



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:54 PM UTC

PDB ID : 1NKQ / pdb_00001nkq
Title : Crystal structure of yeast ynf8, a fumarylacetoacetate hydrolase family protein
Authors : Eswaramoorthy, S.; Kumaran, D.; Daniels, B.; Studier, F.W.; Swaminathan, S.; Burley, S.K.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2003-01-03
Resolution : 2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

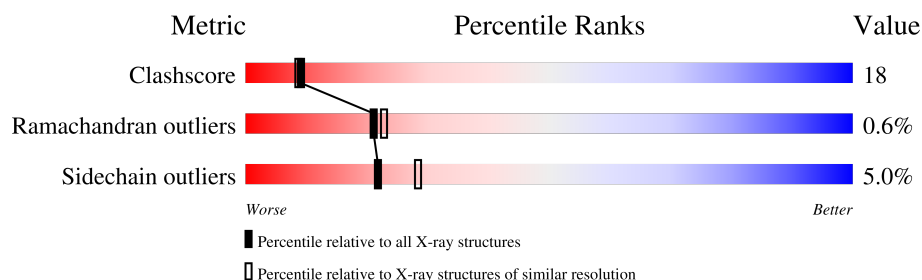
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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))
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	259	64% 27% 5%
1	B	259	66% 26% 6%
1	C	259	61% 30% 5%
1	D	259	61% 29% 6%
1	E	259	59% 32% 5%
1	F	259	58% 30% 7%

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ACY	B	703	-	-	X	-
4	ACY	C	705	-	-	X	-
4	ACY	E	709	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12088 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 Hypothetical 28.8 kDa protein in PSD1-SKO1 intergenic region.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	247	Total	C	N	O	S	Se	0	0	0
			1911	1214	328	360	4	5			
1	B	244	Total	C	N	O	S	Se	0	0	0
			1894	1204	326	355	4	5			
1	C	245	Total	C	N	O	S	Se	0	0	0
			1894	1204	324	357	4	5			
1	D	244	Total	C	N	O	S	Se	0	0	0
			1888	1201	323	355	4	5			
1	E	246	Total	C	N	O	S	Se	0	0	0
			1908	1212	330	357	4	5			
1	F	240	Total	C	N	O	S	Se	0	0	0
			1870	1187	325	349	4	5			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP P53889
A	104	MSE	MET	modified residue	UNP P53889
A	148	MSE	MET	modified residue	UNP P53889
A	189	MSE	MET	modified residue	UNP P53889
A	203	MSE	MET	modified residue	UNP P53889
A	243	MSE	MET	modified residue	UNP P53889
B	301	MSE	MET	modified residue	UNP P53889
B	404	MSE	MET	modified residue	UNP P53889
B	448	MSE	MET	modified residue	UNP P53889
B	489	MSE	MET	modified residue	UNP P53889
B	503	MSE	MET	modified residue	UNP P53889
B	543	MSE	MET	modified residue	UNP P53889
C	1	MSE	MET	modified residue	UNP P53889
C	104	MSE	MET	modified residue	UNP P53889
C	148	MSE	MET	modified residue	UNP P53889
C	189	MSE	MET	modified residue	UNP P53889
C	203	MSE	MET	modified residue	UNP P53889

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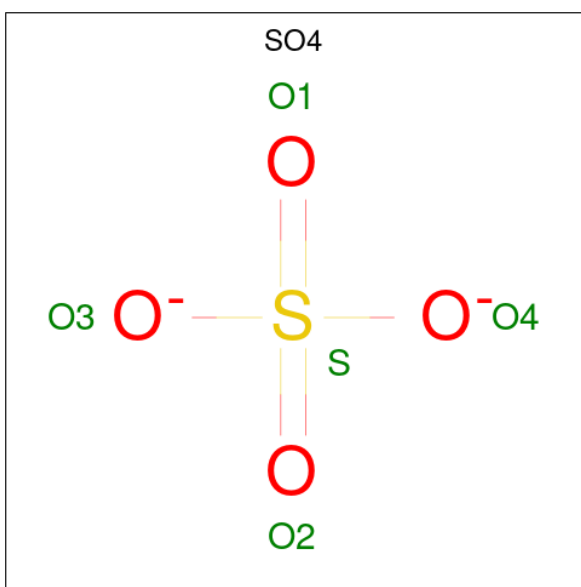
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Chain	Residue	Modelled	Actual	Comment	Reference
C	243	MSE	MET	modified residue	UNP P53889
D	301	MSE	MET	modified residue	UNP P53889
D	404	MSE	MET	modified residue	UNP P53889
D	448	MSE	MET	modified residue	UNP P53889
D	489	MSE	MET	modified residue	UNP P53889
D	503	MSE	MET	modified residue	UNP P53889
D	543	MSE	MET	modified residue	UNP P53889
E	1	MSE	MET	modified residue	UNP P53889
E	104	MSE	MET	modified residue	UNP P53889
E	148	MSE	MET	modified residue	UNP P53889
E	189	MSE	MET	modified residue	UNP P53889
E	203	MSE	MET	modified residue	UNP P53889
E	243	MSE	MET	modified residue	UNP P53889
F	301	MSE	MET	modified residue	UNP P53889
F	404	MSE	MET	modified residue	UNP P53889
F	448	MSE	MET	modified residue	UNP P53889
F	489	MSE	MET	modified residue	UNP P53889
F	503	MSE	MET	modified residue	UNP P53889
F	543	MSE	MET	modified residue	UNP P53889

