



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 23, 2017 – 01:54 PM EST

PDB ID : 5FQ8
Title : Crystal structure of the SusCD complex BT2261-2264 from Bacteroides thetaiotaomicron
Authors : Glenwright, A.J.; Pothula, K.R.; Chorev, D.S.; Basle, A.; Robinson, C.V.; Kleinekathoefer, U.; Bolam, D.N.; van den Berg, B.
Deposited on : 2015-12-07
Resolution : 2.75 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20028442

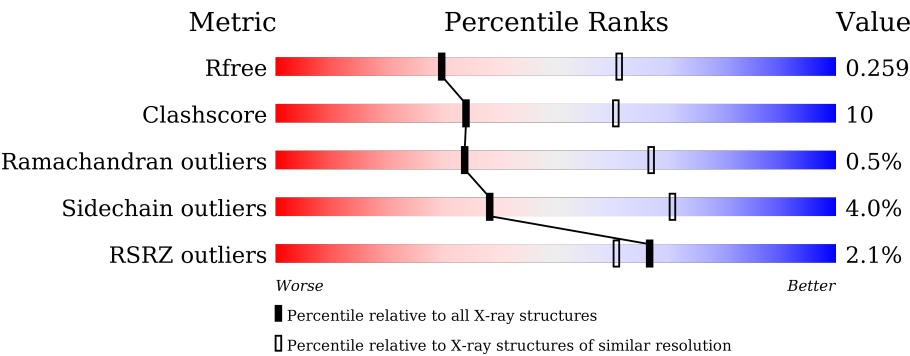
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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.



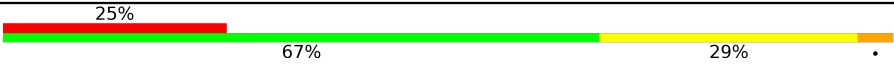


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3340 (2.80-2.72)
Clashscore	102246	3829 (2.80-2.72)
Ramachandran outliers	100387	3767 (2.80-2.72)
Sidechain outliers	100360	3770 (2.80-2.72)
RSRZ outliers	91569	3352 (2.80-2.72)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	480	<div><div></div><div>78%21%.</div></div>
1	C	480	<div><div>%</div><div>77%21%.</div></div>
2	B	984	<div><div></div><div>71%24%. .</div></div>
2	D	984	<div><div>%</div><div>70%24%. .</div></div>
3	E	148	<div><div></div><div>79%19%. .</div></div>
3	F	148	<div><div>%</div><div>85%14%. .</div></div>

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Mol	Chain	Length	Quality of chain
4	G	212	
5	P	10	
6	Q	9	

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
10	C8E	B	1989	-	-	-	X
10	C8E	D	1991	-	-	-	X
8	KR0	B	1985	-	-	-	X
8	KR0	D	1985	-	-	-	X
9	CA	B	1987	-	-	-	X
9	CA	D	1987	-	-	-	X

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 27220 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 PUTATIVE LIPOPROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	480	Total	C	N	O	S	0	1	0
			3749	2373	616	743	17			
1	C	479	Total	C	N	O	S	0	0	0
			3734	2364	614	739	17			

- Molecule 2 is a protein called OUTER MEMBRANE PROTEIN OMP121.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	945	Total	C	N	O	S	0	0	0
			7373	4666	1230	1447	30			
2	D	941	Total	C	N	O	S	0	0	0
			7341	4646	1224	1441	30			

- Molecule 3 is a protein called UNCHARACTERIZED PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	145	Total	C	N	O	S	0	0	0
			1134	717	178	234	5			
3	F	146	Total	C	N	O	S	0	0	0
			1142	721	180	236	5			

- Molecule 4 is a protein called BT_2262 (UNCHARACTERISED LIPOPROTEIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	212	Total	C	N	O	S	0	0	0
			1646	1052	253	335	6			

- Molecule 5 is a protein called UNCHARACTERISED PROTEIN, BOUND PEPTIDE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	P	10	Total	C	N	O	0	0	0
			40	20	10	10			

