



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2024 – 10:41 am BST

PDB ID : 8OXF
Title : Enantioselective synthesis of fluorine-containing building blocks by employing mutant HHDH in a two-phase system
Authors : Majeric Elenkov, M.; Stefanic, Z.
Deposited on : 2023-05-02
Resolution : 1.77 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.36.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

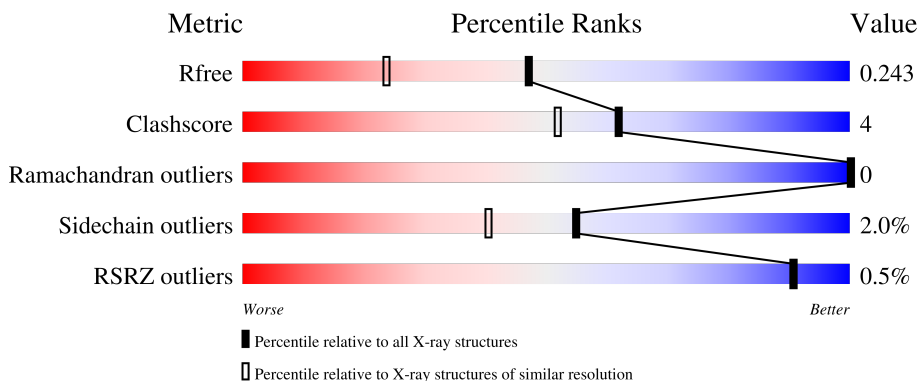
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.77 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.



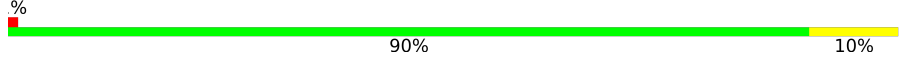


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

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	243	91% 9%
1	B	243	88% 12%
1	C	243	92% 7%
1	D	243	88% 12%
1	E	243	89% 9%

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Mol	Chain	Length	Quality of chain
1	F	243	 <p>% 90% 10%</p>
1	G	243	 <p>89% 10%</p>
1	H	243	 <p>88% 12%</p>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 16731 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 Halohydrin dehalogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	243	1855	1182	322	347	4	0	0	0
1	B	243	1855	1182	322	347	4	0	0	0
1	C	243	1855	1182	322	347	4	0	0	0
1	D	243	1855	1182	322	347	4	0	0	0
1	E	243	1855	1182	322	347	4	0	0	0
1	F	243	1855	1182	322	347	4	0	0	0
1	G	243	1855	1182	322	347	4	0	0	0
1	H	243	1855	1182	322	347	4	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	178	ALA	ASN	conflict	UNP Q93MS3
B	178	ALA	ASN	conflict	UNP Q93MS3
C	178	ALA	ASN	conflict	UNP Q93MS3
D	178	ALA	ASN	conflict	UNP Q93MS3
E	178	ALA	ASN	conflict	UNP Q93MS3
F	178	ALA	ASN	conflict	UNP Q93MS3
G	178	ALA	ASN	conflict	UNP Q93MS3
H	178	ALA	ASN	conflict	UNP Q93MS3

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 3 is water.

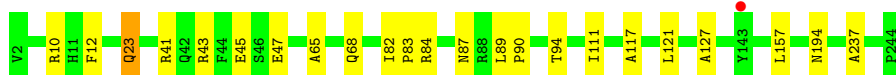
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	229	Total O 229 229	0	0
3	B	253	Total O 253 253	0	0
3	C	240	Total O 240 240	0	0
3	D	252	Total O 252 252	0	0
3	E	247	Total O 247 247	0	0
3	F	213	Total O 213 213	0	0
3	G	213	Total O 213 213	0	0
3	H	236	Total O 236 236	0	0

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.

