 (2%)	8	4
2	B	147/149 (99%)	143 (97%)	4 (3%)	0	100	100
2	D	147/149 (99%)	144 (98%)	3 (2%)	0	100	100
2	F	147/149 (99%)	144 (98%)	3 (2%)	0	100	100
2	H	145/149 (97%)	139 (96%)	6 (4%)	0	100	100
All	All	852/912 (93%)	815 (96%)	34 (4%)	3 (0%)	30	28

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	373	VAL
1	G	373	VAL
1	E	373	VAL

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	60/73 (82%)	57 (95%)	3 (5%)	22	22
1	C	59/73 (81%)	54 (92%)	5 (8%)	10	7
1	E	60/73 (82%)	54 (90%)	6 (10%)	7	5
1	G	62/73 (85%)	57 (92%)	5 (8%)	11	8
2	B	129/131 (98%)	123 (95%)	6 (5%)	23	24
2	D	130/131 (99%)	121 (93%)	9 (7%)	14	12
2	F	129/131 (98%)	123 (95%)	6 (5%)	23	24
2	H	130/131 (99%)	127 (98%)	3 (2%)	44	51
All	All	759/816 (93%)	716 (94%)	43 (6%)	18	17

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

Mol	Chain	Res	Type
1	A	372	ARG
1	A	379	ARG
1	A	427	HIS
2	B	1	MET
2	B	16	ASP
2	B	28	ASP
2	B	89	LEU
2	B	94	SER
2	B	117	ASP
1	C	372	ARG
1	C	373	VAL
1	C	374	LEU
1	C	382	LYS
1	C	405	THR
2	D	5	ARG
2	D	28	ASP
2	D	36	THR
2	D	66	LYS
2	D	72	LYS

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Mol	Chain	Res	Type
2	D	89	LEU
2	D	104	LEU
2	D	109	LEU
2	D	117	ASP
1	E	378	LEU
1	E	379	ARG
1	E	392	GLU
1	E	416	GLN
1	E	437	THR
1	E	440	LEU
2	F	36	THR
2	F	66	LYS
2	F	89	LEU
2	F	94	SER
2	F	104	LEU
2	F	109	LEU
1	G	381	LEU
1	G	383	GLU
1	G	422	ARG
1	G	437	THR
1	G	439	LEU
2	H	1	MET
2	H	66	LYS
2	H	132	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	414	GLN
1	A	427	HIS
1	A	429	GLN
1	A	430	HIS
1	A	436	HIS
2	B	7	GLN
2	B	46	GLN
1	C	414	GLN
1	C	427	HIS
1	C	429	GLN
2	D	20	HIS
2	D	46	GLN
1	E	375	GLN
1	E	416	GLN

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Mol	Chain	Res	Type
1	E	436	HIS
2	F	7	GLN
2	F	46	GLN
2	F	81	ASN
2	F	125	GLN
1	G	429	GLN
1	G	430	HIS
2	H	7	GLN
2	H	20	HIS
2	H	46	GLN
2	H	92	GLN
2	H	137	HIS

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 17 ligands modelled in this entry, 8 are monoatomic - leaving 9 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	ACT	B	1149	-	3,3,3	0.85	0	3,3,3	1.28	0
4	ACT	G	1442	-	3,3,3	0.75	0	3,3,3	1.30	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	ACT	B	1148	-	3,3,3	1.13	0	3,3,3	1.01	0
4	ACT	F	1148	-	3,3,3	0.90	0	3,3,3	0.93	0
4	ACT	A	1440	-	3,3,3	0.81	0	3,3,3	1.31	0
4	ACT	A	1439	-	3,3,3	0.85	0	3,3,3	1.15	0
4	ACT	H	1148	-	3,3,3	1.03	0	3,3,3	1.29	0
4	ACT	H	1149	-	3,3,3	0.79	0	3,3,3	1.40	0
4	ACT	H	1150	-	3,3,3	0.97	0	3,3,3	1.23	0

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.