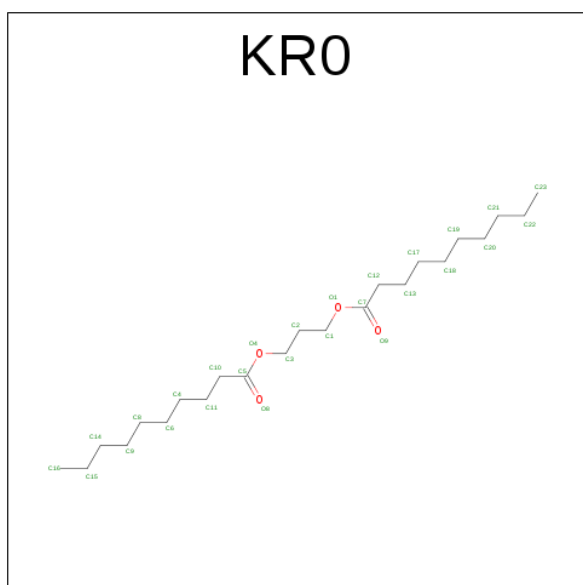
- Molecule 6 is a protein called UNCHARACTERISED PROTEIN, BOUND PEPTIDE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	Q	9	Total	C	N	O	0	0	0
			36	18	9	9			

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Mg	0	0
			1	1		
7	A	1	Total	Mg	0	0
			1	1		
7	D	1	Total	Mg	0	0
			1	1		
7	C	1	Total	Mg	0	0
			1	1		

- Molecule 8 is 3-decanoyloxypropyl decanoate (three-letter code: KR0) (formula: C₂₃H₄₄O₄).

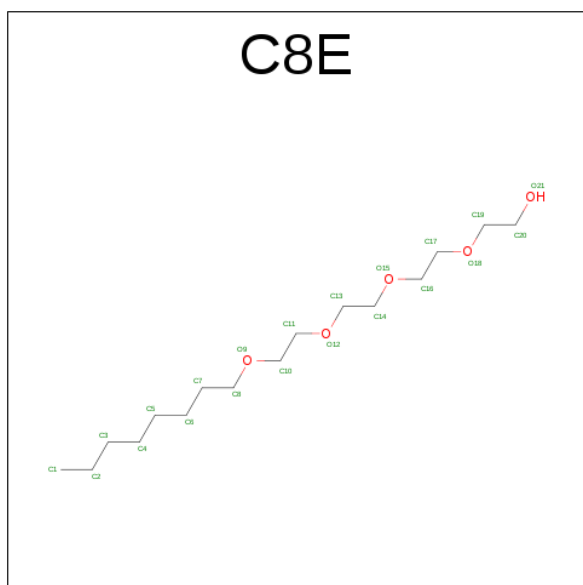


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			27	23	4		
8	D	1	Total	C	O	0	0
			27	23	4		

- Molecule 9 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	2	Total Ca 2 2	0	0
9	D	2	Total Ca 2 2	0	0

- Molecule 10 is (HYDROXYETHYLOXY)TRI(ETHYLOXY)OCTANE (three-letter code: C8E) (formula: C₁₆H₃₄O₅).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	B	1	Total C O 9 8 1	0	0
10	D	1	Total C O 9 6 3	0	0
10	D	1	Total C O 11 7 4	0	0
10	D	1	Total C 6 6	0	0

- Molecule 11 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	179	Total O 179 179	0	0
11	B	292	Total O 292 292	0	0
11	C	123	Total O 123 123	0	0

