



# Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 02:49 PM GMT

PDB ID : 3AQO  
Title : Structure and function of a membrane component SecDF that enhances protein export  
Authors : Echizen, Y.; Tsukazaki, T.; Ishitani, R.; Nureki, O.  
Deposited on : 2010-11-16  
Resolution : 2.60 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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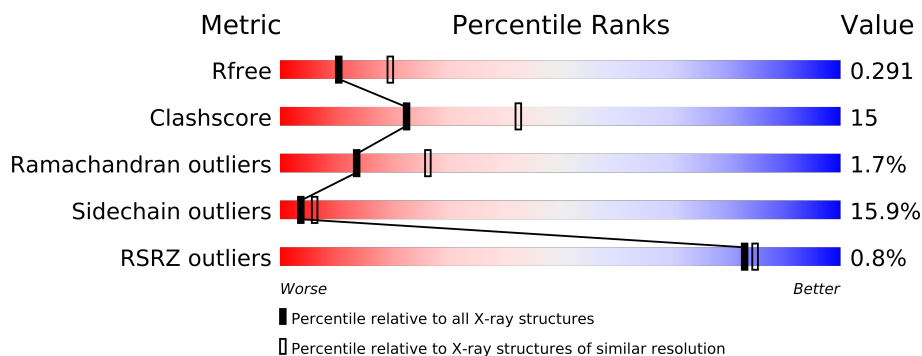
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.60 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))
$R_{free}$	66092	1718 (2.60-2.60)
Clashscore	79885	2154 (2.60-2.60)
Ramachandran outliers	78287	2113 (2.60-2.60)
Sidechain outliers	78261	2113 (2.60-2.60)
RSRZ outliers	66119	1718 (2.60-2.60)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	229	
1	B	229	
1	C	229	
1	D	229	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6860 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Probable SecDF protein-export membrane protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	221	Total	C	N	O	0	0	0
			1691	1062	305	324			
1	B	220	Total	C	N	O	0	0	0
			1687	1060	304	323			
1	C	222	Total	C	N	O	0	0	0
			1695	1064	306	325			
1	D	221	Total	C	N	O	0	0	0
			1691	1062	305	324			

- Molecule 2 is water.

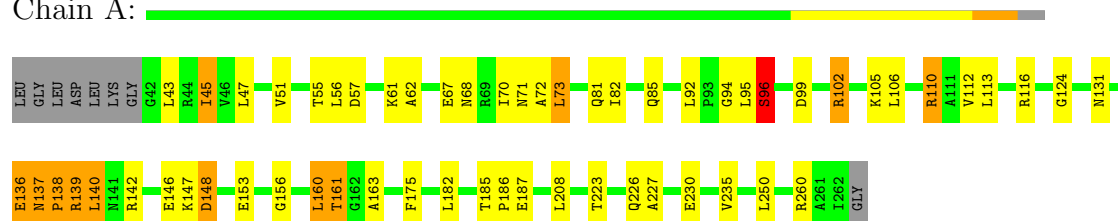
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	31	Total	O	0	0
			31	31		
2	B	34	Total	O	0	0
			34	34		
2	C	17	Total	O	0	0
			17	17		
2	D	14	Total	O	0	0
			14	14		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

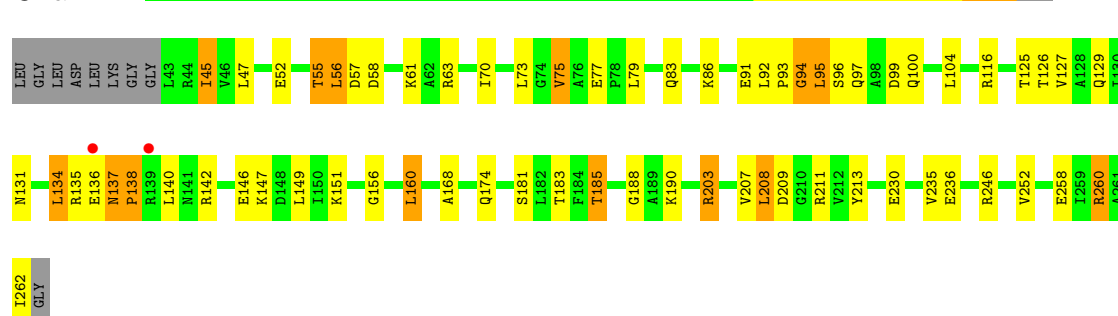
- Molecule 1: Probable SecDF protein-export membrane protein

