



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:40 PM UTC

PDB ID : 4X57 / pdb_00004x57
Title : Structure of an Arabidopsis E2 / Membrane-anchored Ubiquitin-fold Protein Complex
Authors : Korolev, S.; Koroleva, O.; Lu, X.; Downes, B.
Deposited on : 2014-12-04
Resolution : 2.80 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

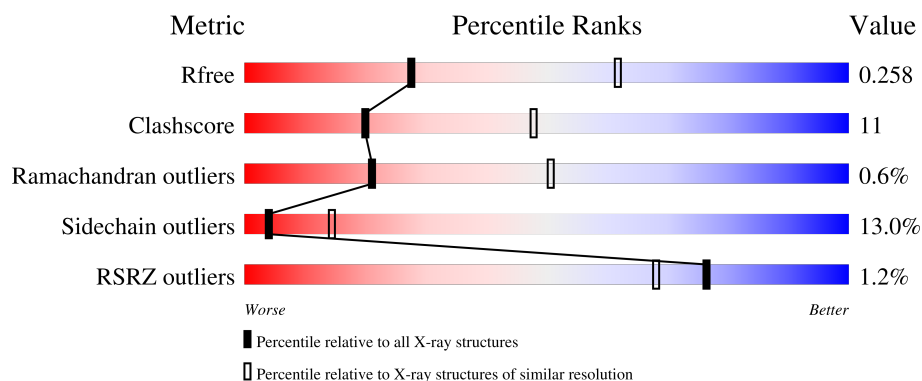
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	179	56% 22% • • 17%
1	C	179	56% 22% • • 17%
2	B	138	46% 20% • 33%
2	D	138	50% 16% • 33%

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
3	SO4	C	202	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3750 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 Ubiquitin-conjugating enzyme E2 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	148	Total	C	N	O	S	0	0	0
			1165	752	192	213	8			
1	C	149	Total	C	N	O	S	0	0	0
			1169	754	193	214	8			

There are 62 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-30	MET	-	initiating methionine	UNP P35131
A	-29	GLY	-	expression tag	UNP P35131
A	-28	SER	-	expression tag	UNP P35131
A	-27	SER	-	expression tag	UNP P35131
A	-26	HIS	-	expression tag	UNP P35131
A	-25	HIS	-	expression tag	UNP P35131
A	-24	HIS	-	expression tag	UNP P35131
A	-23	HIS	-	expression tag	UNP P35131
A	-22	HIS	-	expression tag	UNP P35131
A	-21	HIS	-	expression tag	UNP P35131
A	-20	GLY	-	expression tag	UNP P35131
A	-19	THR	-	expression tag	UNP P35131
A	-18	GLY	-	expression tag	UNP P35131
A	-17	SER	-	expression tag	UNP P35131
A	-16	TYR	-	expression tag	UNP P35131
A	-15	ILE	-	expression tag	UNP P35131
A	-14	THR	-	expression tag	UNP P35131
A	-13	SER	-	expression tag	UNP P35131
A	-12	LEU	-	expression tag	UNP P35131
A	-11	TYR	-	expression tag	UNP P35131
A	-10	LYS	-	expression tag	UNP P35131
A	-9	LYS	-	expression tag	UNP P35131
A	-8	ALA	-	expression tag	UNP P35131
A	-7	GLY	-	expression tag	UNP P35131
A	-6	SER	-	expression tag	UNP P35131