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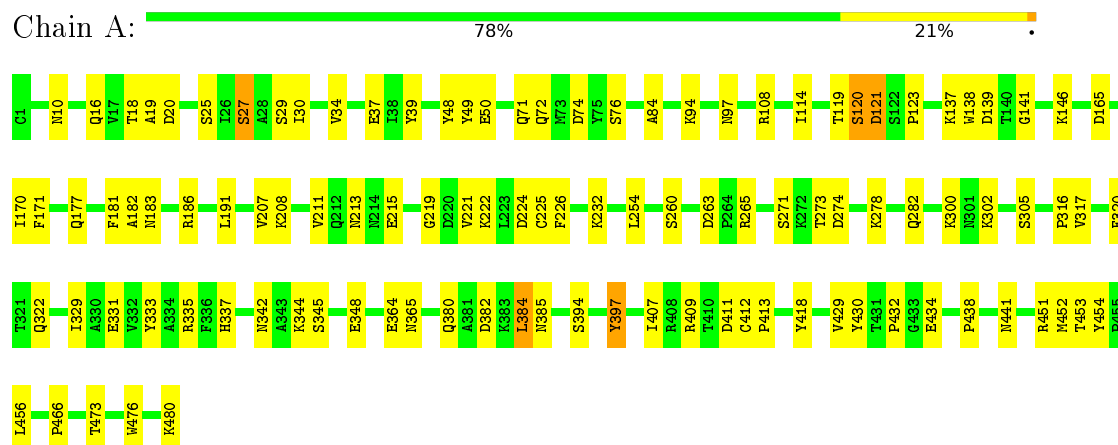
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	D	244	Total 244	O 244	0	0
11	E	41	Total 41	O 41	0	0
11	F	33	Total 33	O 33	0	0
11	G	15	Total 15	O 15	0	0
11	P	1	Total 1	O 1	0	0

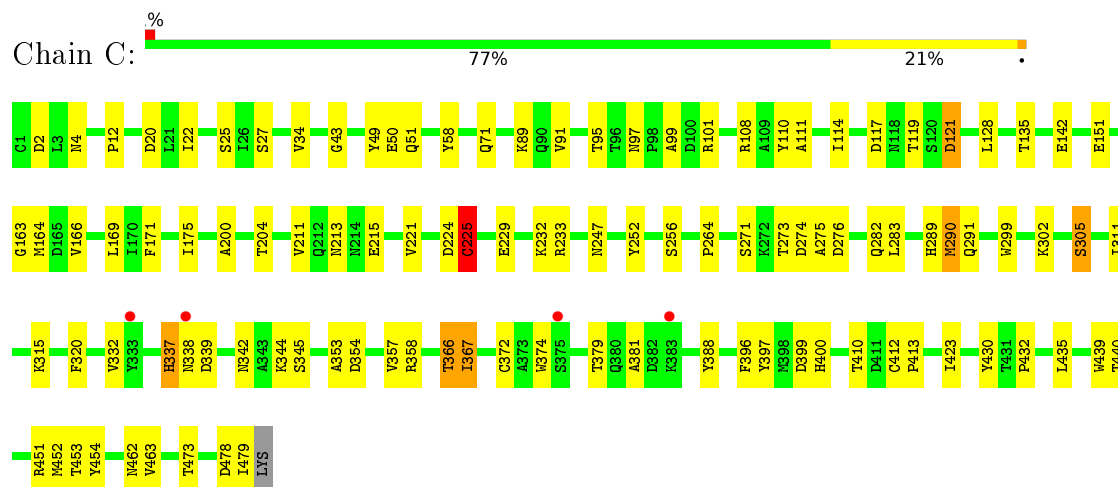
3 Residue-property plots

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 ($\text{RSRZ} > 2$). 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.