Chain A:



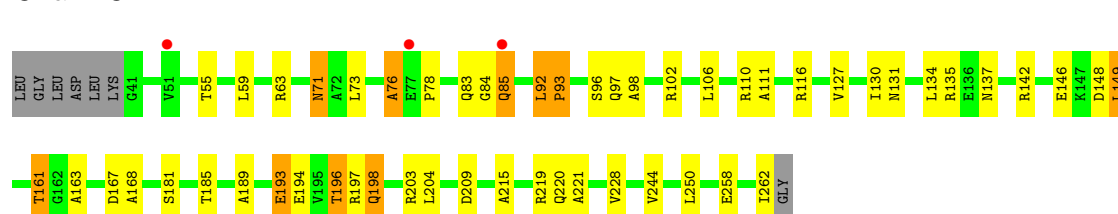
- Molecule 1: Probable SecDF protein-export membrane protein

Chain B:



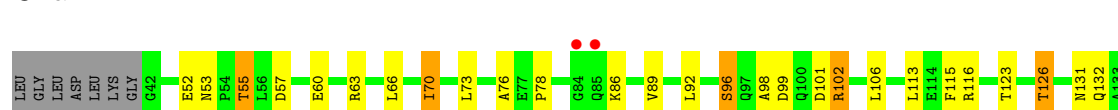
- Molecule 1: Probable SecDF protein-export membrane protein

Chain C:



- Molecule 1: Probable SecDF protein-export membrane protein

Chain D:



L134	R142	L149	A168	D173	T183	F184	T185	A189	E193	T196	R197	Q198	N199	I200	G201	K202	R203	L204	A205	I206	V207	Y213	T214	A215	R219	Q220	T223	V228	L232	V235	V244	L245	R246	I262	GLY
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## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	161.04Å 35.83Å 181.55Å 90.00° 113.68° 90.00°	Depositor
Resolution (Å)	36.86 – 2.60 36.87 – 2.60	Depositor EDS
% Data completeness (in resolution range)	86.8 (36.86-2.60) 86.7 (36.87-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.20 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, $R_{free}$	0.223 , 0.288 0.229 , 0.291	Depositor DCC
$R_{free}$ test set	1341 reflections (5.41%)	DCC
Wilson B-factor (Å <sup>2</sup> )	33.0	Xtriage
Anisotropy	0.164	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 19.7	EDS
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	7 of 26134 reflections (0.027%)	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6860	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 50.70 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 6.2280e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

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	0/1708	0.69	1/2314 (0.0%)
1	B	0.51	0/1704	0.70	1/2309 (0.0%)
1	C	0.45	0/1712	0.64	0/2319
1	D	0.45	0/1708	0.62	0/2314
All	All	0.49	0/6832	0.66	2/9256 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	160	LEU	CA-CB-CG	6.67	130.64	115.30
1	A	160	LEU	CA-CB-CG	5.27	127.43	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1691	0	0	25	1
1	B	1687	0	0	32	0
1	C	1695	0	0	19	0
1	D	1691	0	0	24	0
2	A	31	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	34	0	0	4	0
2	C	17	0	0	0	0
2	D	14	0	0	1	0
All	All	6860	0	0	100	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 15.