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	ALA	-	expression tag	UNP P35131
A	-4	ALA	-	expression tag	UNP P35131
A	-3	ALA	-	expression tag	UNP P35131
A	-2	PRO	-	expression tag	UNP P35131
A	-1	PHE	-	expression tag	UNP P35131
A	0	THR	-	expression tag	UNP P35131
C	-30	MET	-	initiating methionine	UNP P35131
C	-29	GLY	-	expression tag	UNP P35131
C	-28	SER	-	expression tag	UNP P35131
C	-27	SER	-	expression tag	UNP P35131
C	-26	HIS	-	expression tag	UNP P35131
C	-25	HIS	-	expression tag	UNP P35131
C	-24	HIS	-	expression tag	UNP P35131
C	-23	HIS	-	expression tag	UNP P35131
C	-22	HIS	-	expression tag	UNP P35131
C	-21	HIS	-	expression tag	UNP P35131
C	-20	GLY	-	expression tag	UNP P35131
C	-19	THR	-	expression tag	UNP P35131
C	-18	GLY	-	expression tag	UNP P35131
C	-17	SER	-	expression tag	UNP P35131
C	-16	TYR	-	expression tag	UNP P35131
C	-15	ILE	-	expression tag	UNP P35131
C	-14	THR	-	expression tag	UNP P35131
C	-13	SER	-	expression tag	UNP P35131
C	-12	LEU	-	expression tag	UNP P35131
C	-11	TYR	-	expression tag	UNP P35131
C	-10	LYS	-	expression tag	UNP P35131
C	-9	LYS	-	expression tag	UNP P35131
C	-8	ALA	-	expression tag	UNP P35131
C	-7	GLY	-	expression tag	UNP P35131
C	-6	SER	-	expression tag	UNP P35131
C	-5	ALA	-	expression tag	UNP P35131
C	-4	ALA	-	expression tag	UNP P35131
C	-3	ALA	-	expression tag	UNP P35131
C	-2	PRO	-	expression tag	UNP P35131
C	-1	PHE	-	expression tag	UNP P35131
C	0	THR	-	expression tag	UNP P35131

- Molecule 2 is a protein called Membrane-anchored ubiquitin-fold protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	93	Total	C	N	O	S	0	0	0
			703	449	119	133	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	92	Total	C	N	O	S	0	0	0
			683	438	116	127	2			

There are 40 discrepancies between the modelled and reference sequences:

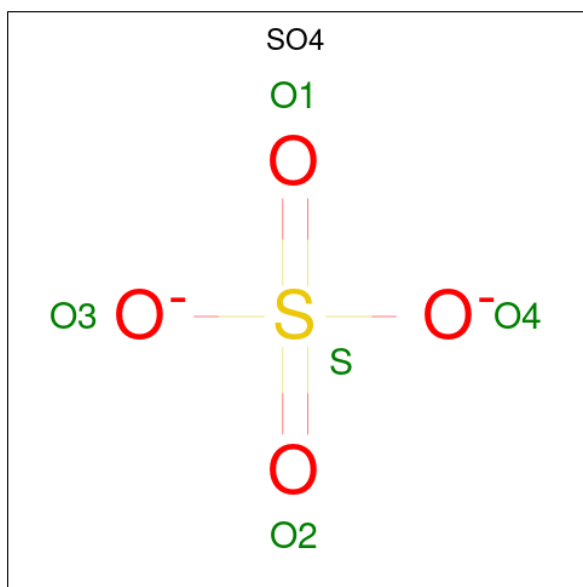
Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	initiating methionine	UNP Q9SW27
B	-18	GLY	-	expression tag	UNP Q9SW27
B	-17	SER	-	expression tag	UNP Q9SW27
B	-16	SER	-	expression tag	UNP Q9SW27
B	-15	HIS	-	expression tag	UNP Q9SW27
B	-14	HIS	-	expression tag	UNP Q9SW27
B	-13	HIS	-	expression tag	UNP Q9SW27
B	-12	HIS	-	expression tag	UNP Q9SW27
B	-11	HIS	-	expression tag	UNP Q9SW27
B	-10	HIS	-	expression tag	UNP Q9SW27
B	-9	SER	-	expression tag	UNP Q9SW27
B	-8	SER	-	expression tag	UNP Q9SW27
B	-7	GLY	-	expression tag	UNP Q9SW27
B	-6	LEU	-	expression tag	UNP Q9SW27
B	-5	VAL	-	expression tag	UNP Q9SW27
B	-4	PRO	-	expression tag	UNP Q9SW27
B	-3	ARG	-	expression tag	UNP Q9SW27
B	-2	GLY	-	expression tag	UNP Q9SW27
B	-1	SER	-	expression tag	UNP Q9SW27
B	0	HIS	-	expression tag	UNP Q9SW27
D	-19	MET	-	initiating methionine	UNP Q9SW27
D	-18	GLY	-	expression tag	UNP Q9SW27
D	-17	SER	-	expression tag	UNP Q9SW27
D	-16	SER	-	expression tag	UNP Q9SW27
D	-15	HIS	-	expression tag	UNP Q9SW27
D	-14	HIS	-	expression tag	UNP Q9SW27
D	-13	HIS	-	expression tag	UNP Q9SW27
D	-12	HIS	-	expression tag	UNP Q9SW27
D	-11	HIS	-	expression tag	UNP Q9SW27
D	-10	HIS	-	expression tag	UNP Q9SW27
D	-9	SER	-	expression tag	UNP Q9SW27
D	-8	SER	-	expression tag	UNP Q9SW27
D	-7	GLY	-	expression tag	UNP Q9SW27
D	-6	LEU	-	expression tag	UNP Q9SW27
D	-5	VAL	-	expression tag	UNP Q9SW27
D	-4	PRO	-	expression tag	UNP Q9SW27