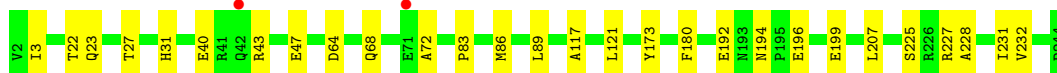
- Molecule 1: Halohydrin dehalogenase

Chain A: 91% 9%



- Molecule 1: Halohydrin dehalogenase

Chain B: 88% 12%



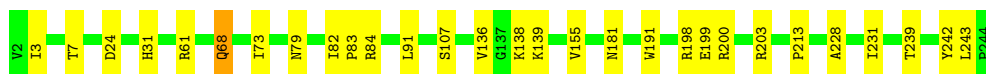
- Molecule 1: Halohydrin dehalogenase

Chain C: 92% 7%



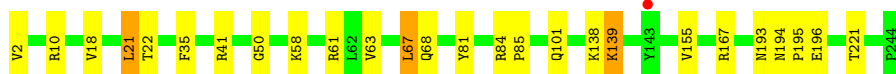
- Molecule 1: Halohydrin dehalogenase

Chain D: 88% 12%

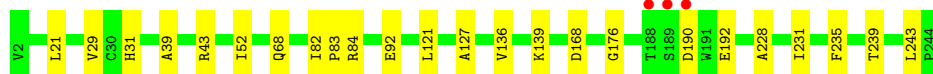
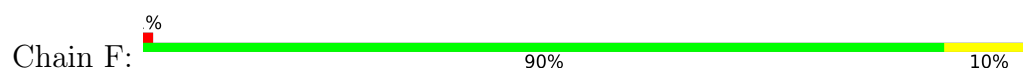


- Molecule 1: Halohydrin dehalogenase

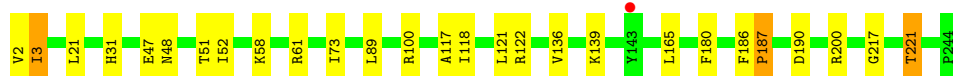
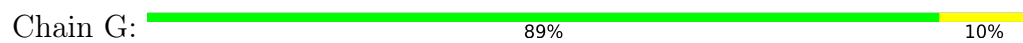
Chain E: 89% 9%



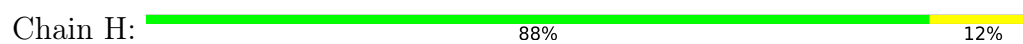
- Molecule 1: Halohydrin dehalogenase



- Molecule 1: Halohydrin dehalogenase



- Molecule 1: Halohydrin dehalogenase



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	60.16Å 60.06Å 137.11Å 81.73° 80.26° 81.72°	Depositor
Resolution (Å)	56.61 – 1.77 56.61 – 1.77	Depositor EDS
% Data completeness (in resolution range)	91.2 (56.61-1.77) 91.1 (56.61-1.77)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 1.76Å)	Xtrriage
Refinement program	PHENIX 1.19	Depositor
R, R_{free}	0.197 , 0.243 0.196 , 0.243	Depositor DCC
R_{free} test set	1991 reflections (1.20%)	wwPDB-VP
Wilson B-factor (Å ²)	20.7	Xtrriage
Anisotropy	0.264	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 35.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.105 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16731	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.41	0/1899	0.65	0/2589
1	B	0.41	0/1899	0.67	0/2589
1	C	0.43	0/1899	0.64	0/2589
1	D	0.42	0/1899	0.64	0/2589
1	E	0.42	0/1899	0.65	1/2589 (0.0%)
1	F	0.42	0/1899	0.66	0/2589
1	G	0.75	3/1899 (0.2%)	0.86	4/2589 (0.2%)
1	H	0.42	0/1899	0.63	0/2589
All	All	0.47	3/15192 (0.0%)	0.68	5/20712 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	187	PRO	CG-CD	-18.17	0.90	1.50
1	G	187	PRO	CB-CG	18.16	2.40	1.50
1	G	187	PRO	N-CD	8.35	1.59	1.47

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	187	PRO	N-CD-CG	-16.40	78.60	103.20
1	G	187	PRO	CB-CG-CD	-16.02	44.01	106.50
1	G	187	PRO	N-CA-CB	-12.41	88.40	103.30
1	G	187	PRO	CA-CB-CG	-10.67	83.72	104.00
1	E	67	LEU	CB-CG-CD2	5.07	119.62	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1855	0	1841	16	0
1	B	1855	0	1841	17	0
1	C	1855	0	1841	10	0
1	D	1855	0	1841	17	0
1	E	1855	0	1841	21	0
1	F	1855	0	1841	17	0
1	G	1855	0	1841	15	0
1	H	1855	0	1841	22	0
2	A	1	0	0	0	0
2	B	1	0	0	1	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
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	229	0	0	3	1
3	B	253	0	0	5	1
3	C	240	0	0	4	0
3	D	252	0	0	6	1
3	E	247	0	0	9	2
3	F	213	0	0	5	2
3	G	213	0	0	2	3
3	H	236	0	0	8	2
All	All	16731	0	14728	131	6

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 4.