All (100) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:136:GLU:O	1:A:138:PRO:CD	1.79	1.29
1:D:70:ILE:CD1	1:D:78:PRO:CB	2.31	1.08
1:D:183:THR:CG2	2:D:272:HOH:O	2.22	0.86
1:B:131:ASN:ND2	2:B:277:HOH:O	2.15	0.78
1:D:131:ASN:ND2	1:D:142:ARG:NH2	2.32	0.78
1:C:167:ASP:OD2	1:C:168:ALA:N	2.17	0.78
1:A:131:ASN:OD1	1:A:142:ARG:NH2	2.18	0.76
1:C:193:GLU:OE1	1:C:197:ARG:NH2	2.19	0.74
1:D:55:THR:CG2	1:D:57:ASP:N	2.54	0.71
1:B:258:GLU:OE2	1:B:260:ARG:NH1	2.24	0.70
1:A:136:GLU:C	1:A:138:PRO:CD	2.60	0.69
1:A:138:PRO:O	1:A:139:ARG:CB	2.41	0.68
1:A:70:ILE:O	1:A:73:LEU:CD2	2.43	0.67
1:B:131:ASN:OD1	1:B:142:ARG:NH2	2.29	0.66
1:B:55:THR:CG2	1:B:58:ASP:CG	2.64	0.66
1:A:137:ASN:O	1:A:138:PRO:O	2.14	0.65
1:A:110:ARG:NH1	1:A:110:ARG:CG	2.59	0.65
1:C:59:LEU:CD1	1:C:85:GLN:O	2.46	0.64
1:B:137:ASN:O	1:B:138:PRO:O	2.15	0.64
1:C:131:ASN:ND2	1:C:142:ARG:NH2	2.45	0.64
1:B:174:GLN:CG	2:B:32:HOH:O	2.49	0.61
1:B:203:ARG:N	2:B:264:HOH:O	2.33	0.61
1:A:161:THR:CG2	1:A:163:ALA:N	2.65	0.59
1:B:70:ILE:CG2	1:B:75:VAL:CG1	2.81	0.58
1:A:110:ARG:N	2:A:273:HOH:O	2.37	0.58
1:B:77:GLU:CG	1:B:77:GLU:O	2.51	0.58
1:C:185:THR:O	1:C:189:ALA:N	2.38	0.57
1:B:262:ILE:CG2	1:B:262:ILE:O	2.53	0.56
1:A:185:THR:CG2	1:A:186:PRO:CD	2.84	0.55
1:C:161:THR:CG2	1:C:163:ALA:N	2.69	0.55
1:C:96:SER:O	1:C:97:GLN:C	2.46	0.54
1:A:185:THR:CG2	1:A:187:GLU:N	2.70	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:125:THR:CG2	1:B:126:THR:N	2.72	0.52
1:C:106:LEU:CD1	1:C:244:VAL:CG1	2.87	0.52
1:A:99:ASP:O	1:A:102:ARG:N	2.43	0.52
1:D:102:ARG:CB	1:D:102:ARG:NH1	2.72	0.52
1:C:110:ARG:NE	1:C:250:LEU:O	2.43	0.52
1:C:76:ALA:O	1:C:78:PRO:CD	2.58	0.51
1:A:110:ARG:NH1	1:A:250:LEU:O	2.43	0.51
1:D:199:ASN:O	1:D:200:ILE:C	2.49	0.51
1:D:70:ILE:CD1	1:D:78:PRO:CG	2.89	0.51
1:D:203:ARG:CD	1:D:215:ALA:O	2.58	0.51
1:D:196:THR:CG2	1:D:197:ARG:N	2.73	0.51
1:A:81:GLN:NE2	1:A:82:ILE:N	2.59	0.50
1:B:125:THR:CG2	1:B:129:GLN:CB	2.88	0.50
1:D:193:GLU:OE2	1:D:197:ARG:NH2	2.45	0.50
1:C:203:ARG:CD	1:C:215:ALA:O	2.60	0.49
1:B:116:ARG:NH1	1:B:156:GLY:O	2.46	0.49
1:B:45:ILE:CD1	1:B:47:LEU:CD2	2.90	0.49