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	ARG	-	expression tag	UNP Q9SW27
D	-2	GLY	-	expression tag	UNP Q9SW27
D	-1	SER	-	expression tag	UNP Q9SW27
D	0	HIS	-	expression tag	UNP Q9SW27

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).

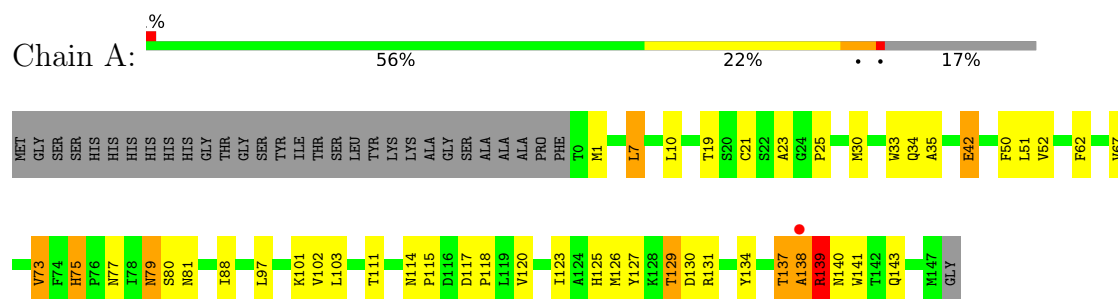


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		

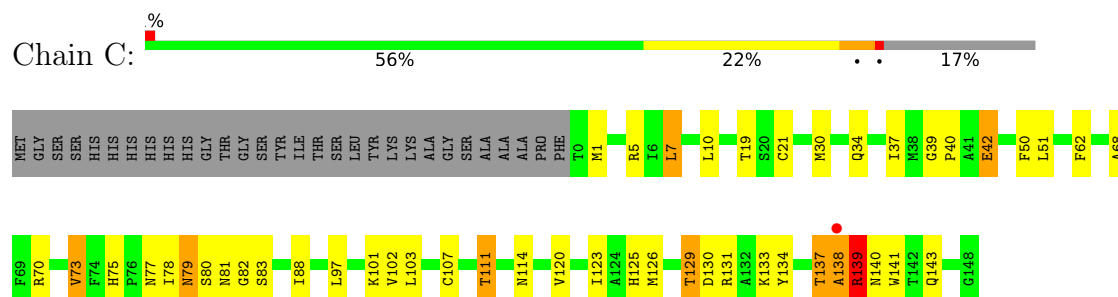
3 Residue-property plots [i](#)

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.