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

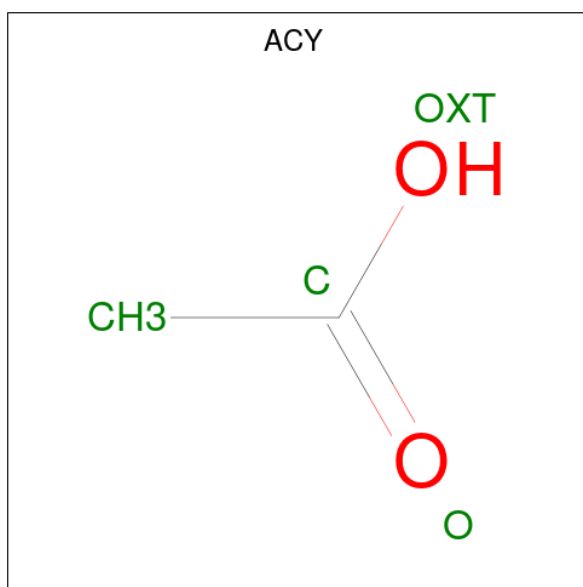
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0
2	B	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0
2	D	1	Total Ca 1 1	0	0
2	E	1	Total Ca 1 1	0	0
2	F	1	Total Ca 1 1	0	0

- 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	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).



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

- Molecule 5 is water.

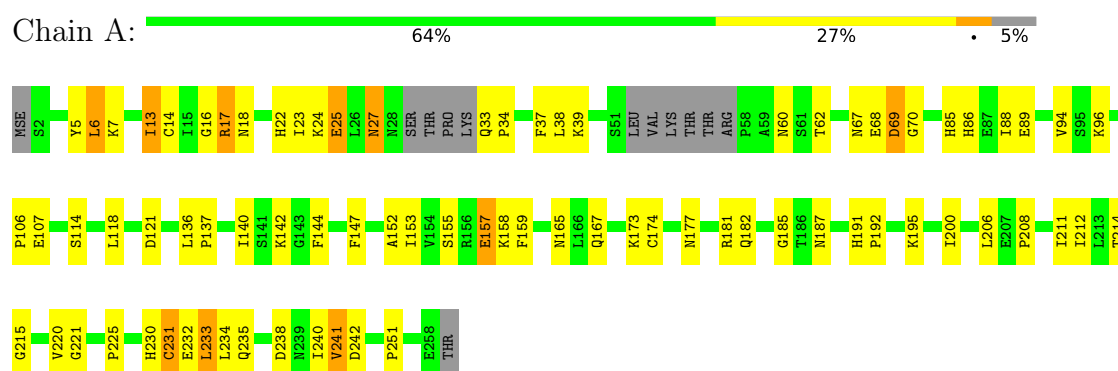
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	112	Total 112	O 112	0	0
5	B	106	Total 106	O 106	0	0
5	C	99	Total 99	O 99	0	0
5	D	122	Total 122	O 122	0	0
5	E	107	Total 107	O 107	0	0
5	F	88	Total 88	O 88	0	0