All (131) 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:C:139:LYS:NZ	3:C:401:HOH:O	2.00	0.94
1:A:84:ARG:O	1:A:87:ASN:ND2	2.06	0.89
1:C:101:GLN:NE2	3:C:402:HOH:O	2.10	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:3:ILE:HD11	1:D:73:ILE:HG12	1.68	0.75
1:D:68:GLN:NE2	3:D:403:HOH:O	2.23	0.71
1:E:68:GLN:NE2	3:E:403:HOH:O	2.23	0.71
1:B:192:GLU:OE2	3:B:401:HOH:O	2.08	0.70
1:E:2:VAL:N	3:E:404:HOH:O	2.24	0.69
1:B:43:ARG:O	1:B:47:GLU:HG3	1.94	0.68
1:H:40:GLU:N	3:H:401:HOH:O	2.12	0.67
1:E:50:GLY:O	3:E:401:HOH:O	2.11	0.67
1:H:2:VAL:N	3:H:407:HOH:O	2.28	0.66
1:F:43:ARG:NH1	3:F:402:HOH:O	2.29	0.65
1:G:2:VAL:N	3:G:402:HOH:O	2.30	0.64
1:H:72:ALA:O	3:H:402:HOH:O	2.15	0.64
1:H:2:VAL:N	3:H:408:HOH:O	2.30	0.63
1:F:239:THR:HG21	1:F:243:LEU:HG	1.79	0.63
1:D:82:ILE:HG13	1:D:83:PRO:HD2	1.81	0.62
1:C:82:ILE:HG13	1:C:83:PRO:HD2	1.82	0.62
1:D:181:ASN:ND2	3:D:408:HOH:O	2.33	0.61
1:E:194:ASN:ND2	3:E:407:HOH:O	2.33	0.61
1:B:225:SER:OG	1:B:227:ARG:HG3	2.02	0.59
1:E:193:ASN:ND2	3:E:410:HOH:O	2.36	0.58
1:E:18:VAL:O	1:E:22:THR:HG23	2.04	0.57
1:E:101:GLN:NE2	3:E:402:HOH:O	2.22	0.56
1:F:228:ALA:O	1:F:231:ILE:HG12	2.06	0.56
1:A:10:ARG:NH1	3:A:406:HOH:O	2.37	0.56
1:G:58:LYS:HB2	1:G:61:ARG:HD2	1.87	0.56
1:E:22:THR:HG22	3:E:401:HOH:O	2.07	0.55
1:A:194:ASN:HB2	3:A:565:HOH:O	2.06	0.55
1:C:2:VAL:N	3:C:405:HOH:O	2.38	0.55
1:B:194:ASN:HB3	1:B:196:GLU:OE2	2.06	0.55
1:E:84:ARG:HG3	1:E:85:PRO:HA	1.88	0.55
1:H:10:ARG:HH22	1:H:43:ARG:HH22	1.54	0.54
1:F:82:ILE:HD12	1:F:83:PRO:HD2	1.88	0.54
1:F:139:LYS:HG2	1:F:243:LEU:HD13	1.90	0.54
1:F:168:ASP:OD2	3:F:401:HOH:O	2.19	0.54
1:H:43:ARG:O	1:H:47:GLU:HG3	2.08	0.54
1:G:3:ILE:HD11	1:G:73:ILE:HG12	1.90	0.53
1:G:100:ARG:NH2	3:G:407:HOH:O	2.36	0.53
1:H:58:LYS:HD3	1:H:60:GLU:OE2	2.09	0.53
1:E:139:LYS:NZ	3:E:405:HOH:O	2.29	0.51
1:H:82:ILE:HG12	1:H:83:PRO:HD2	1.92	0.51
1:H:10:ARG:NH2	1:H:43:ARG:HH22	2.08	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:68:GLN:OE1	1:B:68:GLN:HA	2.11	0.51
1:A:43:ARG:O	1:A:47:GLU:HG3	2.10	0.50
1:H:129:VAL:HB	1:H:172:LEU:HD22	1.94	0.50
1:F:39:ALA:HB1	1:F:43:ARG:HH21	1.77	0.50
1:E:35:PHE:O	1:E:41:ARG:HD3	2.11	0.49
1:E:63:VAL:O	1:E:67:LEU:HD22	2.11	0.49
1:H:40:GLU:HG2	3:H:401:HOH:O	2.13	0.49
1:E:10:ARG:HH11	1:E:10:ARG:HG2	1.78	0.48
1:F:192:GLU:H	1:F:192:GLU:CD	2.17	0.48
1:F:121:LEU:HD13	1:F:127:ALA:HB3	1.96	0.48
1:A:23:GLN:HG3	3:A:578:HOH:O	2.13	0.48
1:B:72:ALA:O	3:B:402:HOH:O	2.20	0.48
1:E:21:LEU:HD13	1:E:221:THR:HG22	1.96	0.47
1:A:41:ARG:O	1:A:45:GLU:HG3	2.15	0.47
1:F:92:GLU:HB2	3:F:523:HOH:O	2.14	0.47
1:D:84:ARG:HB2	3:D:520:HOH:O	2.15	0.47
1:G:89:LEU:HD23	1:G:89:LEU:HA	1.66	0.47
1:H:88:ARG:NE	3:H:415:HOH:O	2.48	0.47
1:H:173:TYR:CE2	1:H:232:VAL:HA	2.50	0.47
1:H:33:ALA:HA	1:H:57:GLN:OE1	2.15	0.46
1:B:3:ILE:HD13	1:B:27:THR:HB	1.97	0.46