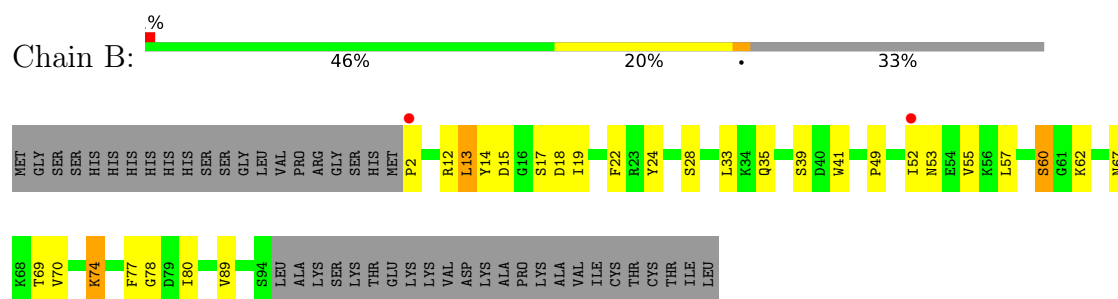
• Molecule 1: Ubiquitin-conjugating enzyme E2 8



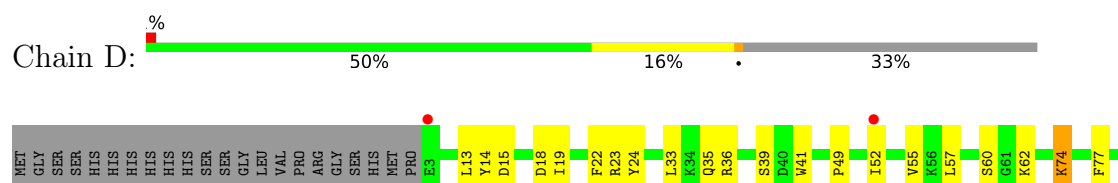
• Molecule 1: Ubiquitin-conjugating enzyme E2 8



• Molecule 2: Membrane-anchored ubiquitin-fold protein 3



• Molecule 2: Membrane-anchored ubiquitin-fold protein 3



T80
V89
S94
LEU
ALA
LYS
SER
LYS
THR
GLU
LYS
VAL
ASP
LYS
ALA
PRO
LYS
ALA
VAL
ILE
CYS
THR
CYS
THR
ILE
LEU

4 Data and refinement statistics

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α , β , γ	135.72Å 135.72Å 202.13Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 2.80 10.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.8 (10.00-2.80) 96.8 (10.00-2.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.92 (at 2.79Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.221 , 0.257 0.228 , 0.258	Depositor DCC
R_{free} test set	1372 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	75.1	Xtriage
Anisotropy	0.087	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3750	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.32% 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: SO4

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	0.83	1/1201 (0.1%)	1.06	6/1638 (0.4%)
1	C	0.77	1/1205 (0.1%)	1.05	4/1643 (0.2%)
2	B	0.73	0/716	1.01	1/969 (0.1%)
2	D	0.60	0/696	0.97	0/944
All	All	0.75	2/3818 (0.1%)	1.03	11/5194 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	138	ALA	CA-C	-7.78	1.43	1.52
1	C	138	ALA	CA-C	-5.48	1.45	1.52

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	138	ALA	N-CA-C	-8.64	94.16	108.76
1	C	138	ALA	N-CA-C	-8.59	94.90	109.24
2	B	2	PRO	N-CA-CB	6.31	109.94	103.00
1	A	139	ARG	N-CA-C	6.23	128.44	111.00
1	C	139	ARG	N-CA-C	5.82	127.30	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	138	ALA	CA-C-N	5.53	131.66	121.70
1	A	138	ALA	C-N-CA	5.53	131.66	121.70
1	C	138	ALA	CA-C-N	5.49	131.58	121.70
1	C	138	ALA	C-N-CA	5.49	131.58	121.70
1	A	75	HIS	CA-C-N	5.40	125.47	119.32
1	A	75	HIS	C-N-CA	5.40	125.47	119.32

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	137	THR	Peptide
1	C	137	THR	Peptide

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	1165	0	1167	29	1
1	C	1169	0	1170	34	1
2	B	703	0	708	14	0
2	D	683	0	683	11	0
3	A	5	0	0	0	0
3	C	20	0	0	2	0
3	D	5	0	0	0	0
All	All	3750	0	3728	85	2

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 11.