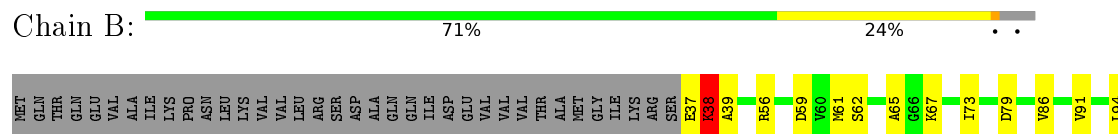
• Molecule 1: PUTATIVE LIPOPROTEIN

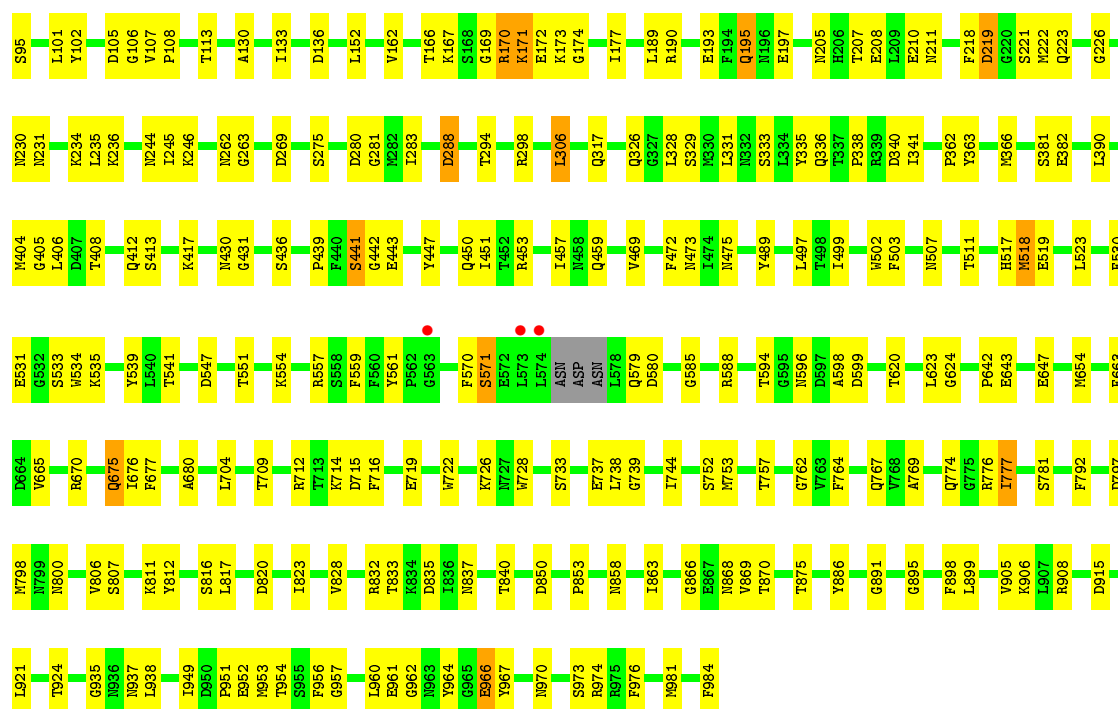


• Molecule 1: PUTATIVE LIPOPROTEIN

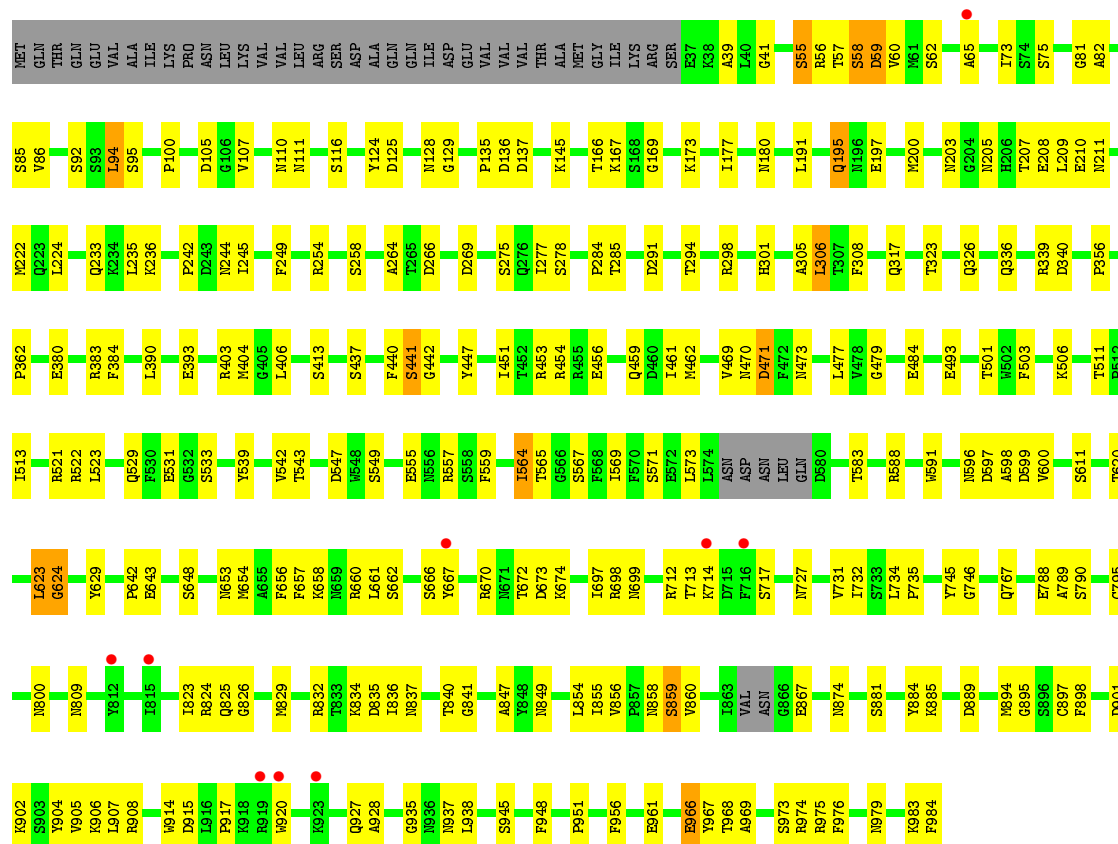


• Molecule 2: OUTER MEMBRANE PROTEIN OMP121






• Molecule 2: OUTER MEMBRANE PROTEIN OMP121




• Molecule 3: UNCHARACTERIZED PROTEIN

Chain E:  79% 19%



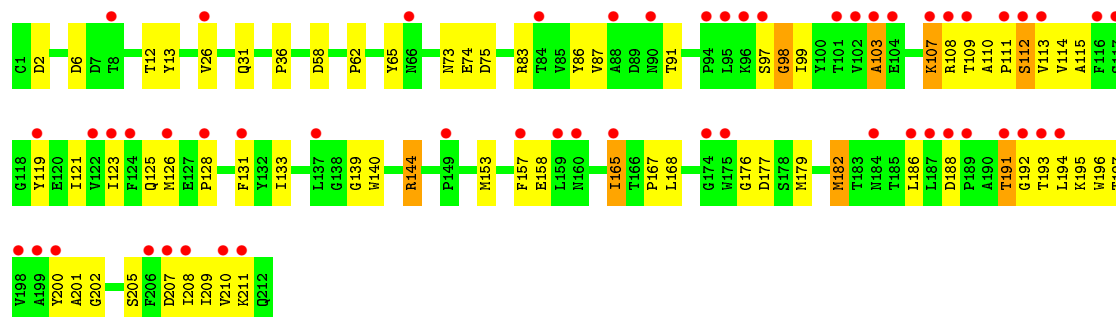
- Molecule 3: UNCHARACTERIZED PROTEIN

Chain F:  85% 14%



- Molecule 4: BT_2262 (UNCHARACTERISED LIPOPROTEIN)

Chain G:  25% 67% 29%




- Molecule 5: UNCHARACTERISED PROTEIN, BOUND PEPTIDE

Chain P:  10% 60% 40%



- Molecule 6: UNCHARACTERISED PROTEIN, BOUND PEPTIDE

Chain Q:  78% 22%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	92.11Å 122.74Å 122.83Å 111.41° 98.33° 98.51°	Depositor
Resolution (Å)	52.93 – 2.75 66.95 – 2.75	Depositor EDS
% Data completeness (in resolution range)	100.0 (52.93-2.75) 80.9 (66.95-2.75)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.94 (at 2.73Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.205 , 0.259 0.206 , 0.259	Depositor DCC
R_{free} test set	5812 reflections (4.97%)	DCC
Wilson B-factor (Å ²)	28.0	Xtriage
Anisotropy	0.681	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 37.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.016 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	27220	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% 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: MG, KR0, CA, C8E

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	0.58	0/3843	0.57	0/5231
1	C	0.53	1/3825 (0.0%)	0.54	0/5209
2	B	0.55	0/7550	0.61	2/10237 (0.0%)
2	D	0.55	1/7517 (0.0%)	0.61	2/10190 (0.0%)
3	E	0.54	0/1162	0.59	0/1578
3	F	0.48	0/1170	0.56	0/1589
4	G	0.38	0/1685	0.53	0/2293
5	P	0.54	0/39	0.92	0/47
6	Q	0.74	0/35	0.72	0/42
All	All	0.54	2/26826 (0.0%)	0.59	4/36416 (0.0%)