1:G:180:PHE:O	1:G:186:PHE:HB2	2.15	0.46
1:H:123:ALA:HB2	3:H:576:HOH:O	2.15	0.46
1:A:65:ALA:HA	1:A:68:GLN:HE21	1.80	0.46
1:B:228:ALA:O	1:B:231:ILE:HG12	2.16	0.46
1:C:173:TYR:CE2	1:C:232:VAL:HA	2.51	0.46
1:E:196:GLU:H	1:E:196:GLU:CD	2.19	0.46
1:A:89:LEU:HD22	1:A:90:PRO:HD2	1.97	0.45
1:E:167:ARG:NH1	3:E:409:HOH:O	2.36	0.45
1:F:136:VAL:HA	1:F:139:LYS:O	2.17	0.45
1:G:217:GLY:O	1:G:221:THR:HB	2.16	0.45
1:D:138:LYS:HE2	1:D:155:VAL:HG11	1.97	0.45
1:F:29:VAL:HG22	1:F:52:ILE:HD12	1.97	0.45
1:G:122:ARG:NH2	1:H:92:GLU:OE2	2.46	0.45
1:A:82:ILE:HD12	1:A:82:ILE:HA	1.86	0.45
1:D:200:ARG:NE	3:D:422:HOH:O	2.49	0.45
1:F:68:GLN:OE1	1:F:68:GLN:HA	2.17	0.45
1:F:82:ILE:HD12	1:F:82:ILE:HA	1.87	0.45
1:F:176:GLY:HA3	1:F:235:PHE:CZ	2.52	0.45
1:G:187:PRO:HG3	1:G:190:ASP:OD2	2.17	0.45
1:D:203:ARG:HD3	3:D:543:HOH:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:LEU:HD13	1:A:94:THR:HG23	1.99	0.44
1:E:10:ARG:HG2	1:E:10:ARG:NH1	2.30	0.44
1:G:47:GLU:HG2	1:G:48:ASN:OD1	2.16	0.44
1:C:10:ARG:HD2	3:C:524:HOH:O	2.17	0.44
1:F:92:GLU:HG2	3:F:424:HOH:O	2.17	0.44
1:B:173:TYR:CE2	1:B:232:VAL:HA	2.52	0.44
1:D:228:ALA:O	1:D:231:ILE:HG12	2.17	0.44
1:H:139:LYS:HD2	1:H:243:LEU:HD22	2.00	0.44
1:G:118:ILE:HD13	1:G:165:LEU:HD21	1.99	0.43
1:A:237:ALA:O	1:C:234:GLN:NE2	2.44	0.43
1:G:117:ALA:O	1:G:121:LEU:HG	2.18	0.43
1:A:89:LEU:HD23	1:A:89:LEU:HA	1.82	0.43
1:E:58:LYS:HE3	1:E:61:ARG:NE	2.34	0.43
1:B:22:THR:HG21	3:B:473:HOH:O	2.18	0.43
1:B:40:GLU:OE1	1:B:43:ARG:NH2	2.52	0.43
1:A:111:ILE:HG13	1:A:157:LEU:HD22	2.01	0.43
1:A:117:ALA:O	1:A:121:LEU:HB2	2.18	0.43
1:H:40:GLU:OE1	1:H:43:ARG:NH2	2.52	0.43
1:G:51:THR:C	1:G:52:ILE:HD12	2.39	0.43
1:A:82:ILE:HD12	1:A:83:PRO:HD2	2.01	0.43
1:H:243:LEU:HB2	3:H:403:HOH:O	2.18	0.42
1:B:23:GLN:NE2	3:B:418:HOH:O	2.51	0.42
1:D:239:THR:HB	1:D:242:TYR:HB3	2.01	0.42
1:E:139:LYS:NZ	1:H:139:LYS:HZ1	2.18	0.42
1:B:199:GLU:OE1	3:B:403:HOH:O	2.21	0.42
1:H:64:ASP:HA	1:H:67:LEU:HD12	2.01	0.42
1:G:187:PRO:CG	1:G:190:ASP:HB2	2.50	0.42
1:E:193:ASN:O	1:E:195:PRO:HD3	2.20	0.41
1:D:7:THR:O	1:D:79:ASN:HB3	2.20	0.41
1:F:84:ARG:NH1	3:F:421:HOH:O	2.53	0.41
1:D:136:VAL:HA	1:D:139:LYS:O	2.20	0.41
1:D:191:TRP:CZ2	1:D:198:ARG:HG2	2.55	0.41
1:E:138:LYS:HE2	1:E:155:VAL:HG11	2.03	0.41
1:C:117:ALA:O	1:C:121:LEU:HG	2.20	0.41
1:H:7:THR:O	1:H:79:ASN:HB3	2.21	0.41
1:A:121:LEU:HG	1:A:127:ALA:HB3	2.03	0.41
1:D:181:ASN:HB3	1:D:213:PRO:HD3	2.03	0.41
1:D:239:THR:HG21	1:D:243:LEU:HD13	2.02	0.41
1:B:180:PHE:HB3	2:B:301:CL:CL	2.58	0.41
1:G:136:VAL:HA	1:G:139:LYS:O	2.20	0.41
1:C:118:ILE:HD11	1:D:91:LEU:HD13	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:217:GLY:O	1:C:221:THR:HB	2.21	0.40
1:B:83:PRO:O	1:B:86:MET:HG3	2.21	0.40
1:B:89:LEU:HD23	1:B:89:LEU:HA	1.89	0.40
1:B:117:ALA:HB1	1:B:121:LEU:HD22	2.04	0.40
1:D:61:ARG:NH1	3:D:401:HOH:O	2.22	0.40