3 Residue-property plots [i](#)

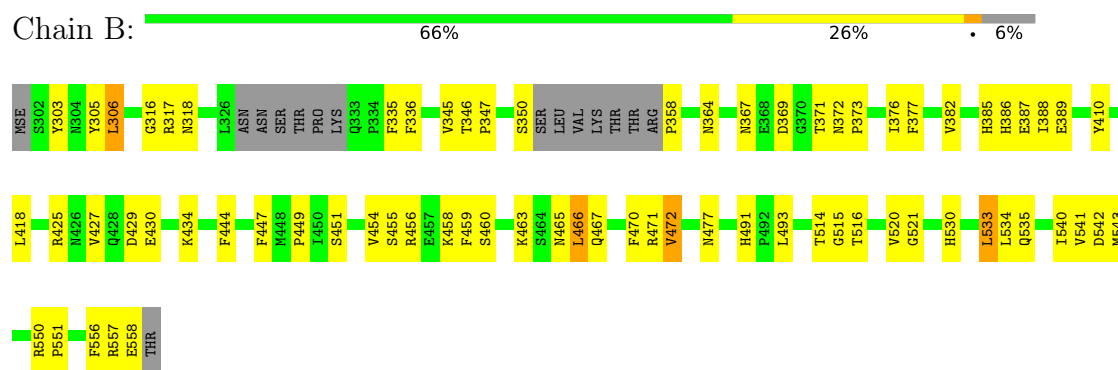
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

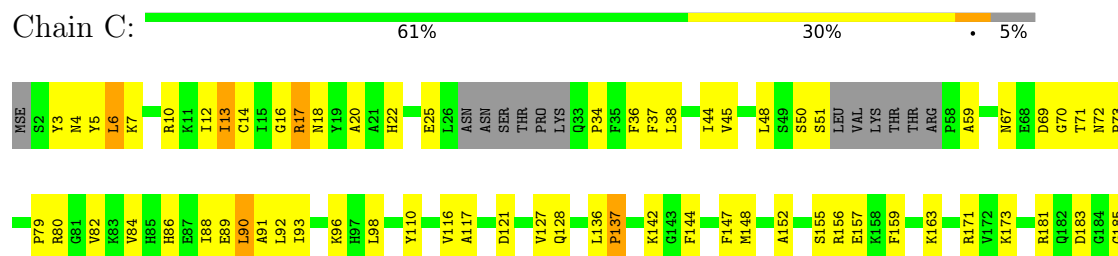
- Molecule 1: Hypothetical 28.8 kDa protein in PSD1-SKO1 intergenic region

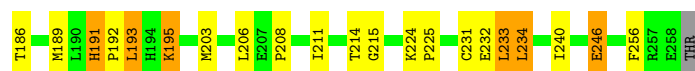


- Molecule 1: Hypothetical 28.8 kDa protein in PSD1-SKO1 intergenic region



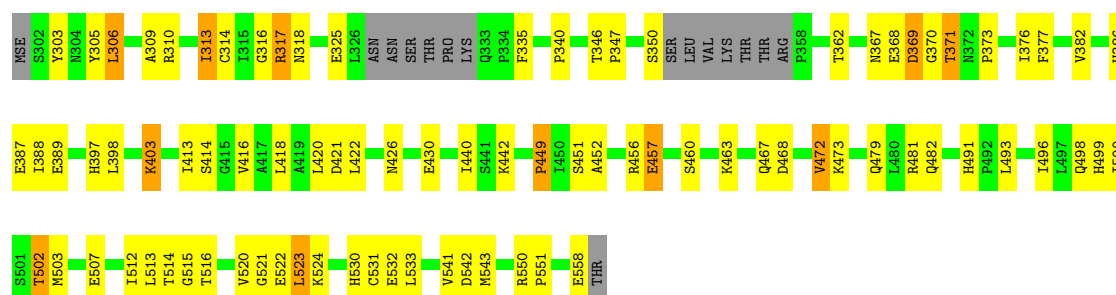
- Molecule 1: Hypothetical 28.8 kDa protein in PSD1-SKO1 intergenic region





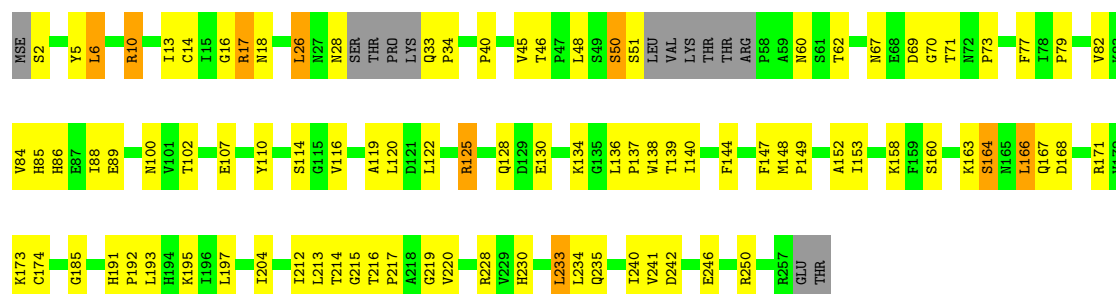
- Molecule 1: Hypothetical 28.8 kDa protein in PSD1-SKO1 intergenic region