All (85) 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:7:LEU:HD22	1:A:30:MET:HE1	1.33	1.09
1:C:7:LEU:HD22	1:C:30:MET:HE1	1.40	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:ALA:HB2	1:A:141:TRP:HB2	1.58	0.85
1:C:138:ALA:HB2	1:C:141:TRP:HB2	1.60	0.83
1:C:1:MET:HE1	1:C:62:PHE:CE2	2.18	0.79
1:C:70:ARG:NH2	3:C:202:SO4:O2	2.18	0.76
1:A:126:MET:HE2	1:A:134:TYR:HA	1.66	0.76
1:A:7:LEU:HD22	1:A:30:MET:CE	2.12	0.75
1:C:7:LEU:HD22	1:C:30:MET:CE	2.18	0.73
1:C:126:MET:HE2	1:C:134:TYR:HA	1.71	0.72
1:C:79:ASN:C	1:C:79:ASN:HD22	1.99	0.71
1:A:77:ASN:HD21	1:A:114:ASN:H	1.39	0.69
1:A:1:MET:HE1	1:A:62:PHE:CE2	2.28	0.68
1:A:79:ASN:C	1:A:79:ASN:HD22	2.02	0.67
2:B:77:PHE:HD1	2:B:80:ILE:HD11	1.63	0.64
1:A:75:HIS:HD2	1:A:77:ASN:H	1.46	0.63
1:C:70:ARG:NH2	3:C:202:SO4:S	2.72	0.63
1:C:1:MET:HE1	1:C:62:PHE:HE2	1.62	0.63
1:C:77:ASN:HD21	1:C:114:ASN:H	1.49	0.60
2:D:74:LYS:HE3	2:D:74:LYS:HA	1.84	0.59
1:A:126:MET:HE2	1:A:134:TYR:CA	2.37	0.55
1:C:79:ASN:C	1:C:79:ASN:ND2	2.65	0.55
1:C:125:HIS:O	1:C:129:THR:HB	2.07	0.54
2:B:74:LYS:HE3	2:B:74:LYS:HA	1.90	0.54
1:A:125:HIS:O	1:A:129:THR:HB	2.08	0.53
1:C:120:VAL:HG11	1:C:123:ILE:HD12	1.90	0.53
1:A:75:HIS:CD2	1:A:77:ASN:H	2.24	0.53
1:A:50:PHE:CE1	1:A:73:VAL:HG13	2.44	0.52
1:A:79:ASN:C	1:A:79:ASN:ND2	2.68	0.51
2:B:41:TRP:CE2	2:B:49:PRO:HD3	2.44	0.51
1:C:50:PHE:CE1	1:C:73:VAL:HG13	2.46	0.51
1:A:120:VAL:HG11	1:A:123:ILE:HD12	1.93	0.51
1:C:40:PRO:HG2	1:C:111:THR:HG22	1.93	0.51
1:C:79:ASN:ND2	1:C:81:ASN:H	2.08	0.51
1:C:126:MET:HE2	1:C:134:TYR:CA	2.39	0.50
1:C:120:VAL:HG11	1:C:123:ILE:CD1	2.42	0.49
2:B:77:PHE:CD1	2:B:80:ILE:HD11	2.46	0.49
1:A:30:MET:HE3	1:A:30:MET:HB2	1.60	0.48
2:B:12:ARG:HA	2:B:18:ASP:HB3	1.95	0.48
2:D:77:PHE:HD1	2:D:80:ILE:HD11	1.78	0.48
1:C:75:HIS:CD2	1:C:77:ASN:H	2.32	0.48
1:A:126:MET:HE1	1:A:137:THR:OG1	2.14	0.48
2:B:67:ASN:HB3	2:D:36:ARG:NH2	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:24:TYR:OH	2:D:36:ARG:HG2	2.13	0.47