1:B:97:GLN:CA	1:B:97:GLN:OE1	2.59	0.49
1:A:185:THR:CG2	1:A:186:PRO:N	2.76	0.49
1:C:130:ILE:CD1	1:C:149:LEU:CD1	2.91	0.48
1:D:106:LEU:CD1	1:D:244:VAL:CG1	2.92	0.48
1:B:55:THR:CG2	1:B:58:ASP:OD2	2.63	0.47
1:B:79:LEU:CD2	1:B:91:GLU:OE2	2.63	0.47
1:D:168:ALA:O	1:D:246:ARG:NH1	2.48	0.47
1:B:185:THR:CG2	1:B:188:GLY:N	2.78	0.47
1:B:146:GLU:OE1	1:B:211:ARG:NH1	2.48	0.47
1:B:136:GLU:O	1:B:138:PRO:CD	2.63	0.47
1:C:96:SER:O	1:C:98:ALA:N	2.48	0.46
1:D:185:THR:O	1:D:189:ALA:N	2.49	0.46
1:B:93:PRO:O	1:B:95:LEU:CD2	2.63	0.46
1:D:232:LEU:N	1:D:232:LEU:CD2	2.78	0.46
1:D:76:ALA:C	1:D:78:PRO:CD	2.85	0.45
1:B:174:GLN:N	2:B:32:HOH:O	2.50	0.45
1:B:134:LEU:O	1:B:138:PRO:CD	2.64	0.45
1:D:126:THR:CG2	1:D:213:TYR:O	2.65	0.45
1:A:146:GLU:O	1:A:148:ASP:N	2.50	0.45
1:D:96:SER:C	1:D:98:ALA:N	2.70	0.45
1:A:45:ILE:O	1:A:45:ILE:CG2	2.65	0.45
1:B:137:ASN:OD1	1:B:137:ASN:N	2.49	0.45
1:B:93:PRO:O	1:B:94:GLY:C	2.55	0.45
1:B:147:LYS:O	1:B:151:LYS:NZ	2.50	0.45
1:D:116:ARG:O	1:D:205:ALA:N	2.50	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:111:ALA:N	1:C:209:ASP:OD2	2.51	0.44
1:A:116:ARG:NH1	1:A:156:GLY:O	2.51	0.44
1:D:173:ASP:C	1:D:173:ASP:OD1	2.56	0.44
1:B:55:THR:OG1	1:B:56:LEU:N	2.51	0.43
1:A:124:GLY:CA	2:A:282:HOH:O	2.66	0.43
1:B:168:ALA:O	1:B:246:ARG:NH1	2.52	0.43
1:C:194:GLU:OE1	1:C:198:GLN:NE2	2.51	0.43
1:B:127:VAL:CG2	1:B:213:TYR:CE1	3.01	0.43
1:C:92:LEU:O	1:C:93:PRO:O	2.36	0.43
1:A:153:GLU:OE1	1:A:153:GLU:N	2.52	0.43
1:C:71:ASN:ND2	1:C:76:ALA:O	2.52	0.43
1:B:61:LYS:N	1:B:61:LYS:CD	2.81	0.42
1:D:96:SER:O	1:D:98:ALA:N	2.53	0.42
1:A:68:ASN:O	1:A:72:ALA:N	2.53	0.42
1:D:55:THR:CG2	1:D:57:ASP:CB	2.98	0.42
1:D:199:ASN:N	1:D:199:ASN:ND2	2.68	0.41
1:D:66:LEU:O	1:D:70:ILE:CG2	2.68	0.41
1:B:99:ASP:O	1:B:100:GLN:C	2.59	0.41
1:D:113:LEU:CD1	1:D:115:PHE:CE1	3.04	0.41
1:A:182:LEU:N	1:A:227:ALA:O	2.54	0.41
1:C:196:THR:CG2	1:C:221:ALA:CA	2.99	0.41
1:A:45:ILE:CD1	1:A:47:LEU:CD2	2.99	0.41
1:A:95:LEU:O	1:A:96:SER:C	2.59	0.41
1:A:61:LYS:O	1:A:62:ALA:C	2.60	0.40
1:C:142:ARG:O	1:C:146:GLU:CG	2.70	0.40
1:B:208:LEU:O	1:B:209:ASP:C	2.59	0.40