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
2	B	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	225	CYS	CB-SG	-5.91	1.72	1.81
2	D	795	CYS	CB-SG	-5.34	1.73	1.81

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	81	GLY	N-CA-C	-6.22	97.56	113.10
2	D	624	GLY	N-CA-C	-6.21	97.56	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	623	LEU	CA-CB-CG	6.00	129.10	115.30
2	B	624	GLY	N-CA-C	-5.57	99.17	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	38	LYS	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	3749	0	3565	69	0
1	C	3734	0	3548	68	0
2	B	7373	0	7059	157	0
2	D	7341	0	7024	159	0
3	E	1134	0	1050	16	0
3	F	1142	0	1056	11	0
4	G	1646	0	1565	51	0
5	P	40	0	32	2	0
6	Q	36	0	29	2	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	B	27	0	0	0	0
8	D	27	0	0	0	0
9	B	2	0	0	0	0
9	D	2	0	0	0	0
10	B	9	0	17	0	0
10	D	26	0	30	3	0
11	A	179	0	0	12	0
11	B	292	0	0	18	0
11	C	123	0	0	6	0
11	D	244	0	0	22	0
11	E	41	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	F	33	0	0	0	0
11	G	15	0	0	4	0
11	P	1	0	0	0	0
All	All	27220	0	24975	515	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 10.

The worst 5 of 515 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:D:800:ASN:HA	2:D:826:GLY:HA3	1.53	0.90
2:B:170:ARG:HB3	2:B:171:LYS:HA	1.55	0.87
2:B:833:THR:OG1	2:B:966:GLU:OE2	2.00	0.78
2:D:856:VAL:O	2:D:859:SER:OG	2.00	0.78
2:D:236:LYS:NZ	2:D:340:ASP:OD2	2.17	0.77

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	479/480 (100%)	448 (94%)	30 (6%)	1 (0%)	52	83
1	C	477/480 (99%)	442 (93%)	32 (7%)	3 (1%)	30	62
2	B	941/984 (96%)	886 (94%)	51 (5%)	4 (0%)	39	72
2	D	935/984 (95%)	870 (93%)	64 (7%)	1 (0%)	56	86
3	E	143/148 (97%)	137 (96%)	4 (3%)	2 (1%)	14	38
3	F	144/148 (97%)	138 (96%)	6 (4%)	0	100	100
4	G	210/212 (99%)	187 (89%)	20 (10%)	3 (1%)	14	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	P	8/10 (80%)	6 (75%)	0	2 (25%)	0	0
6	Q	7/9 (78%)	7 (100%)	0	0	100	100
All	All	3344/3455 (97%)	3121 (93%)	207 (6%)	16 (0%)	34	67

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	38	LYS
4	G	201	ALA
1	A	120	SER
3	E	92	GLU
5	P	2	GLY

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	393/392 (100%)	376 (96%)	17 (4%)	35	68
1	C	391/392 (100%)	376 (96%)	15 (4%)	40	73
2	B	800/836 (96%)	775 (97%)	25 (3%)	47	79
2	D	796/836 (95%)	761 (96%)	35 (4%)	35	67
3	E	121/124 (98%)	119 (98%)	2 (2%)	68	90
3	F	122/124 (98%)	118 (97%)	4 (3%)	45	77
4	G	176/177 (99%)	163 (93%)	13 (7%)	17	40
All	All	2799/2881 (97%)	2688 (96%)	111 (4%)	38	71

5 of 111 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	305	SER
2	D	94	LEU
4	G	107	LYS
1	C	320	PHE

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Mol	Chain	Res	Type
1	C	463	VAL