1:C:88:ILE:HD11	1:C:102:VAL:HA	1.96	0.47
2:B:67:ASN:CB	2:D:36:ARG:NH2	2.77	0.47
2:B:57:LEU:CD2	2:B:89:VAL:HG22	2.45	0.47
1:C:5:ARG:NH1	1:C:97:LEU:O	2.48	0.47
2:D:57:LEU:CD2	2:D:89:VAL:HG22	2.44	0.47
1:C:126:MET:HE1	1:C:137:THR:OG1	2.15	0.47
1:C:138:ALA:HA	1:C:140:ASN:N	2.30	0.46
1:A:1:MET:HE1	1:A:62:PHE:HE2	1.76	0.46
2:D:41:TRP:CE2	2:D:49:PRO:HD3	2.51	0.46
1:C:138:ALA:HA	1:C:139:ARG:C	2.41	0.46
1:C:126:MET:HE3	1:C:133:LYS:HD3	1.97	0.46
2:B:22:PHE:HB2	2:B:24:TYR:CE1	2.52	0.44
2:D:14:TYR:CG	2:D:15:ASP:N	2.85	0.44
1:A:120:VAL:HG11	1:A:123:ILE:CD1	2.47	0.44
1:A:138:ALA:HA	1:A:139:ARG:C	2.42	0.44
2:B:74:LYS:HE2	2:B:78:GLY:HA3	1.99	0.44
1:C:37:ILE:HG23	1:C:107:CYS:SG	2.58	0.44
1:C:68:ALA:HA	1:C:82:GLY:O	2.18	0.44
1:A:79:ASN:ND2	1:A:81:ASN:H	2.16	0.43
1:C:129:THR:HG22	1:C:130:ASP:HB2	2.01	0.43
1:A:88:ILE:HD12	1:A:97:LEU:HD13	2.01	0.43
1:A:138:ALA:HA	1:A:140:ASN:N	2.33	0.43
2:B:52:ILE:HD13	2:D:23:ARG:HH12	1.84	0.43
2:D:14:TYR:CD1	2:D:15:ASP:N	2.87	0.42
1:C:7:LEU:HD13	1:C:7:LEU:HA	1.87	0.42
1:C:39:GLY:HA2	1:C:40:PRO:HD3	1.90	0.42
2:D:22:PHE:HB2	2:D:24:TYR:CE1	2.55	0.42
1:A:23:ALA:HB2	1:A:35:ALA:HB2	2.02	0.42
2:B:13:LEU:HB2	2:B:17:SER:O	2.19	0.42
2:B:69:THR:O	2:B:70:VAL:C	2.62	0.42
2:B:14:TYR:CG	2:B:15:ASP:N	2.88	0.42
1:C:78:ILE:HA	1:C:83:SER:O	2.21	0.41
1:A:25:PRO:HA	1:A:33:TRP:HA	2.02	0.41
1:C:75:HIS:HD2	1:C:77:ASN:H	1.68	0.41
1:A:129:THR:HG22	1:A:130:ASP:HB2	2.03	0.41
1:C:30:MET:HE3	1:C:30:MET:HB2	1.59	0.41
1:C:126:MET:HE2	1:C:134:TYR:N	2.36	0.41
1:A:52:VAL:CG1	1:A:67:VAL:HG13	2.51	0.40
1:A:115:PRO:HG3	1:A:127:TYR:CD2	2.56	0.40
1:A:117:ASP:N	1:A:118:PRO:HD3	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:ILE:HD11	1:A:102:VAL:HA	2.03	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:42:GLU:OE2	1:C:42:GLU:OE2[7_555]	1.99	0.21
1:A:42:GLU:OE2	1:A:42:GLU:OE2[12_555]	2.03	0.17