5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	1442	ACT	2	0
4	B	1148	ACT	1	0
4	F	1148	ACT	3	0
4	H	1148	ACT	2	0
4	H	1150	ACT	1	0

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	67/79 (84%)	0.35	5 (7%) 20 21	17, 24, 59, 71	0
1	C	67/79 (84%)	0.58	7 (10%) 11 12	18, 27, 65, 77	0
1	E	70/79 (88%)	0.65	6 (8%) 16 17	21, 29, 64, 74	0
1	G	70/79 (88%)	0.60	10 (14%) 6 6	20, 30, 66, 70	0
2	B	149/149 (100%)	0.32	8 (5%) 31 33	18, 28, 50, 63	0
2	D	149/149 (100%)	0.07	0 100 100	17, 26, 40, 48	0
2	F	149/149 (100%)	0.17	0 100 100	18, 28, 41, 47	0
2	H	147/149 (98%)	0.15	2 (1%) 73 75	19, 28, 45, 54	0
All	All	868/912 (95%)	0.29	38 (4%) 39 41	17, 28, 53, 77	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	373	VAL	5.6
1	E	374	LEU	5.1
2	B	0	ALA	5.0
1	C	373	VAL	5.0
2	B	-1	GLY	4.8
1	C	437	THR	4.6
1	G	373	VAL	4.2
1	A	373	VAL	4.2
1	G	437	THR	4.2
1	A	438	SER	4.2
1	G	441	ASN	4.0
1	E	372	ARG	3.7
1	A	437	THR	3.7
1	C	438	SER	3.6
1	E	439	LEU	3.6
1	C	372	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	372	ARG	3.3
1	G	439	LEU	3.2
2	B	131	LYS	3.1
2	B	115	PRO	3.0
2	B	1	MET	3.0
1	G	374	LEU	2.8
2	B	126	ILE	2.8
1	G	376	GLU	2.7
2	B	122	ASP	2.7
1	G	438	SER	2.7
1	G	440	LEU	2.7
2	B	28	ASP	2.7
2	H	42	ASP	2.7
1	C	374	LEU	2.6
1	C	375	GLN	2.6
1	C	378	LEU	2.3
1	E	375	GLN	2.3
1	G	372	ARG	2.2
2	H	29	ASP	2.2
1	A	378	LEU	2.1
1	G	416	GLN	2.1
1	E	436	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 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($\text{\AA}^2$)	Q<0.9
4	ACT	G	1442	4/4	0.60	0.20	29,40,41,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	ACT	B	1148	4/4	0.70	0.19	24,28,38,40	0
4	ACT	H	1148	4/4	0.70	0.16	27,30,39,42	0
4	ACT	A	1439	4/4	0.72	0.18	30,33,36,42	0
4	ACT	F	1148	4/4	0.75	0.15	25,33,35,37	0
4	ACT	H	1150	4/4	0.76	0.20	20,30,31,34	0
4	ACT	H	1149	4/4	0.77	0.17	34,34,36,41	0
4	ACT	A	1440	4/4	0.85	0.14	43,44,45,46	0
4	ACT	B	1149	4/4	0.91	0.14	34,35,39,40	0
3	ZN	G	1002	1/1	0.99	0.03	26,26,26,26	0
3	ZN	C	1002	1/1	1.00	0.02	19,19,19,19	0
3	ZN	E	1001	1/1	1.00	0.02	27,27,27,27	0
3	ZN	E	1002	1/1	1.00	0.02	21,21,21,21	0
3	ZN	G	1001	1/1	1.00	0.01	24,24,24,24	0
3	ZN	A	1001	1/1	1.00	0.02	21,21,21,21	0
3	ZN	A	1002	1/1	1.00	0.01	21,21,21,21	0
3	ZN	C	1001	1/1	1.00	0.01	26,26,26,26	0

6.5 Other polymers

There are no such residues in this entry.