All (6) 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)
3:F:549:HOH:O	3:H:576:HOH:O[1_545]	1.98	0.22
3:B:569:HOH:O	3:D:549:HOH:O[1_455]	2.01	0.19
3:A:622:HOH:O	3:G:583:HOH:O[1_556]	2.12	0.08
3:E:494:HOH:O	3:G:462:HOH:O[1_545]	2.12	0.08
3:F:447:HOH:O	3:H:439:HOH:O[1_655]	2.15	0.05
3:E:487:HOH:O	3:G:558:HOH:O[1_545]	2.19	0.01

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	241/243 (99%)	230 (95%)	11 (5%)	0	100	100
1	B	241/243 (99%)	233 (97%)	8 (3%)	0	100	100
1	C	241/243 (99%)	231 (96%)	10 (4%)	0	100	100
1	D	241/243 (99%)	233 (97%)	8 (3%)	0	100	100
1	E	241/243 (99%)	232 (96%)	9 (4%)	0	100	100
1	F	241/243 (99%)	232 (96%)	9 (4%)	0	100	100
1	G	241/243 (99%)	231 (96%)	10 (4%)	0	100	100
1	H	241/243 (99%)	231 (96%)	10 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1928/1944 (99%)	1853 (96%)	75 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	191/191 (100%)	189 (99%)	2 (1%)	76	68
1	B	191/191 (100%)	188 (98%)	3 (2%)	62	51
1	C	191/191 (100%)	185 (97%)	6 (3%)	40	22
1	D	191/191 (100%)	186 (97%)	5 (3%)	46	29
1	E	191/191 (100%)	188 (98%)	3 (2%)	62	51
1	F	191/191 (100%)	188 (98%)	3 (2%)	62	51
1	G	191/191 (100%)	186 (97%)	5 (3%)	46	29
1	H	191/191 (100%)	188 (98%)	3 (2%)	62	51
All	All	1528/1528 (100%)	1498 (98%)	30 (2%)	55	40