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	146/179 (82%)	139 (95%)	6 (4%)	1 (1%)	18	47
1	C	147/179 (82%)	138 (94%)	8 (5%)	1 (1%)	18	47
2	B	91/138 (66%)	83 (91%)	7 (8%)	1 (1%)	11	36
2	D	90/138 (65%)	84 (93%)	6 (7%)	0	100	100
All	All	474/634 (75%)	444 (94%)	27 (6%)	3 (1%)	21	51

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	139	ARG
1	C	139	ARG
2	B	60	SER

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	131/153 (86%)	115 (88%)	16 (12%)	5	16
1	C	131/153 (86%)	115 (88%)	16 (12%)	5	16
2	B	78/120 (65%)	67 (86%)	11 (14%)	3	12
2	D	74/120 (62%)	63 (85%)	11 (15%)	3	10
All	All	414/546 (76%)	360 (87%)	54 (13%)	4	14

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	10	LEU
1	A	19	THR
1	A	21	CYS
1	A	34	GLN
1	A	42	GLU
1	A	51	LEU
1	A	73	VAL
1	A	79	ASN
1	A	80	SER
1	A	101	LYS
1	A	103	LEU
1	A	111	THR
1	A	129	THR
1	A	131	ARG
1	A	143	GLN
2	B	13	LEU
2	B	19	ILE
2	B	28	SER
2	B	33	LEU
2	B	35	GLN
2	B	39	SER
2	B	53	ASN
2	B	55	VAL
2	B	60	SER
2	B	62	LYS
2	B	74	LYS
1	C	7	LEU

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Mol	Chain	Res	Type
1	C	10	LEU
1	C	19	THR
1	C	21	CYS
1	C	34	GLN
1	C	42	GLU
1	C	51	LEU
1	C	73	VAL
1	C	79	ASN
1	C	80	SER
1	C	101	LYS
1	C	103	LEU
1	C	111	THR
1	C	129	THR
1	C	131	ARG
1	C	143	GLN
2	D	13	LEU
2	D	18	ASP
2	D	19	ILE
2	D	33	LEU
2	D	35	GLN
2	D	39	SER
2	D	52	ILE
2	D	55	VAL
2	D	60	SER
2	D	62	LYS
2	D	74	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	77	ASN
1	A	79	ASN
1	C	77	ASN
1	C	79	ASN

5.3.3 RNA ⓘ

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](#)

6 ligands are modelled in this entry.

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	$\# Z > 2$
3	SO4	D	201	-	4,4,4	0.46	0	6,6,6	0.39	0
3	SO4	C	203	-	4,4,4	0.49	0	6,6,6	0.37	0
3	SO4	C	202	-	4,4,4	0.49	0	6,6,6	0.23	0
3	SO4	C	201	-	4,4,4	0.51	0	6,6,6	0.26	0
3	SO4	C	204	-	4,4,4	0.49	0	6,6,6	0.29	0
3	SO4	A	201	-	4,4,4	0.61	0	6,6,6	0.30	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.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	202	SO4	2	0

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	148/179 (82%)	-0.64	1 (0%) 84 77	42, 58, 87, 104	0
1	C	149/179 (83%)	-0.29	1 (0%) 84 77	49, 73, 104, 128	0
2	B	93/138 (67%)	-0.29	2 (2%) 62 52	51, 76, 104, 117	0
2	D	92/138 (66%)	-0.05	2 (2%) 62 52	55, 92, 126, 157	0
All	All	482/634 (76%)	-0.35	6 (1%) 76 68	42, 72, 109, 157	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	3	GLU	5.1
1	C	138	ALA	3.8
2	B	52	ILE	2.3
2	B	2	PRO	2.2
1	A	138	ALA	2.1
2	D	52	ILE	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](#)

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
3	SO4	C	202	5/5	0.86	0.08	106,113,138,139	0
3	SO4	C	203	5/5	0.88	0.18	112,118,139,158	0
3	SO4	C	204	5/5	0.88	0.11	126,126,140,144	0
3	SO4	D	201	5/5	0.89	0.10	105,111,129,138	0
3	SO4	A	201	5/5	0.91	0.15	91,97,105,114	0
3	SO4	C	201	5/5	0.92	0.14	103,108,121,139	0

6.5 Other polymers [i](#)

There are no such residues in this entry.