Chain D: 61% 29% 6%



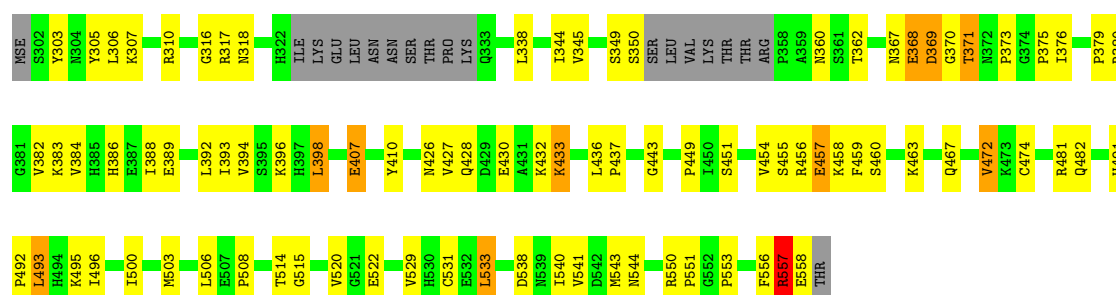
- Molecule 1: Hypothetical 28.8 kDa protein in PSD1-SKO1 intergenic region

Chain E: 59% 32% 5%



- Molecule 1: Hypothetical 28.8 kDa protein in PSD1-SKO1 intergenic region

Chain F: 58% 30% 7%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.70Å 85.99Å 316.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20	Depositor
% Data completeness (in resolution range)	(Not available) (50.00-2.20)	Depositor
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.216 , 0.262	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12088	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, ACY, 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	0.44	0/1946	0.95	6/2625 (0.2%)
1	B	0.42	0/1929	0.92	5/2602 (0.2%)
1	C	0.41	0/1929	0.93	6/2603 (0.2%)
1	D	0.43	0/1923	0.95	6/2595 (0.2%)
1	E	0.42	0/1943	0.95	8/2620 (0.3%)
1	F	0.53	2/1905 (0.1%)	1.00	7/2568 (0.3%)
All	All	0.44	2/11575 (0.0%)	0.95	38/15613 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	557	ARG	CA-C	10.42	1.65	1.53
1	F	557	ARG	C-O	5.65	1.30	1.23

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	370	GLY	N-CA-C	-8.24	104.53	115.40
1	A	70	GLY	N-CA-C	-7.84	104.73	114.92
1	D	370	GLY	N-CA-C	-7.56	105.30	115.36
1	E	50	SER	N-CA-C	7.44	119.47	111.36
1	E	70	GLY	N-CA-C	-7.03	106.07	115.21

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	1911	0	1905	70	0
1	B	1894	0	1892	55	0
1	C	1894	0	1886	79	0
1	D	1888	0	1881	65	0
1	E	1908	0	1910	82	0
1	F	1870	0	1873	93	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	10	0	0	1	0
3	B	15	0	0	0	0
3	C	5	0	0	0	0
3	E	5	0	0	1	0
4	A	8	0	6	1	0
4	B	8	0	6	2	0
4	C	8	0	6	3	0
4	D	8	0	6	1	0
4	E	8	0	6	3	0
4	F	8	0	6	1	0
5	A	112	0	0	4	0
5	B	106	0	0	2	0
5	C	99	0	0	5	0
5	D	122	0	0	3	0
5	E	107	0	0	4	0
5	F	88	0	0	6	0
All	All	12088	0	11383	418	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 18.