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	PHE
1	A	23	GLN
1	B	31	HIS
1	B	64	ASP
1	B	207	LEU
1	C	3	ILE
1	C	21	LEU
1	C	31	HIS
1	C	61	ARG
1	C	199	GLU
1	C	221	THR
1	D	24	ASP

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Mol	Chain	Res	Type
1	D	31	HIS
1	D	68	GLN
1	D	107	SER
1	D	199	GLU
1	E	21	LEU
1	E	81	TYR
1	E	139	LYS
1	F	21	LEU
1	F	31	HIS
1	F	190	ASP
1	G	3	ILE
1	G	21	LEU
1	G	31	HIS
1	G	200	ARG
1	G	221	THR
1	H	12	PHE
1	H	46	SER
1	H	85	PRO

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

Mol	Chain	Res	Type
1	B	23	GLN
1	E	68	GLN
1	E	193	ASN
1	G	42	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 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 [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](#)

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	243/243 (100%)	-0.37	1 (0%) 92 92	15, 22, 35, 41	0
1	B	243/243 (100%)	-0.34	2 (0%) 86 86	15, 21, 35, 45	0
1	C	243/243 (100%)	-0.33	1 (0%) 92 92	14, 21, 33, 43	0
1	D	243/243 (100%)	-0.25	0 100 100	13, 21, 38, 57	0
1	E	243/243 (100%)	-0.34	1 (0%) 92 92	14, 21, 33, 42	0
1	F	243/243 (100%)	-0.21	3 (1%) 79 79	13, 22, 41, 52	0
1	G	243/243 (100%)	-0.23	1 (0%) 92 92	15, 21, 33, 41	0
1	H	243/243 (100%)	-0.21	0 100 100	14, 21, 33, 44	0
All	All	1944/1944 (100%)	-0.28	9 (0%) 91 91	13, 21, 35, 57	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	190	ASP	3.4
1	F	189	SER	3.1
1	G	143	TYR	2.6
1	A	143	TYR	2.4
1	F	188	THR	2.2
1	B	42	GLN	2.2
1	E	143	TYR	2.1
1	C	143	TYR	2.0
1	B	71	GLU	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 monosaccharides 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	CL	C	301	1/1	0.98	0.09	29,29,29,29	0
2	CL	B	301	1/1	0.99	0.05	22,22,22,22	0
2	CL	A	301	1/1	0.99	0.03	28,28,28,28	0
2	CL	E	301	1/1	0.99	0.03	26,26,26,26	0
2	CL	G	301	1/1	0.99	0.04	24,24,24,24	0
2	CL	F	301	1/1	1.00	0.06	22,22,22,22	0
2	CL	D	301	1/1	1.00	0.06	23,23,23,23	0
2	CL	H	301	1/1	1.00	0.04	19,19,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.