All (1) 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	Distance(Å)	Clash(Å)
1:A:139:ARG:NH2	1:A:140:LEU:O[2_555]	1.65	0.55

## 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	219/229 (96%)	199 (91%)	14 (6%)	6 (3%)	8	13
1	B	218/229 (95%)	196 (90%)	19 (9%)	3 (1%)	16	32
1	C	220/229 (96%)	203 (92%)	12 (6%)	5 (2%)	10	17
1	D	219/229 (96%)	208 (95%)	10 (5%)	1 (0%)	38	67
All	All	876/916 (96%)	806 (92%)	55 (6%)	15 (2%)	14	26

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	137	ASN
1	A	138	PRO
1	B	138	PRO
1	C	76	ALA
1	C	93	PRO
1	D	52	GLU
1	A	94	GLY
1	A	96	SER
1	A	136	GLU
1	B	94	GLY
1	B	135	ARG
1	A	147	LYS
1	C	84	GLY
1	C	85	GLN
1	C	220	GLN

### 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	181/186 (97%)	151 (83%)	30 (17%)	3	5
1	B	181/186 (97%)	150 (83%)	31 (17%)	3	5
1	C	181/186 (97%)	157 (87%)	24 (13%)	6	10
1	D	181/186 (97%)	151 (83%)	30 (17%)	3	5
All	All	724/744 (97%)	609 (84%)	115 (16%)	4	6

All (115) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	LEU
1	A	45	ILE
1	A	51	VAL
1	A	55	THR
1	A	56	LEU
1	A	57	ASP
1	A	67	GLU
1	A	71	ASN
1	A	73	LEU
1	A	85	GLN
1	A	92	LEU
1	A	96	SER
1	A	102	ARG
1	A	105	LYS
1	A	106	LEU
1	A	110	ARG
1	A	112	VAL
1	A	113	LEU
1	A	139	ARG
1	A	140	LEU
1	A	148	ASP
1	A	160	LEU
1	A	161	THR
1	A	175	PHE
1	A	208	LEU
1	A	223	THR
1	A	226	GLN
1	A	230	GLU
1	A	235	VAL
1	A	260	ARG
1	B	45	ILE
1	B	52	GLU
1	B	55	THR
1	B	56	LEU
1	B	57	ASP
1	B	63	ARG
1	B	73	LEU
1	B	75	VAL
1	B	83	GLN
1	B	86	LYS
1	B	92	LEU
1	B	95	LEU

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Mol	Chain	Res	Type
1	B	96	SER
1	B	104	LEU
1	B	134	LEU
1	B	137	ASN
1	B	140	LEU
1	B	149	LEU
1	B	160	LEU
1	B	181	SER
1	B	183	THR
1	B	185	THR
1	B	190	LYS
1	B	203	ARG
1	B	207	VAL
1	B	208	LEU
1	B	230	GLU
1	B	235	VAL
1	B	236	GLU
1	B	252	VAL
1	B	260	ARG
1	C	55	THR
1	C	63	ARG
1	C	71	ASN
1	C	73	LEU
1	C	83	GLN
1	C	92	LEU
1	C	102	ARG
1	C	116	ARG
1	C	127	VAL
1	C	134	LEU
1	C	135	ARG
1	C	137	ASN
1	C	148	ASP
1	C	149	LEU
1	C	161	THR
1	C	181	SER
1	C	193	GLU
1	C	196	THR
1	C	198	GLN
1	C	204	LEU
1	C	219	ARG
1	C	228	VAL
1	C	258	GLU

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Mol	Chain	Res	Type
1	C	262	ILE
1	D	53	ASN
1	D	55	THR
1	D	60	GLU
1	D	63	ARG
1	D	70	ILE
1	D	73	LEU
1	D	86	LYS
1	D	89	VAL
1	D	92	LEU
1	D	96	SER
1	D	99	ASP
1	D	101	ASP
1	D	102	ARG
1	D	123	THR
1	D	126	THR
1	D	132	GLN
1	D	134	LEU
1	D	149	LEU
1	D	183	THR
1	D	193	GLU
1	D	196	THR
1	D	202	LYS
1	D	204	LEU
1	D	207	VAL
1	D	219	ARG
1	D	220	GLN
1	D	223	THR
1	D	228	VAL
1	D	235	VAL
1	D	262	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

There are no ligands in this entry.

## 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 ⓘ

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	221/229 (96%)	-0.32	0 100 100	13, 29, 69, 81	0
1	B	220/229 (96%)	-0.37	2 (0%) 81 82	13, 28, 65, 77	0
1	C	222/229 (96%)	-0.07	3 (1%) 72 72	21, 42, 74, 94	0
1	D	221/229 (96%)	-0.16	2 (0%) 81 82	21, 42, 65, 85	0
All	All	884/916 (96%)	-0.23	7 (0%) 83 85	13, 38, 69, 94	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	85	GLN	4.4
1	C	51	VAL	3.7
1	C	85	GLN	3.5
1	C	77	GLU	2.6
1	B	139	ARG	2.3
1	D	84	GLY	2.3
1	B	136	GLU	2.0

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

There are no ligands in this entry.



## 6.5 Other polymers ⓘ

There are no such residues in this entry.