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

Mol	Chain	Res	Type
1	A	461	GLN
2	B	464	ASN
2	B	475	ASN
1	C	51	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 8 are monoatomic - leaving 6 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	$\# Z > 2$
8	KR0	B	1985	1	26,26,26	1.22	2 (7%)	27,27,27	1.24	3 (11%)
10	C8E	B	1989	-	8,8,20	0.27	0	7,7,19	0.43	0
8	KR0	D	1985	1,2	26,26,26	1.23	2 (7%)	27,27,27	1.27	5 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	C8E	D	1989	-	8,8,20	0.42	0	7,7,19	0.45	0
10	C8E	D	1990	-	9,9,20	0.41	0	7,7,19	0.58	0
10	C8E	D	1991	-	5,5,20	0.22	0	4,4,19	0.46	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	KR0	B	1985	1	-	0/26/26/26	0/0/0/0
10	C8E	B	1989	-	-	0/6/6/18	0/0/0/0
8	KR0	D	1985	1,2	-	0/26/26/26	0/0/0/0
10	C8E	D	1989	-	-	0/6/6/18	0/0/0/0
10	C8E	D	1990	-	-	0/5/5/18	0/0/0/0
10	C8E	D	1991	-	-	0/3/3/18	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	D	1985	KR0	O1-C7	4.12	1.45	1.33
8	B	1985	KR0	O4-C5	4.21	1.45	1.33
8	B	1985	KR0	O1-C7	4.21	1.45	1.33
8	D	1985	KR0	O4-C5	4.29	1.46	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	1985	KR0	O4-C5-O8	-2.27	117.56	123.51
8	D	1985	KR0	O4-C5-O8	-2.23	117.66	123.51
8	D	1985	KR0	O4-C3-C2	2.01	114.71	108.58
8	D	1985	KR0	C1-O1-C7	2.37	124.20	117.04
8	D	1985	KR0	O1-C7-C12	2.79	120.42	111.85

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	D	1990	C8E	3	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](#)

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	480/480 (100%)	-0.34	0 100 100	22, 29, 41, 60	0
1	C	479/480 (99%)	-0.07	4 (0%) 87 83	25, 39, 61, 81	0
2	B	945/984 (96%)	-0.17	3 (0%) 94 93	22, 31, 48, 86	0
2	D	941/984 (95%)	-0.09	9 (0%) 84 80	26, 34, 54, 85	0
3	E	145/148 (97%)	-0.17	0 100 100	29, 35, 49, 58	0
3	F	146/148 (98%)	0.08	1 (0%) 89 86	27, 40, 61, 88	0
4	G	212/212 (100%)	1.30	54 (25%) 1 0	32, 74, 115, 130	0
5	P	10/10 (100%)	0.67	1 (10%) 9 6	28, 29, 50, 67	0
6	Q	9/9 (100%)	0.52	0 100 100	26, 27, 31, 34	0
All	All	3367/3455 (97%)	-0.05	72 (2%) 67 61	22, 34, 66, 130	0

The worst 5 of 72 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	G	111	PRO	7.8
4	G	191	THR	4.9
4	G	192	GLY	4.7
4	G	95	LEU	4.6
4	G	187	LEU	4.6

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
9	CA	B	1987	1/1	0.86	0.45	8.83	107,107,107,107	0
10	C8E	B	1989	9/21	0.92	0.27	6.84	19,26,27,29	0
10	C8E	D	1991	6/21	0.91	0.47	6.04	18,21,24,25	0
8	KR0	D	1985	27/27	0.89	0.26	3.66	37,43,54,74	0
9	CA	D	1987	1/1	0.65	0.22	3.43	67,67,67,67	0
8	KR0	B	1985	27/27	0.88	0.25	2.08	41,46,54,57	0
10	C8E	D	1989	9/21	0.90	0.22	1.30	23,38,41,42	0
10	C8E	D	1990	11/21	0.88	0.20	0.33	26,31,36,37	0
7	MG	D	1986	1/1	0.91	0.16	0.07	10,10,10,10	0
9	CA	D	1988	1/1	0.95	0.10	-1.27	35,35,35,35	0
9	CA	B	1988	1/1	0.78	0.10	-1.45	46,46,46,46	0
7	MG	B	1986	1/1	0.96	0.09	-2.06	13,13,13,13	0
7	MG	A	1481	1/1	0.88	0.09	-2.49	23,23,23,23	0
7	MG	C	1480	1/1	0.92	0.05	-5.48	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.