The worst 5 of 418 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:E:148:MSE:HE3	1:E:213:LEU:HD11	1.38	1.01
1:F:367:ASN:HD22	1:F:371:THR:HG22	1.23	0.99
1:C:224:LYS:HD3	1:C:225:PRO:HD2	1.45	0.98
1:F:318:ASN:HD21	1:F:491:HIS:H	1.12	0.96
1:E:67:ASN:HD22	1:E:71:THR:HG23	1.31	0.94

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	241/259 (93%)	229 (95%)	10 (4%)	2 (1%)	16	16
1	B	238/259 (92%)	223 (94%)	14 (6%)	1 (0%)	30	34
1	C	239/259 (92%)	229 (96%)	8 (3%)	2 (1%)	16	16
1	D	238/259 (92%)	230 (97%)	6 (2%)	2 (1%)	16	16
1	E	240/259 (93%)	229 (95%)	9 (4%)	2 (1%)	16	16
1	F	234/259 (90%)	222 (95%)	12 (5%)	0	100	100
All	All	1430/1554 (92%)	1362 (95%)	59 (4%)	9 (1%)	21	23

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	59	ALA
1	B	551	PRO
1	A	17	ARG
1	C	17	ARG
1	A	165	ASN

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	214/224 (96%)	204 (95%)	10 (5%)	23	31
1	B	212/224 (95%)	205 (97%)	7 (3%)	33	45
1	C	212/224 (95%)	204 (96%)	8 (4%)	29	40
1	D	211/224 (94%)	196 (93%)	15 (7%)	13	16
1	E	214/224 (96%)	204 (95%)	10 (5%)	23	31
1	F	210/224 (94%)	196 (93%)	14 (7%)	15	17
All	All	1273/1344 (95%)	1209 (95%)	64 (5%)	22	28

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	457	GLU
1	F	493	LEU
1	C	246	GLU
1	C	234	LEU
1	F	531	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	367	ASN
1	F	491	HIS
1	E	18	ASN
1	F	482	GLN
1	F	367	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](#)

Of 25 ligands modelled in this entry, 6 are monoatomic - leaving 19 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	$\# Z > 2$
3	SO4	B	802	-	4,4,4	0.36	0	6,6,6	0.16	0
4	ACY	F	710	-	3,3,3	1.31	1 (33%)	3,3,3	1.62	1 (33%)
4	ACY	C	704	-	3,3,3	1.27	0	3,3,3	1.64	1 (33%)
3	SO4	A	801	-	4,4,4	0.37	0	6,6,6	0.17	0
3	SO4	A	803	-	4,4,4	0.36	0	6,6,6	0.10	0
3	SO4	B	805	-	4,4,4	0.38	0	6,6,6	0.10	0
4	ACY	A	701	2	3,3,3	1.38	1 (33%)	3,3,3	1.62	1 (33%)
4	ACY	D	707	2	3,3,3	1.30	1 (33%)	3,3,3	1.70	1 (33%)
4	ACY	E	709	2	3,3,3	1.31	1 (33%)	3,3,3	1.66	1 (33%)
4	ACY	F	711	2	3,3,3	1.29	1 (33%)	3,3,3	1.67	1 (33%)
3	SO4	B	800	-	4,4,4	0.38	0	6,6,6	0.11	0
3	SO4	C	806	-	4,4,4	0.40	0	6,6,6	0.18	0
3	SO4	E	807	-	4,4,4	0.34	0	6,6,6	0.08	0
4	ACY	A	700	-	3,3,3	1.26	0	3,3,3	1.63	1 (33%)
4	ACY	D	706	-	3,3,3	1.29	0	3,3,3	1.61	1 (33%)
4	ACY	B	703	2	3,3,3	1.30	1 (33%)	3,3,3	1.67	1 (33%)
4	ACY	B	702	-	3,3,3	1.29	1 (33%)	3,3,3	1.61	1 (33%)
4	ACY	C	705	2	3,3,3	1.36	1 (33%)	3,3,3	1.62	1 (33%)
4	ACY	E	708	-	3,3,3	1.31	0	3,3,3	1.65	1 (33%)

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	701	ACY	O-C	2.17	1.31	1.22
4	C	705	ACY	O-C	2.16	1.31	1.22
4	E	709	ACY	O-C	2.06	1.31	1.22
4	B	703	ACY	O-C	2.05	1.31	1.22
4	F	710	ACY	O-C	2.05	1.31	1.22

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	707	ACY	O-C-CH3	-2.31	113.07	122.53
4	B	703	ACY	O-C-CH3	-2.28	113.19	122.53
4	F	711	ACY	O-C-CH3	-2.28	113.20	122.53
4	E	709	ACY	O-C-CH3	-2.25	113.29	122.53
4	E	708	ACY	O-C-CH3	-2.25	113.30	122.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	704	ACY	1	0
3	A	801	SO4	1	0
4	A	701	ACY	1	0
4	D	707	ACY	1	0
4	E	709	ACY	2	0
4	F	711	ACY	1	0
3	E	807	SO4	1	0
4	B	703	ACY	2	0
4	C	705	ACY	2	0
4	E	708	ACY	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.